

SEQUENCE LISTING

<110> Tang, Y. Tom
 Zhou, Ping
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 Zhang, Jie
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 Yang, Yonghong
 Wehrman, Tom
 Drmanac, Radoje T.

<120> Novel Nucleic Acids and
 Polypeptides

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gga gtg atg gat ggc gtt ccc tcg gct aat aac tat cag ggt gga ttt 930																
Gly	Val	Met	Asp	Gly	Val	Pro	Ser	Ala	Asn	Asn	Tyr	Gln	Gly	Gly	Phe	
			265					270					275			
gga aca aca ctc atg gct aag gat ctg gga ttg gca caa gac tct gct 978																
Gly	Thr	Thr	Leu	Met	Ala	Lys	Asp	Leu	Gly	Leu	Ala	Gln	Asp	Ser	Ala	
		280					285					290				
acc agc aca aag agc cca atc ctt ctt ggc agt ctg gcc cat cag atc 1026																
Thr	Ser	Thr	Lys	Ser	Pro	Ile	Leu	Leu	Gly	Ser	Leu	Ala	His	Gln	Ile	

295	300	305	
tac agg atg atg tgt gca aag ggc tac tca aag	aaa gac ttc tca tcc	1074	
Tyr Arg Met Met Cys Ala Lys Gly Tyr Ser Lys	Lys Asp Phe Ser Ser		
310	315 320 325		
gtg ttc cag ttc cta cga gag gag gag acc ttc	tga gtgt gccctttggc	1124	
Val Phe Gln Phe Leu Arg Glu Glu Glu Thr Phe	*		
330	335		
cacggacact gttgggaacc aaactctgtc ttggagcctc	cttttagctc actccacaag	1184	
taaatggatt taatcaaagg tcacctatct gcttttgatt	gtctaggtca cagtaatccc	1244	
taggattttt caccgcttat tctttttgtc tttttaacaa	acatattatc cgaatttttt	1304	
ttctgcaagc cactgatagt ctctgctaac tagcttaatt	gaccttttta caaagtttga	1364	
tccccaagca tcctcaacta aatcattgaa tacttcaatc	aggatattat ctgctttact	1424	
ttacaaataa aaccaaactc tttgtcaaca ggatgaaacc	catcttaaag gaaagaaaag	1484	
gaattggtgt gaagagagaa gttagagaag ggaaatgcag	tgaattacta tctgtgtcca	1544	
tcaggaagtt tgtcctgtta accaaatggt tactgcacta	ccagggttac tggttttatt	1604	
tccagggagc tgataaagca ggagaactgt tgctgcatgt	tttctatttg gactccgtca	1664	
caatatggtg ggatatccct caccaactcc cgacactcag	cagacttggt tttatatatt	1724	
tttctttctt gttcattctt actacgtatt ttttgactta	agaatgacat ctttagatgc	1784	
atttcagagc caatgatgat atttgcttta gataattatt	atattattat aaatatagcc	1844	
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Lys Asn Ile Lys Ala Leu Val Ala Phe His Ser Thr Ala Leu Asp Lys	
5 10 15	

gaa att aca tca gca aat tat gct ggt gtc tgt aca tca tct gtg att	153
Glu Ile Thr Ser Ala Asn Tyr Ala Gly Val Cys Thr Ser Ser Val Ile	
20 25 30	
aaa gaa gaa aac att gat caa cca gga tac tgt tat ctc tca cct gat	201
Lys Glu Glu Asn Ile Asp Gln Pro Gly Tyr Cys Tyr Leu Ser Pro Asp	
35 40 45	
gga aag aga aaa act atg ctc tgc ttg gct tgt gga caa tcc atg aga	249
Gly Lys Arg Lys Thr Met Leu Cys Leu Ala Cys Gly Gln Ser Met Arg	
50 55 60 65	
aca gag aaa gga ctg aaa caa ttg ctt cca ggg gtt cca ttc ctc tgt	297
Thr Glu Lys Gly Leu Lys Gln Leu Leu Pro Gly Val Pro Phe Leu Cys	
70 75 80	
att tca ggc acc aag act cag aag ccc ttc tta caa ggg ccc ttc aag	345
Ile Ser Gly Thr Lys Thr Gln Lys Pro Phe Leu Gln Gly Pro Phe Lys	
85 90 95	
gtc atc agt gtg gct gag gtt gat ttg tgc tgt gac aag gct gaa aaa	393
Val Ile Ser Val Ala Glu Val Asp Leu Ser Cys Asp Lys Ala Glu Lys	
100 105 110	
act cta agt tac tac caa gca cgt cta ttg tct tta cgg atg aag acc	441
Thr Leu Ser Tyr Tyr Gln Ala Arg Leu Leu Ser Leu Arg Met Lys Thr	
115 120 125	
tgc acg caa gct gca tct cac agt ggc atg gca gcc aca cac cag aag	489
Cys Thr Gln Ala Ala Ser His Ser Gly Met Ala Ala Thr His Gln Lys	
130 135 140 145	
gca gtg aaa ata att gca tac aaa aat ggg gat ggg tat cgt aat ggg	537
Ala Val Lys Ile Ile Ala Tyr Lys Asn Gly Asp Gly Tyr Arg Asn Gly	
150 155 160	
aag tta att gtg gct gga aca ttc ccc atg ctt ctt aca gaa tgc acg	585
Lys Leu Ile Val Ala Gly Thr Phe Pro Met Leu Leu Thr Glu Cys Thr	
165 170 175	
gaa caa ctt ggg ctt gcc aga gca gcc tcc aaa gta tat acc aaa gat	633
Glu Gln Leu Gly Leu Ala Arg Ala Ala Ser Lys Val Tyr Thr Lys Asp	
180 185 190	
gga acc cca atc ttt acc ttg cgt gat ttg gtt tta tgg gct cta gat	681
Gly Thr Pro Ile Phe Thr Leu Arg Asp Leu Val Leu Trp Ala Leu Asp	
195 200 205	
gaa tcc ttt ctc cag aga gac tct gag aaa caa aag caa gat gca gct	729
Glu Ser Phe Leu Gln Arg Asp Ser Glu Lys Gln Lys Gln Asp Ala Ala	
210 215 220 225	
cct gtt gga aaa gaa cag ata att gtt gaa agt atg gaa gaa aat cca	777
Pro Val Gly Lys Glu Gln Ile Ile Val Glu Ser Met Glu Glu Asn Pro	
230 235 240	
aga atg aaa gtg aaa aac aga tta ttt gca aaa tct gtg aca tcc gat	825

Arg Met Lys Val Lys Asn Arg Leu Phe Ala Lys Ser Val Thr Ser Asp	
245	250 255
agt ttg gat ggt ata gac aag tct ttg ctt acc ctc atc ctc aga aat	873
Ser Leu Asp Gly Ile Asp Lys Ser Leu Leu Thr Leu Ile Leu Arg Asn	
260	265 270
cct att gcc atc tgg gtg tct tgt ggt gaa cca ttt cta cct cca aat	921
Pro Ile Ala Ile Trp Val Ser Cys Gly Glu Pro Phe Leu Pro Pro Asn	
275	280 285
gct ttg cag aaa gca gaa aaa tta gag aaa cag aac tgg cta aaa aag	969
Ala Leu Gln Lys Ala Glu Lys Leu Glu Lys Gln Asn Trp Leu Lys Lys	
290	295 300 305
gac aga att ttg gct gat cta gat acc atg aga cac aaa atg aga cag	1017
Asp Arg Ile Leu Ala Asp Leu Asp Thr Met Arg His Lys Met Arg Gln	
310	315 320
tta aaa ggg cgg cga gta gcg gca tgt cag cca gcc acc atg gtt cct	1065
Leu Lys Gly Arg Arg Val Ala Ala Cys Gln Pro Ala Thr Met Val Pro	
325	330 335
acc aag agc cct gtg cag ccc gtg gtg gtt gaa gga ggc tgg acc gaa	1113
Thr Lys Ser Pro Val Gln Pro Val Val Val Glu Gly Gly Trp Thr Glu	
340	345 350
cag act caa cag gaa att aaa ctc atg gaa ctt ata aga cat aca gag	1161
Gln Thr Gln Gln Glu Ile Lys Leu Met Glu Leu Ile Arg His Thr Glu	
355	360 365
gca cac ctt tct gaa atc caa gaa atg gaa tcc aaa ata aat ttt cca	1209
Ala His Leu Ser Glu Ile Gln Glu Met Glu Ser Lys Ile Asn Phe Pro	
370	375 380 385
att gca acc aaa cgt ata gca gtc aag ccg agc aac ctg tat aag cag	1257
Ile Ala Thr Lys Arg Ile Ala Val Lys Pro Ser Asn Leu Tyr Lys Gln	
390	395 400
ccc aac aca aaa cga gtg tgg att tat cta aat gga ggc aga cct gaa	1305
Pro Asn Thr Lys Arg Val Trp Ile Tyr Leu Asn Gly Gly Arg Pro Glu	
405	410 415
gat ggc act tat gcc tgg ggc aaa act att tca gag ctg ctg caa gac	1353
Asp Gly Thr Tyr Ala Trp Gly Lys Thr Ile Ser Glu Leu Leu Gln Asp	
420	425 430
tgc tcc tct cgt ctc aaa atg acc cac cca gct aga gca ctg tac acc	1401
Cys Ser Ser Arg Leu Lys Met Thr His Pro Ala Arg Ala Leu Tyr Thr	
435	440 445
ccc agt gga gag cca att cag tcc tgg gac gac ata gag cga gat atg	1449
Pro Ser Gly Glu Pro Ile Gln Ser Trp Asp Asp Ile Glu Arg Asp Met	
450	455 460 465
gtc atc tgt gtg tct atg gga cat ggt ttc aaa acc cca aaa gag tta	1497
Val Ile Cys Val Ser Met Gly His Gly Phe Lys Thr Pro Lys Glu Leu	

470	475	480	
aaa caa ctg atg gag atc aga gca aat tat gcc aga atc cga agg cag			1545
Lys Gln Leu Met Glu Ile Arg Ala Asn Tyr Ala Arg Ile Arg Arg Gln			
485	490	495	
cag ggc cct caa gcc aca gac att gtg gtg tca cca tcc acg aag ctg			1593
Gln Gly Pro Gln Ala Thr Asp Ile Val Val Ser Pro Ser Thr Lys Leu			
500	505	510	
ctg tct ctg gca cat ctc cac aat taa ctctc atcagaacca tcggattttc			1645
Leu Ser Leu Ala His Leu His Asn *			
515	520		
tgctgtatattt ttctggaaag aaaacttttct ttaccactt ataaacagaa gactgtgaca			1705
agaaggccaa ttattttccat cgctgaagac tctaaatttg gcaaattcttc taaataacaa			1765
tcctgcatag tttattaaaa aaaattagtc gtaaaattta tccttcaaaa atctgcattt			1825
taaataaaacc ctgacagtga tttctcaaga ctgtaaagat attagtctga gaatgcaact			1885
ctaacagact gctctgggca tctttttctct ttgccttggc caggcctctc agaattgagt			1945
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Lys Leu Gly Ser Ser Gly Gly Trp Phe Leu Arg Val Leu Gly Pro Gly			
10 15 20			
ggc tgt aat aca aaa gct gcg cgt ccc tta att tcc tcg gcg gtt tat			149
Gly Cys Asn Thr Lys Ala Ala Arg Pro Leu Ile Ser Ser Ala Val Tyr			
25 30 35			
gtg aag aac cag ctc agt ggg act cta cag att aaa cca ggg gtt ttc			197
Val Lys Asn Gln Leu Ser Gly Thr Leu Gln Ile Lys Pro Gly Val Phe			
40 45 50			

aat gaa tac aga acc ata tgg ttc aaa tcc tac agg acg atc ttt tcc Asn Glu Tyr Arg Thr Ile Trp Phe Lys Ser Tyr Arg Thr Ile Phe Ser 55 60 65	245
tgt ttg aac aga ata aag agt ttc agg tac cct tgg gcg aga ctg tac Cys Leu Asn Arg Ile Lys Ser Phe Arg Tyr Pro Trp Ala Arg Leu Tyr 70 75 80 85	293
agt act tcc caa acc act gtc gac agc ggt gag gta aaa acc ttc ttg Ser Thr Ser Gln Thr Thr Val Asp Ser Gly Glu Val Lys Thr Phe Leu 90 95 100	341
gcc ctg gct cac aaa tgg tgg gat gaa caa gga gta tat gca cct ctt Ala Leu Ala His Lys Trp Trp Asp Glu Gln Gly Val Tyr Ala Pro Leu 105 110 115	389
cat tcc atg aat gac ctg agg gtg cca ttt att agg gac aat ctt ctg His Ser Met Asn Asp Leu Arg Val Pro Phe Ile Arg Asp Asn Leu Leu 120 125 130	437
aaa aca att cct aat cac cag cca gga aaa cct ttg ttg ggg atg aag Lys Thr Ile Pro Asn His Gln Pro Gly Lys Pro Leu Leu Gly Met Lys 135 140 145	485
att ctt gac gtt ggc tgt ggt ggt ggg ctg tta act gaa cct cta ggg Ile Leu Asp Val Gly Cys Gly Gly Gly Leu Leu Thr Glu Pro Leu Gly 150 155 160 165	533
cgg ctt ggg gct tca gtt att gga atc gac cct gtg gat gag aac att Arg Leu Gly Ala Ser Val Ile Gly Ile Asp Pro Val Asp Glu Asn Ile 170 175 180	581
aaa aca gca caa tgc cat aaa tca ttt gat cca gtc cgg gat aag aga Lys Thr Ala Gln Cys His Lys Ser Phe Asp Pro Val Arg Asp Lys Arg 185 190 195	629
ata gag tac aga gtg tgt tcc ctg gaa gag att gtg gaa gag act gca Ile Glu Tyr Arg Val Cys Ser Leu Glu Glu Ile Val Glu Glu Thr Ala 200 205 210	677
gaa aca ttt gat gct gtt gta gct tct gaa gtt gta gaa cat gtg att Glu Thr Phe Asp Ala Val Val Ala Ser Glu Val Val Glu His Val Ile 215 220 225	725
gat cta gaa aca ttt tta cag tgc tgc tgt caa gtg tta aaa ccc ggt Asp Leu Glu Thr Phe Leu Gln Cys Cys Cys Gln Val Leu Lys Pro Gly 230 235 240 245	773
ggt tct tta ttc att act aca atc aac aaa aca caa ctt tcc tat gcc Gly Ser Leu Phe Ile Thr Thr Ile Asn Lys Thr Gln Leu Ser Tyr Ala 250 255 260	821
ttg gga att gtt ttt tca gag caa att gca ggt att gta cca aaa ggt Leu Gly Ile Val Phe Ser Glu Gln Ile Ala Gly Ile Val Pro Lys Gly 265 270 275	869
act cat aca tgg gag aag ttt gtt tca cct gaa aca cta gag agc att	917

Thr	His	Thr	Trp	Glu	Lys	Phe	Val	Ser	Pro	Glu	Thr	Leu	Glu	Ser	Ile		
		280					285					290					
ctg	gaa	tca	aat	ggt	ctg	tca	gtt	caa	aca	gtg	gta	gga	atg	ctc	tat		965
Leu	Glu	Ser	Asn	Gly	Leu	Ser	Val	Gln	Thr	Val	Val	Gly	Met	Leu	Tyr		
		295					300				305						
aac	ccc	ttc	tca	ggt	tac	tgg	cat	tgg	agt	gaa	aat	acc	agc	ctt	aac		1013
Asn	Pro	Phe	Ser	Gly	Tyr	Trp	His	Trp	Ser	Glu	Asn	Thr	Ser	Leu	Asn		
		310				315				320					325		
tat	gca	gct	cat	gct	gtg	aaa	tcc	agg	gtc	cag	gaa	cac	cca	gcc	tct		1061
Tyr	Ala	Ala	His	Ala	Val	Lys	Ser	Arg	Val	Gln	Glu	His	Pro	Ala	Ser		
					330				335					340			
gct	gag	ttt	gtt	tta	aag	gga	gaa	aca	gaa	gag	ctc	caa	gct	aat	gcc		1109
Ala	Glu	Phe	Val	Leu	Lys	Gly	Glu	Thr	Glu	Glu	Leu	Gln	Ala	Asn	Ala		
			345					350					355				
tgc	acc	aat	cca	gct	gtg	cat	gaa	aag	ctg	aag	aaa	tga	attg	tttctg			1158
Cys	Thr	Asn	Pro	Ala	Val	His	Glu	Lys	Leu	Lys	Lys	*					
		360					365					370					
agaactatag	taatatggct	tgatatactg	atgttttcaa	atacaagaaa	tgtacaattt												1218
atcctttgag	agagaatcat	gaagaaaaga	aggtcaataa	aaagggctaa	aaccttggac												1278
aaaagttttt	gttatttcgt	ctaatagcta	ctttcaaggg	attctgtgaa	taaaaagttt												1338
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tgcgtctcct	tgtagcat	gttttggc	atatctttcg	tatctatgcc	ccagaagctc												120
catatacttc	ccatgataa	cttaagtggc	gagtaagaaa	agaagct	atg atg ggt												176
					Met Met Gly												
					1												
ctg gct cag	ctt tat aag	aaa tac	tgt ctt	cat ggt	gaa gca	gga aag											224
Leu Ala Gln	Leu Tyr Lys	Lys Tyr	Cys Leu	His Gly	Glu Ala	Gly Lys											
	5		10		15												
gaa gct gca	gag aaa gtc	agc tgg	ata aag	gac aaa	ctt ctg	cat att											272

Glu	Ala	Ala	Glu	Lys	Val	Ser	Trp	Ile	Lys	Asp	Lys	Leu	Leu	His	Ile		
20					25					30					35		
tat	tat	cag	aac	agc	att	gac	gac	aaa	ctg	ttg	gta	gag	aaa	atc	ttt	320	
Tyr	Tyr	Gln	Asn	Ser	Ile	Asp	Asp	Lys	Leu	Leu	Val	Glu	Lys	Ile	Phe		
				40					45					50			
gct	cag	tat	ctt	gtc	ccc	cac	aac	ctg	gaa	aca	gaa	gag	aga	atg	aaa	368	
Ala	Gln	Tyr	Leu	Val	Pro	His	Asn	Leu	Glu	Thr	Glu	Glu	Arg	Met	Lys		
			55					60					65				
tgc	tta	tat	tac	tta	tat	gct	agt	ttg	gat	cca	aat	gct	gta	aaa	gct	416	
Cys	Leu	Tyr	Tyr	Leu	Tyr	Ala	Ser	Leu	Asp	Pro	Asn	Ala	Val	Lys	Ala		
		70					75					80					
ctc	aac	gaa	atg	tgg	aag	tgt	cag	aac	atg	ctt	cgg	agc	cat	gta	cgc	464	
Leu	Asn	Glu	Met	Trp	Lys	Cys	Gln	Asn	Met	Leu	Arg	Ser	His	Val	Arg		
	85					90					95						
gaa	cta	ttg	gat	ttg	cac	aag	cag	cct	aca	tca	gag	gct	aac	tgt	tct	512	
Glu	Leu	Leu	Asp	Leu	His	Lys	Gln	Pro	Thr	Ser	Glu	Ala	Asn	Cys	Ser		
100					105					110				115			
gcc	atg	ttt	gga	aaa	ctg	atg	acc	ata	gca	aag	aat	ttg	cct	gac	ccc	560	
Ala	Met	Phe	Gly	Lys	Leu	Met	Thr	Ile	Ala	Lys	Asn	Leu	Pro	Asp	Pro		
				120					125					130			
ggg	aaa	gca	caa	gat	ttt	gtg	aag	aaa	ttt	aac	cag	gtt	ctc	ggc	gat	608	
Gly	Lys	Ala	Gln	Asp	Phe	Val	Lys	Lys	Phe	Asn	Gln	Val	Leu	Gly	Asp		
			135					140					145				
gat	gag	aaa	ctt	cgg	tct	cag	ttg	gag	tta	tta	att	agc	cca	acc	tgt	656	
Asp	Glu	Lys	Leu	Arg	Ser	Gln	Leu	Glu	Leu	Leu	Ile	Ser	Pro	Thr	Cys		
		150					155					160					
tct	tgc	aaa	caa	gca	gat	att	tgt	gtg	aga	gaa	ata	gcc	cgg	aaa	ctt	704	
Ser	Cys	Lys	Gln	Ala	Asp	Ile	Cys	Val	Arg	Glu	Ile	Ala	Arg	Lys	Leu		
	165					170					175						
gca	aat	cct	aag	caa	cca	aca	aat	cct	ttt	cta	gag	atg	gtc	aaa	ttt	752	
Ala	Asn	Pro	Lys	Gln	Pro	Thr	Asn	Pro	Phe	Leu	Glu	Met	Val	Lys	Phe		
180					185					190					195		
ctg	ttg	gaa	aga	atc	gca	cct	gtg	cac	att	gat	tca	gaa	gcc	ata	agt	800	
Leu	Leu	Glu	Arg	Ile	Ala	Pro	Val	His	Ile	Asp	Ser	Glu	Ala	Ile	Ser		
				200					205					210			
gcg	cta	gtg	aaa	ttg	atg	aat	aag	tca	ata	gag	ggg	aca	gca	gat	gat	848	
Ala	Leu	Val	Lys	Leu	Met	Asn	Lys	Ser	Ile	Glu	Gly	Thr	Ala	Asp	Asp		
			215					220					225				
gaa	gag	gag	ggt	gta	agt	cca	gat	aca	gct	atc	cgt	tca	gga	ctt	gaa	896	
Glu	Glu	Glu	Gly	Val	Ser	Pro	Asp	Thr	Ala	Ile	Arg	Ser	Gly	Leu	Glu		
		230					235					240					
ctt	ctt	aag	gtt	ctg	tct	ttt	aca	cat	cct	acc	tcg	ttc	cac	tct	gca	944	
Leu	Leu	Lys	Val	Leu	Ser	Phe	Thr	His	Pro	Thr	Ser	Phe	His	Ser	Ala		

245	250	255	
gag aca tat gag tcc ttg tta cag tgc cta aga atg gag gat gac aag Glu Thr Tyr Glu Ser Leu Leu Gln Cys Leu Arg Met Glu Asp Asp Lys 260 265 270 275			992
gta gca gaa gct gct att caa att ttt aga aat aca ggt cac aaa ata Val Ala Glu Ala Ala Ile Gln Ile Phe Arg Asn Thr Gly His Lys Ile 280 285 290			1040
gaa aca gac ctt ccc cag ata cga tcg acc tta att ccc att tta cat Glu Thr Asp Leu Pro Gln Ile Arg Ser Thr Leu Ile Pro Ile Leu His 295 300 305			1088
caa aaa gca aag agg ggt act cca cac caa gca aaa cag gct gtg cac Gln Lys Ala Lys Arg Gly Thr Pro His Gln Ala Lys Gln Ala Val His 310 315 320			1136
tgt ata cac gcc ata ttc aca aat aaa gaa gtc cag ctt gca cag att Cys Ile His Ala Ile Phe Thr Asn Lys Glu Val Gln Leu Ala Gln Ile 325 330 335			1184
ttt gag cca ctc agt agg agt ctg aat gct gat gtg cca gaa caa ctt Phe Glu Pro Leu Ser Arg Ser Leu Asn Ala Asp Val Pro Glu Gln Leu 340 345 350 355			1232
ata act cca tta gtt tca ttg ggc cac att tct atg tta gca cca gat Ile Thr Pro Leu Val Ser Leu Gly His Ile Ser Met Leu Ala Pro Asp 360 365 370			1280
cag ttt gct tcc cca atg aaa tct gta gta gca aat ttt att gtg aaa Gln Phe Ala Ser Pro Met Lys Ser Val Val Ala Asn Phe Ile Val Lys 375 380 385			1328
gat ctg cta atg aat gac agg tca aca ggt gaa aag aat gga aaa ctg Asp Leu Leu Met Asn Asp Arg Ser Thr Gly Glu Lys Asn Gly Lys Leu 390 395 400			1376
tgg tct cca gat gaa gag gtt tcc cct gaa gta cta gca aag gta cag Trp Ser Pro Asp Glu Glu Val Ser Pro Glu Val Leu Ala Lys Val Gln 405 410 415			1424
gca att aaa ctt ctg gta agg tgg ctg ttg ggt atg aaa aac aac cag Ala Ile Lys Leu Leu Val Arg Trp Leu Leu Gly Met Lys Asn Asn Gln 420 425 430 435			1472
tct aaa tct gcc aat tca acc ctt cgg tta tta tca gcg atg ttg gtt Ser Lys Ser Ala Asn Ser Thr Leu Arg Leu Leu Ser Ala Met Leu Val 440 445 450			1520
agt gag ggt gac ctg aca gag caa aag agg atc agt aaa tct gat atg Ser Glu Gly Asp Leu Thr Glu Gln Lys Arg Ile Ser Lys Ser Asp Met 455 460 465			1568
tct cgc ttg cga tta gct gct ggt agt gcc ata atg aag ctt gct cag Ser Arg Leu Arg Leu Ala Ala Gly Ser Ala Ile Met Lys Leu Ala Gln 470 475 480			1616

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Glu Pro Cys Tyr His Glu Ile Ile Thr Pro Glu Gln Phe Gln Leu Cys	
485 490 495	
gca ctt gtt att aat gat gag tgt tac caa gta agg cag ata ttt gct	1712
Ala Leu Val Ile Asn Asp Glu Cys Tyr Gln Val Arg Gln Ile Phe Ala	
500 505 510 515	
cag aag ctg cat aag gca ctt gtg aag tta ctg ctc cca ttg gag tat	1760
Gln Lys Leu His Lys Ala Leu Val Lys Leu Leu Leu Pro Leu Glu Tyr	
520 525 530	
atg gcg atc ttt gcc ttg tgt gcc aaa gat cct gtg aag gag aga aga	1808
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Ser	Arg	Ser	Arg	Arg	Ser	Ser	Ile	Gly	Leu	Arg	Val	Ala	Phe	Gln	Phe			
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ccc	acc	aag	aag	ctg	gcc	aac	aaa	cca	gat	aaa	aac	agt	tct	tcc	gag			295
Pro	Thr	Lys	Lys	Leu	Ala	Asn	Lys	Pro	Asp	Lys	Asn	Ser	Ser	Ser	Glu			
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Gln	Leu	Phe	Ser	Ser	Ala	Arg	Leu	Gln	Asn	Glu	Lys	Lys	Thr	Ile	Leu			
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Glu	Arg	Lys	Lys	Asp	Cys	Arg	Gln	Val	Ile	Gln	Arg	Glu	Asp	Ser	Thr			
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Ser	Glu	Ser	Glu	Asp	Asp	Ser	Arg	Asp	Glu	Ser	Gln	Glu	Ser	Ser	Asp			
			120					125					130					
gct	ttg	ctg	aaa	agg	acc	atg	aac	atc	aag	gag	aac	aaa	gcc	atg	ctt			487
Ala	Leu	Leu	Lys	Arg	Thr	Met	Asn	Ile	Lys	Glu	Asn	Lys	Ala	Met	Leu			
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gcc	cag	tta	ttg	gcg	gaa	ttg	aac	tcg	atg	cca	gat	ttc	ttc	cca	gta			535
Ala	Gln	Leu	Leu	Ala	Glu	Leu	Asn	Ser	Met	Pro	Asp	Phe	Phe	Pro	Val			
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Ser	Glu	Gly	Gln	Ile	Thr	Arg	Arg	Met	Asn	Pro	Thr	Arg	Ser	Ala	Arg			
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Pro	Pro	Glu	Lys	Phe	Ala	Leu	Glu	Asn	Phe	Thr	Val	Ser	Ala	Ala	Lys			
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Phe	Ala	Glu	Glu	Phe	Tyr	Ser	Phe	Arg	Arg	Arg	Lys	Thr	Ile	Gly	Gly			
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Lys	Cys	Arg	Glu	Tyr	Arg	Arg	Arg	His	Arg	Ile	Ser	Ser	Phe	Arg	Pro			
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Val	Glu	Asp	Ile	Thr	Glu	Glu	Asp	Leu	Glu	Asn	Val	Ala	Ile	Thr	Val			
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Arg	Asp	Lys	Ile	Tyr	Asp	Lys	Val	Leu	Gly	Asn	Thr	Cys	His	Gln	Cys			

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Cys Gly Val Arg Gly Gln Phe Cys	Gly Pro Cys Leu Arg Asn Arg Tyr		
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Gly Glu Asp Val Arg Ser Ala Leu	Leu Asp Pro Asp Trp Val Cys Pro		
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Pro Cys Arg Gly Ile Cys Asn Cys	Ser Tyr Cys Arg Lys Arg Asp Gly		
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Asp Asn Val Lys Glu Tyr Leu Glu	Ser Leu Gln Lys Glu Leu Val Glu		
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 Glu Thr Gln Thr Leu Ser Ala Glu Thr Ser Ser Arg Ala Ser Thr Pro
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 gcc ggc ccc att cca gaa gca gag acc agg gga gcc aag aga att tcc 557

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Pro Ala Arg Glu Thr Arg Ser Phe Thr Lys Thr Ser Pro Asn Phe Met	
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Val Leu Ile Ala Thr Ser Val Glu Thr Ser Ala Ala Ser Gly Ser Pro	
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Glu Gly Ala Gly Met Thr Thr Val Gln Thr Ile Thr Gly Ser Asp Pro	
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Glu Glu Ala Ile Phe Asp Thr Leu Cys Thr Asp Asp Ser Ser Glu Glu	
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Thr Pro Ser Arg Ala Ser Glu Ser Ser Ala Ser Ser Asp Gly Pro His	
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Pro Val Ile Thr Pro Ser Trp Ser Pro Gly Ser Asp Val Thr Leu Leu	
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Pro Ser Glu Thr Pro Thr Met Asp Ile Ala Thr Lys Gly Pro Phe Pro			
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Ser Arg Gly Thr Asn Ser Thr Leu Ala Lys Ile Thr Thr Ser Ala Lys			
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Lys Thr Thr Met Lys Pro Pro Thr Ala Thr Pro Thr Thr Ala Arg Thr			
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Ala Glu Arg Leu Met Gln Gln Leu His Arg Glu Leu His Ala His Ala			
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Pro His Phe Gln Val Ser Leu Leu Arg Val Arg Arg Gly *			
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 Met Gln Val Trp Leu Leu Thr
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 Leu Glu Arg Leu Arg Val Leu Pro Lys Pro Arg Ser Glu Phe Asp Phe
 10 15 20
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 Phe Pro Ile Ser His Thr His Pro Arg Arg His Pro Asn Pro Arg Ile
 25 30 35
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 Ser His Val Arg Leu Pro Leu Pro Pro Arg Trp Ala Leu Gln Asp Pro
 40 45 50 55
 cca tcg cat ccc ctc tca ctc cac aga aaa ctc gtg ggg ccg tgt tcc 606
 Pro Ser His Pro Leu Ser Leu His Arg Lys Leu Val Gly Pro Cys Ser
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 ccc tgc cac tga ccacgctttc cttgcaga 636

Pro Cys His *
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tttctgtgag ctctccttag ttgtccacat tggaagcaaa cttttaaatg ctgtgtatgc      240
gtggcccaag caaaacacat ctggaggcca gattgaatcc acaggctgaa agcagtcaac      300
caggcctgat gtc      atg acc ctg tat cct ctc cac tgg cag gaa gag atg      349
                  Met Thr Leu Tyr Pro Leu His Trp Gln Glu Glu Met
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tca gga gaa agt gtg gtg agc tca gcg gtg cca gcg gct gct acc cgc      397
Ser Gly Glu Ser Val Val Ser Ser Ala Val Pro Ala Ala Ala Thr Arg
                   15              20              25

acc act tcc ttc aag ggc acg agc ccc agc tcc aaa tac gtg aag ctg      445
Thr Thr Ser Phe Lys Gly Thr Ser Pro Ser Ser Lys Tyr Val Lys Leu
                   30              35              40

aat gtg ggt gga gcc ctc tac tat acc acc atg cag acg ctg acc aag      493
Asn Val Gly Gly Ala Leu Tyr Tyr Thr Thr Met Gln Thr Leu Thr Lys
                   45              50              55              60

cag gac acc atg ctg aag gcc atg ttc agc ggg cgc atg gaa gtg ctc      541
Gln Asp Thr Met Leu Lys Ala Met Phe Ser Gly Arg Met Glu Val Leu
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acc gac agt gaa ggc tgg atc ctc att gac cgc tgt ggg aag cac ttt      589
Thr Asp Ser Glu Gly Trp Ile Leu Ile Asp Arg Cys Gly Lys His Phe
                   80              85              90

ggt acg ata ctc aac tac ctt cga gac ggg gcg gtg cct tta ccc gag      637
Gly Thr Ile Leu Asn Tyr Leu Arg Asp Gly Ala Val Pro Leu Pro Glu
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agc cgc cgg gag atc gag gag ctg cta gca gaa gcc aag tac tac cta      685
Ser Arg Arg Glu Ile Glu Glu Leu Leu Ala Glu Ala Lys Tyr Tyr Leu
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110	115	120	
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Val Gln Gly Leu Val Glu Glu Cys Gln Ala Ala Leu Gln Asn Lys Asp			
125	130	135	140
act tat gag cct ttc tgc aag gtc cct gtg atc acc tca tcc aag gaa			781
Thr Tyr Glu Pro Phe Cys Lys Val Pro Val Ile Thr Ser Ser Lys Glu			
	145	150	155
gaa caa aaa ctt ata gcg act tca aat aag cca gcc gtg aag ttg ctc			829
Glu Gln Lys Leu Ile Ala Thr Ser Asn Lys Pro Ala Val Lys Leu Leu			
	160	165	170
tac aac aga agt aac aac aaa tac tca tat acc agc aat tct gac gac			877
Tyr Asn Arg Ser Asn Asn Lys Tyr Ser Tyr Thr Ser Asn Ser Asp Asp			
	175	180	185
aat atg ttg aaa aac att gaa ctg ttt gat aag ctg tct ctg cgc ttt			925
Asn Met Leu Lys Asn Ile Glu Leu Phe Asp Lys Leu Ser Leu Arg Phe			
	190	195	200
aac gga agg gtc ctg ttc ata aag gat gtt att ggg gat gaa atc tgc			973
Asn Gly Arg Val Leu Phe Ile Lys Asp Val Ile Gly Asp Glu Ile Cys			
205	210	215	220
tgc tgg tcc ttt tat ggt cag ggc cgg aag att gct gaa gtc tgt tgt			1021
Cys Trp Ser Phe Tyr Gly Gln Gly Arg Lys Ile Ala Glu Val Cys Cys			
	225	230	235
acc tcc atc gtc tat gcc act gag aag aaa cag acc aag gtg gag ttt			1069
Thr Ser Ile Val Tyr Ala Thr Glu Lys Lys Gln Thr Lys Val Glu Phe			
	240	245	250
ccc gaa gcc cgg att tat gag gag acc ctg aac att ttg ctg tat gag			1117
Pro Glu Ala Arg Ile Tyr Glu Glu Thr Leu Asn Ile Leu Leu Tyr Glu			
	255	260	265
gcc cag gat ggc cgg gga cct gac aat gcg ctc ctg gag gcc aca ggc			1165
Ala Gln Asp Gly Arg Gly Pro Asp Asn Ala Leu Leu Glu Ala Thr Gly			
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ggg gcg gcg ggg cgc tcc cac cac ctg gac gag gac gag gag cgg gag			1213
Gly Ala Ala Gly Arg Ser His His Leu Asp Glu Asp Glu Glu Arg Glu			
285	290	295	300
cgg atc gag cgc gtg cgg agg atc cac atc aag cgc cct gat gac cgg			1261
Arg Ile Glu Arg Val Arg Arg Ile His Ile Lys Arg Pro Asp Asp Arg			
	305	310	315
gcc cac ctc cac cag tga gcaggc aagagaccga gccgccctcc tctcaccgcc			1315
Ala His Leu His Gln *			
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acaataaaac tttaaaacaa aaaaaaaaaa 2905

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<213> Homo sapiens

<220>

<221> CDS

<222> (287)..(1924)

<400> 14

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actcatcctc atcctcttcc tctgataaag cccctaccag tgctgataaa gtcttttctcg      180
tgagagccta gaggccttaa aaaaaaaagt gcttgaaaga gaagggggaca aaggaacacc      240
agtattaaga ggattttcca gtgtttctgg cagttgggtcc agaagg  atg cct cca      295
                                     Met Pro Pro
                                     1

ttc ctg ctt ctc acc tgc ctc ttc atc aca ggc acc tcc gtg tca ccc      343
Phe Leu Leu Leu Thr Cys Leu Phe Ile Thr Gly Thr Ser Val Ser Pro
      5                      10                      15

gtg gcc cta gat cct tgt tct gct tac atc agc ctg aat gag ccc tgg      391
Val Ala Leu Asp Pro Cys Ser Ala Tyr Ile Ser Leu Asn Glu Pro Trp
      20                      25                      30                      35

agg aac act gac cac cag ttg gat gag tct caa ggt cct cct cta tgt      439
Arg Asn Thr Asp His Gln Leu Asp Glu Ser Gln Gly Pro Pro Leu Cys
                        40                      45                      50

gac aac cat gtg aat ggg gag tgg tac cac ttc acg ggc atg gcg gga      487
Asp Asn His Val Asn Gly Glu Trp Tyr His Phe Thr Gly Met Ala Gly
                        55                      60                      65

gat gcc atg cct acc ttc tgc ata cca gaa aac cac tgt gga acc cac      535
Asp Ala Met Pro Thr Phe Cys Ile Pro Glu Asn His Cys Gly Thr His
      70                      75                      80

gca cct gtc tgg ctc aat ggc agc cac ccc cta gaa ggc gac ggc att      583
Ala Pro Val Trp Leu Asn Gly Ser His Pro Leu Glu Gly Asp Gly Ile
      85                      90                      95

gtg caa cgc cag gct tgt gcc agc ttc aat ggg aac tgc tgt ctc tgg      631
Val Gln Arg Gln Ala Cys Ala Ser Phe Asn Gly Asn Cys Cys Leu Trp
      100                      105                      110                      115

aac acc acg gtg gaa gtc aag gct tgc cct gga ggc tac tat gtg tat      679
Asn Thr Thr Val Glu Val Lys Ala Cys Pro Gly Gly Tyr Tyr Val Tyr
                        120                      125                      130

cgt ctg acc aag ccc agc gtc tgc ttc cac gtc tac tgt ggt cat ttt      727
Arg Leu Thr Lys Pro Ser Val Cys Phe His Val Tyr Cys Gly His Phe
                        135                      140                      145

tat gac atc tgc gac gag gac tgc cat ggc agc tgc tca gat acc agc      775
Tyr Asp Ile Cys Asp Glu Asp Cys His Gly Ser Cys Ser Asp Thr Ser
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gag tgc aca tgc gct cca gga act gtg cta ggc cct gac agg cag aca			823
Glu Cys Thr Cys Ala Pro Gly Thr Val Leu Gly Pro Asp Arg Gln Thr			
165	170	175	
tgc ttt gat gaa aat gaa tgt gag caa aac aac ggt ggc tgc agt gag			871
Cys Phe Asp Glu Asn Glu Cys Glu Gln Asn Asn Gly Gly Cys Ser Glu			
180	185	190	195
atc tgt gtg aac ctc aaa aac tcc tac cgc tgt gag tgt ggg gtt ggc			919
Ile Cys Val Asn Leu Lys Asn Ser Tyr Arg Cys Glu Cys Gly Val Gly			
	200	205	210
cgt gtg cta aga agt gat ggc aag act tgt gaa gac gtt gaa gga tgc			967
Arg Val Leu Arg Ser Asp Gly Lys Thr Cys Glu Asp Val Glu Gly Cys			
	215	220	225
cac aat aac aat ggt ggc tgc agc cac tct tgc ctt gga tct gag aaa			1015
His Asn Asn Asn Gly Gly Cys Ser His Ser Cys Leu Gly Ser Glu Lys			
	230	235	240
ggc tac cag tgt gaa tgt ccc cgg ggc ctg gtg ctg tct gag gat aac			1063
Gly Tyr Gln Cys Glu Cys Pro Arg Gly Leu Val Leu Ser Glu Asp Asn			
	245	250	255
cac act tgc caa gtc cct gtg ttg tgc aaa tca aat gcc att gaa gtg			1111
His Thr Cys Gln Val Pro Val Leu Cys Lys Ser Asn Ala Ile Glu Val			
	260	265	270
aac atc ccc agg gag ctg gtt ggt ggc ctg gag ctc ttc ctg acc aac			1159
Asn Ile Pro Arg Glu Leu Val Gly Gly Leu Glu Leu Phe Leu Thr Asn			
	280	285	290
acc tcc tgc cga gga gtg tcc aac ggc acc cat gtc aac atc ctc ttc			1207
Thr Ser Cys Arg Gly Val Ser Asn Gly Thr His Val Asn Ile Leu Phe			
	295	300	305
tct ctc aag aca tgt ggt aca gtg gtc gat gtg gtg aat gac aag att			1255
Ser Leu Lys Thr Cys Gly Thr Val Val Asp Val Val Asn Asp Lys Ile			
	310	315	320
gtg gcc agc aac ctc gtg aca ggt cta ccc aag cag acc ccg ggg agc			1303
Val Ala Ser Asn Leu Val Thr Gly Leu Pro Lys Gln Thr Pro Gly Ser			
	325	330	335
agc ggg gac ttc atc atc cga acc agc aag ctg ctg atc ccg gtg acc			1351
Ser Gly Asp Phe Ile Ile Arg Thr Ser Lys Leu Leu Ile Pro Val Thr			
	340	345	350
tgc gag ttt cca cgc ctg tac acc att tct gaa gga tac gtt ccc aac			1399
Cys Glu Phe Pro Arg Leu Tyr Thr Ile Ser Glu Gly Tyr Val Pro Asn			
	360	365	370
ctt cga aac tcc cca ctg gaa atc atg agc cga aat cat ggg atc ttc			1447
Leu Arg Asn Ser Pro Leu Glu Ile Met Ser Arg Asn His Gly Ile Phe			
	375	380	385

cca ttc act ctg gag atc ttc aag gac aat gag ttt gaa gag cct tac	1495
Pro Phe Thr Leu Glu Ile Phe Lys Asp Asn Glu Phe Glu Glu Pro Tyr	
390 395 400	
cgg gaa gct ctg ccc acc ctc aag ctt cgt gac tcc ctc tac ttt ggc	1543
Arg Glu Ala Leu Pro Thr Leu Lys Leu Arg Asp Ser Leu Tyr Phe Gly	
405 410 415	
att gag ccc gtg gtg cac gtg agc ggc ttg gaa agc ttg gtg gag agc	1591
Ile Glu Pro Val Val His Val Ser Gly Leu Glu Ser Leu Val Glu Ser	
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tgc ttt gcc acc ccc acc tcc aag atc gac gag gtc ctg aaa tac tac	1639
Cys Phe Ala Thr Pro Thr Ser Lys Ile Asp Glu Val Leu Lys Tyr Tyr	
440 445 450	
ctc atc cgg gat ggc tgt gtt tca gat gac tcg gta aag cag tac aca	1687
Leu Ile Arg Asp Gly Cys Val Ser Asp Asp Ser Val Lys Gln Tyr Thr	
455 460 465	
tcc cgg gat cac cta gca aag cac ttc cag gtc cct gtc ttc aag ttt	1735
Ser Arg Asp His Leu Ala Lys His Phe Gln Val Pro Val Phe Lys Phe	
470 475 480	
gtg ggc aaa gac cac aag gaa gtg ttt ctg cac tgc cgg gtt ctt gtc	1783
Val Gly Lys Asp His Lys Glu Val Phe Leu His Cys Arg Val Leu Val	
485 490 495	
tgt gga gtg ttg gac gag cgt tcc cgc tgt gcc cag ggt tgc cac cgg	1831
Cys Gly Val Leu Asp Glu Arg Ser Arg Cys Ala Gln Gly Cys His Arg	
500 505 510 515	
cga atg cgt cgt ggg gca gga gga gag gac tca gcc ggt cta cag ggc	1879
Arg Met Arg Arg Gly Ala Gly Gly Glu Asp Ser Ala Gly Leu Gln Gly	
520 525 530	
cag acg cta aca ggc ggc ccg atc cgc atc gac tgg gag gac tag ttc	1927
Gln Thr Leu Thr Gly Gly Pro Ile Arg Ile Asp Trp Glu Asp *	
535 540 545	
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2444

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atg ggg gca aag gat cca agc att gag cct tca tcc tct att ccc cat 165

Met Gly Ala Lys Asp Pro Ser Ile Glu Pro Ser Ser Ser Ile Pro His

1 5 10 15

cca gtg ggg tgc cga ggc tca ggc agc atg acg acg gag acc ttt gtg 213

Pro Val Gly Cys Arg Gly Ser Gly Ser Met Thr Thr Glu Thr Phe Val

20 25 30

aag gat atc aag cct ggg ctc aag aat ctg aac ctt atc ttc att gtg 261

Lys Asp Ile Lys Pro Gly Leu Lys Asn Leu Asn Leu Ile Phe Ile Val

35 40 45

ctg gag aca ggc cga gtg acc aag aca aag gac ggg cat gag gtt cgg 309

Leu Glu Thr Gly Arg Val Thr Lys Thr Lys Asp Gly His Glu Val Arg

50 55 60

acc tgc aaa gtg gcg gac aaa aca ggc agc atc aat atc tct gtc tgg 357

Thr Cys Lys Val Ala Asp Lys Thr Gly Ser Ile Asn Ile Ser Val Trp

65 70 75 80

gac gat gtt ggc aat ctg atc cag cct ggg gac att atc cgg ctc acc 405

Asp Asp Val Gly Asn Leu Ile Gln Pro Gly Asp Ile Ile Arg Leu Thr

85 90 95

aaa ggg tac gct tca gtt ttc aaa ggt tgt ctg aca cta tat act ggc 453

Lys Gly Tyr Ala Ser Val Phe Lys Gly Cys Leu Thr Leu Tyr Thr Gly

100 105 110

cgt ggg ggt gat ctg cag aag att gga gaa ttc tgt atg gtt tat tct 501

Arg Gly Gly Asp Leu Gln Lys Ile Gly Glu Phe Cys Met Val Tyr Ser

115 120 125

gag gtt cct aac ttc agt gag cca aac cca gag tac agc acc cag cag 549

Glu Val Pro Asn Phe Ser Glu Pro Asn Pro Glu Tyr Ser Thr Gln Gln

130 135 140

gca ccc aac aag gcg gtg cag aac gac agc aac cct tca gct tcc cag 597

Ala Pro Asn Lys Ala Val Gln Asn Asp Ser Asn Pro Ser Ala Ser Gln

145 150 155 160

cct acc act gga ccc tct gct gcc tct cca gcc tct gag aac cag aat	645
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Gly Asn Gly Leu Ser Ala Pro Pro Gly Pro Gly Gly Gly Pro His Pro	
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Pro His Thr Pro Ser His Pro Pro Ser Thr Arg Ile Thr Arg Ser Gln	
195 200 205	
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Pro Asn His Thr Pro Ala Gly Pro Pro Gly Pro Phe Ser Asn Pro Val	
210 215 220	
agt aac ggc aaa gaa acc cgg agg agc agc aag aga tag catgacattc	838
Ser Asn Gly Lys Glu Thr Arg Arg Ser Ser Lys Arg *	
225 230 235	
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cccatatccc atttcagct gcaaattact gcagaatctg aaccaggaa agaaacccat	180
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atg gcc cag aag ccg aag gtg gac ccc cac gtc ggg cgg ctg gga tac	348
Met Ala Gln Lys Pro Lys Val Asp Pro His Val Gly Arg Leu Gly Tyr	
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ctg cag gcg ctg gtc acg gaa ttc cag gag acc caa agc caa gac gcc	396
Leu Gln Ala Leu Val Thr Glu Phe Gln Glu Thr Gln Ser Gln Asp Ala	
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Lys Glu Gln Val Leu Ala Asn Leu Ala Asn Phe Ala Tyr Asp Pro Ser	
35 40 45	
aac tac gag tat ctg cgg cag ctg cag gtc ctg gat tta ttt ctc gat	492
Asn Tyr Glu Tyr Leu Arg Gln Leu Gln Val Leu Asp Leu Phe Leu Asp	
50 55 60	
tcg ctg tcg gag gag aat gag acc ctg gtg gag ttt gct att gga ggc	540
Ser Leu Ser Glu Glu Asn Glu Thr Leu Val Glu Phe Ala Ile Gly Gly	
65 70 75 80	
ctg tgc aac ctg tgc cca gac agg gcc aac aag gag cac atc ctg cac	588
Leu Cys Asn Leu Cys Pro Asp Arg Ala Asn Lys Glu His Ile Leu His	
85 90 95	
gca gga ggt gtc cca ctc atc atc aac tgc cta tcc agc ccc aat gag	636
Ala Gly Gly Val Pro Leu Ile Ile Asn Cys Leu Ser Ser Pro Asn Glu	
100 105 110	
gag acg gtg ctg tct gcc atc acc acg ctc atg cac ctg agc ccg ccg	684
Glu Thr Val Leu Ser Ala Ile Thr Thr Leu Met His Leu Ser Pro Pro	
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ggc cgc agc ttt ctc cca gag ctg acc gcc acg ccc gtg gtg cag tgc	732
Gly Arg Ser Phe Leu Pro Glu Leu Thr Ala Thr Pro Val Val Gln Cys	
130 135 140	
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Met Leu Arg Phe Ser Leu Ser Ala Ser Ala Arg Leu Arg Asn Leu Ala	
145 150 155 160	
cag atc ttc ctg gag gac ttc tgc tcc ccc cgc cag gtg gcc gag gcc	828
Gln Ile Phe Leu Glu Asp Phe Cys Ser Pro Arg Gln Val Ala Glu Ala	
165 170 175	
cgc agc cgg cag gcg cac tct gcc ctg ggt atc cca ctg ccg agg agc	876
Arg Ser Arg Gln Ala His Ser Ala Leu Gly Ile Pro Leu Pro Arg Ser	
180 185 190	

gtg gcc cca cgg cag cgc tga tc catggagact gcgagaccgt ggcaccccta 929
 Val Ala Pro Arg Gln Arg *
 195

ctgctgggga ccacagtcct gatgtggacg cagggaaagg ggagcacata ctgccccatt 989
 ggtgcctttt cagccatctg aaaggcgggt tctttcagca ggacaggcat ttacactgat 1049
 gaaacgccac tgggagtgag gaagccagac tccagagaca cggagaagat caaactggag 1109
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 taacagaagt gtctggagta gttttcagggt ataggaatga gatgcctcgt ggtgaaagga 1349
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 ggggctctcc aagctgggca tttgggcctg gtggatgcc aacctggataa cctgtggccc 1469
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 tccctgccct tgagtgcag cccagggtact taatgtggcc atcgggcac aagcacaagg 1589
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 aaaaaaatgg taccacgtg ggcattgaaa tggggcagat taggggacca ctggactcag 2009
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 aaagggtcct agaagaaaaa aaaaaaaaaa 2098

<210> 17
 <211> 2099
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (119)..(580)

<400> 17

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ccgggaaccg ttcccggggcc gttgatcttc ggccccacac gcagagaggg gcagcagg      118
atg aat gtg ggc aca gcg cac agc gag gtg aac ccc aac acg cgg gtg      166
Met Asn Val Gly Thr Ala His Ser Glu Val Asn Pro Asn Thr Arg Val
  1             5             10             15

atg aac agc cgt ggc atc tgg ctc tcc tac gtg ctg gcc atc ggt ctc      214
Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu
             20             25             30

ctc cac atc gtg ctg ctg agc atc ccg ttt gtg agt gtc cct gtc gtc      262
Leu His Ile Val Leu Leu Ser Ile Pro Phe Val Ser Val Pro Val Val
             35             40             45

tgg acc ctc acc aac ctc att cac aac atg ggc atg tat atc ttc ctg      310
Trp Thr Leu Thr Asn Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu
             50             55             60

cac acg gtg aag ggg aca ccc ttt gag acc ccg gac cag ggc aag gcg      358
His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala
             65             70             75             80

agg ctg cta acc cac tgg gag cag atg gat tat ggg gtc cag ttc acg      406
Arg Leu Leu Thr His Trp Glu Gln Met Asp Tyr Gly Val Gln Phe Thr
             85             90             95

gcc tct cgg aag ttc ttg acc atc aca ccc atc gtg ctg tac ttc ctc      454
Ala Ser Arg Lys Phe Leu Thr Ile Thr Pro Ile Val Leu Tyr Phe Leu
             100             105             110

acc agc ttc tac act aag tac gac cag atc cat ttt gtg ctc aac acc      502
Thr Ser Phe Tyr Thr Lys Tyr Asp Gln Ile His Phe Val Leu Asn Thr
             115             120             125

gtg tcc ctg atg agc gtg ctt atc ccc aag ctg ccc cag ctc cac gga      550
Val Ser Leu Met Ser Val Leu Ile Pro Lys Leu Pro Gln Leu His Gly
             130             135             140

gtc cgg att ttt gga atc aat aag tac tga g agtgcagccc cttccccctgc      601
Val Arg Ile Phe Gly Ile Asn Lys Tyr *
145             150

ccaggggtggc aggggagggg tagggtaaaa ggcattgtgct gcaacactga agacagaaag      661

aagaagcctc tggacactgc cagagatggg gggttagcct ctggcctaata tccccccctc      721

gcttccccca gtagccaact tggagtagct tgtagtgggg ttggggtagg ccccttgggc      781

tctgaccttt tctgaatttt ttgatctttt ccttttgctt tttgaataga gactccatgg      841

agttggtcat ggaatgggct gggctcctgg gctgaacatg gaccacgcag ttgcgacagg      901

aggccagggg aaaaaccctt gctcatttgt ttgcctcag gcagccaaag cactttaacc      961

cctgcatagg gagcagaggg cggtacggct tctggattgt ttcactgtga ttcctaggtt      1021

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ttttcgatgc cacgcagtgt gtgcttttgt gtatggaagc aagtgtggga tgggtctttg 1081
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ccaccgtggg tcctggttgg gagtggggag ggtcagggtt gggaaagatg gggtagagtg 1201
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gttggggagc tgtaggagag ctagtgagtc gagacttaga agaatggggc cacatagcag 1321
cagaggactg gtgtaaggga gggaggggta gggacagaag ctagacccaa tctccttttg 1381
gatgtgggca gggaggggaag caggccttga gggtaattt acccacagaa tgtgatagta 1441
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ggaaaaggcc cgtgagtcac tgtaagcaca ggtccaactt ggccctgact cctgcggggg 1561
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gtgttaattt tgaaaagggt tgggtccctg tgcctcttc caggggtcca agggaacagg 1921
agaggtcact gggcctgttt tctccctcct gaccctgcat ctcccacccc gtgtatcata 1981
gggaactttc accttaaaat ctttctaagc aaagtgtgaa taggattttt actccctttg 2041
tacagtattc tgagaaacgc aaataaaagg gcaacatggt tctgttaaaa aaaaaaaaa 2099

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<210> 18
<211> 1605
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (535)..(1050)

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gctggtaact ttggcgctc cgccaagccc tgccagactc ccctggctgt gatggcattc 180
tgtgccatcc tccttgctcc cagcctctgc aggatgcct ccctaccac ctctccctgg 240

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gccttccctg tccactgggc tggattcatg ttcaaaccac tggactggca gggcaacgac 300
 ttcttccccc ctcaagatga ggtcctcgcc cccttgtctt ggcataaaaa cacctttaaa 360
 gcatgagcca tgtgcttctt tgcccttctc tgtcctgttc caatcttctg cctcccagtc 420
 actccctggg gactatggga tcaactgtccc cccacctgtg tggccacacc atgtgtcctg 480
 tcaatccaga actgcctctg agctccaggc tgaccacaga tcagccacag cctg atg 537
 Met
 1
 cct gca gcc cca ctt tgc tca ccc ttc ccc tcc cct cct cct tcc ttc 585
 Pro Ala Ala Pro Leu Cys Ser Pro Phe Pro Ser Pro Pro Pro Ser Phe
 5 10 15
 cac aca gca agc cta cct ttc tcc atc cat gct cac cat agc ccc ctt 633
 His Thr Ala Ser Leu Pro Phe Ser Ile His Ala His His Ser Pro Leu
 20 25 30
 cct tgt gac ttg gac cct cca ttg tac ctg gct gag act gtc agc ctc 681
 Pro Cys Asp Leu Asp Pro Pro Leu Tyr Leu Ala Glu Thr Val Ser Leu
 35 40 45
 ctg gag gag tgg ggt cca cct tct tct tgc cct atg cag tgc aag ctc 729
 Leu Glu Glu Trp Gly Pro Pro Ser Ser Cys Pro Met Gln Cys Lys Leu
 50 55 60 65
 act tct cac cca gca agg ttg act cat ctg cct cca tgt ctc tgg ggc 777
 Thr Ser His Pro Ala Arg Leu Thr His Leu Pro Pro Cys Leu Trp Gly
 70 75 80
 ttt gct gtt gcc ctg aaa cct agc tgg gct ggt ctt gct ccc agc ttg 825
 Phe Ala Val Ala Leu Lys Pro Ser Trp Ala Gly Leu Ala Pro Ser Leu
 85 90 95
 ctt ccc cct cct cgg atg tcc ctt tgc agg ccc ctg tgg ttc ctc cgg 873
 Leu Pro Pro Pro Arg Met Ser Leu Cys Arg Pro Leu Ser Phe Leu Arg
 100 105 110
 cac cag tgt cct tgg ctg cca tgg caa gct cat cag ggg ctt gta ccc 921
 His Gln Cys Pro Trp Leu Pro Trp Gln Ala His Gln Gly Leu Val Pro
 115 120 125
 tgg tca cca agc atg gta gca gct gcc tgc att gta tct cca tct ggt 969
 Trp Ser Pro Ser Met Val Ala Ala Ala Cys Ile Val Ser Pro Ser Gly
 130 135 140 145
 cac tgc agg tgc caa ccc ttc atc ccc cat gtt ttc ctg ggc cat gga 1017
 His Cys Arg Cys Gln Pro Phe Ile Pro His Val Phe Leu Gly His Gly
 150 155 160
 ggg ctg acc tcc gtt tct ggg gaa tgt ggc tga gctgtggt aaccagctac 1068
 Gly Leu Thr Ser Val Ser Gly Glu Cys Gly *
 165 170
 accccaggtg ctctttccat ggtggtgcct gctcatcttg ctgatgcaaa ctaggaagtt 1128

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aggctgcatc tcggagtggc tttcgctgga gaggtgcttt gctgtctctc agactcagtc 1188
actgtgttcc ctccccgcct ctcttatctc catggctggt tgcagctctc ccaggtactt 1248
tgggggtctga gctggaattc ctttgtgggt tgctcttctg cttctcactc ttgtattaag 1308
aaggattcca caaagggaga gtggcatccc tgctgctgct gtgccagacc agagtttccct 1368
gagggggccct gaccctaacc ctccagctca gccctgtaca cctgaccctg taaatgagtg 1428
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gtgagagcca gggttaccta ctctgccaag tgaggacaaa ctgctaggct gtatcccata 1548
atttcaggat gagaaacatt aacaataaaa atttgtagta aacataaaaa aaaaaaa 1605

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<210> 19
<211> 1497
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (210)..(1172)

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tgggcggggag cccttgctctg ggtctcgcg gggtctgcca gatgcgtagg ccacactgac 180
tagttccttc ttgtcgcttt tcccagcaa atg gcg gat gac gcc ggt gca gcg 233
Met Ala Asp Asp Ala Gly Ala Ala
1 5

ggg ggg ccc ggg ggc cct ggt ggc cct ggg atg ggg aac cgc ggt ggc 281
Gly Gly Pro Gly Gly Pro Gly Gly Pro Gly Met Gly Asn Arg Gly Gly
10 15 20

ttc cgc gga ggt ttc ggc agt ggc atc cgg ggc cgg ggt cgc ggc cgt 329
Phe Arg Gly Gly Phe Gly Ser Gly Ile Arg Gly Arg Gly Arg Gly Arg
25 30 35 40

gga cgg ggc cgg ggc cga ggc cgc gga gct cgc gga ggc aag gcc gag 377
Gly Arg Gly Arg Gly Arg Gly Arg Gly Ala Arg Gly Gly Lys Ala Glu
45 50 55

gat aag gag tgg atg ccc gtc acc aag ttg ggc cgc ttg gtc aag gac 425
Asp Lys Glu Trp Met Pro Val Thr Lys Leu Gly Arg Leu Val Lys Asp
60 65 70

atg aag atc aag tcc ctg gag gag atc tat ctc ttc tcc ctg ccc att 473

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Met	Lys	Ile	Lys	Ser	Leu	Glu	Glu	Ile	Tyr	Leu	Phe	Ser	Leu	Pro	Ile		
		75					80					85					
aag	gaa	tca	gag	atc	att	gat	ttc	ttc	ctg	ggg	gcc	tct	ctc	aag	gat	521	
Lys	Glu	Ser	Glu	Ile	Ile	Asp	Phe	Phe	Leu	Gly	Ala	Ser	Leu	Lys	Asp		
	90					95				100							
gag	gtt	ttg	aag	att	atg	cca	gtg	cag	aag	cag	acc	cgt	gcc	ggc	cag	569	
Glu	Val	Leu	Lys	Ile	Met	Pro	Val	Gln	Lys	Gln	Thr	Arg	Ala	Gly	Gln		
105					110					115					120		
cgc	acc	agg	ttc	aag	gca	ttt	gtt	gct	atc	ggg	gac	tac	aat	ggc	cac	617	
Arg	Thr	Arg	Phe	Lys	Ala	Phe	Val	Ala	Ile	Gly	Asp	Tyr	Asn	Gly	His		
				125					130					135			
gtc	ggc	ctg	ggc	gtt	aag	tgc	tcc	aag	gag	gtg	gcc	acc	gcc	atc	cgt	665	
Val	Gly	Leu	Gly	Val	Lys	Cys	Ser	Lys	Glu	Val	Ala	Thr	Ala	Ile	Arg		
			140					145					150				
ggg	gcc	atc	atc	ctg	gcc	aag	ctc	tcc	atc	gtc	ccc	gtg	cgc	aga	ggc	713	
Gly	Ala	Ile	Ile	Leu	Ala	Lys	Leu	Ser	Ile	Val	Pro	Val	Arg	Arg	Gly		
		155					160					165					
tac	tgg	ggg	aac	aag	atc	ggc	aag	ccc	cac	act	gtc	cct	tgc	aag	gtg	761	
Tyr	Trp	Gly	Asn	Lys	Ile	Gly	Lys	Pro	His	Thr	Val	Pro	Cys	Lys	Val		
	170					175					180						
aca	gcg	tgg	ggc	cat	cat	cct	ggc	caa	gct	ctc	cat	cgt	ccc	cgt	gcg	809	
Thr	Ala	Trp	Gly	His	His	Pro	Gly	Gln	Ala	Leu	His	Arg	Pro	Arg	Ala		
185					190					195					200		
cag	agg	cta	ctg	ggg	gaa	caa	gat	cgg	caa	gcc	cca	cac	tgt	cac	ctt	857	
Gln	Arg	Leu	Leu	Gly	Glu	Gln	Asp	Arg	Gln	Ala	Pro	His	Cys	His	Leu		
				205				210						215			
gca	agg	gac	agt	gtg	ggg	ctt	gcc	gat	ctt	gtt	ccc	cca	gta	gcc	tct	905	
Ala	Arg	Asp	Ser	Val	Gly	Leu	Ala	Asp	Leu	Val	Pro	Pro	Val	Ala	Ser		
			220					225					230				
gcg	cac	ggg	gac	gat	gga	gag	ctt	ggc	cag	gat	gat	ggc	ccc	acg	gat	953	
Ala	His	Gly	Asp	Asp	Gly	Glu	Leu	Gly	Gln	Asp	Asp	Gly	Pro	Thr	Asp		
		235					240					245					
ggc	ggc	ggc	cac	ctc	ctt	gga	gca	ctt	aac	acc	cag	acc	gac	gtg	gcc	1001	
Gly	Gly	Gly	His	Leu	Leu	Gly	Ala	Leu	Asn	Thr	Gln	Thr	Asp	Val	Ala		
		250				255					260						
att	gta	gtc	ccc	gat	agc	aac	aaa	tgc	ctt	gaa	cct	ggc	gcg	ctg	gcc	1049	
Ile	Val	Val	Pro	Asp	Ser	Asn	Lys	Cys	Leu	Glu	Pro	Gly	Ala	Leu	Ala		
265					270					275					280		
ggc	acg	ggc	ctg	ctt	ctg	cac	tgg	cat	aat	ctt	caa	aac	ctc	atc	ctt	1097	
Gly	Thr	Gly	Leu	Leu	Leu	His	Trp	His	Asn	Leu	Gln	Asn	Leu	Ile	Leu		
				285				290						295			
gag	aga	ggg	cac	cac	aca	gtg	aac	gaa	agt	caa	atg	agt	gct	gct	gat	1145	
Glu	Arg	Gly	His	His	Thr	Val	Asn	Glu	Ser	Gln	Met	Ser	Ala	Ala	Asp		

300	305	310	
tcc tta ata ggc agg gag aag aga tag atcac cactccaggg acttagatct			1197
Ser Leu Ile Gly Arg Glu Lys Arg *			
315	320		

tcatgtcctt ggaccaagcg gccacaactt cggtgacggg gcatccactc cttatcgctc	1257
ggccttgcgc tccagcgagc tccgcaggca catcgggcca caggccacac agtcacacag	1317
gccgcagacc accaggccac cagagtgcac agcatgcaca gaaacactgc cgcaggaagc	1377
acacacagcg gcttcccaca tcacaagggc cacaatgggc ccccagggcc caccgctg	1437
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<210> 20
 <211> 907
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
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	Met
	1

acg aac gtg tac tcc ttg gat ggg att ctg gtg ttt ggt ttg ctc ttt	164
Thr Asn Val Tyr Ser Leu Asp Gly Ile Leu Val Phe Gly Leu Leu Phe	
5 10 15	

gtt tgc acc tgt gcc tac ttc aag aaa gta cct cgt ctc aaa acc tgg	212
Val Cys Thr Cys Ala Tyr Phe Lys Lys Val Pro Arg Leu Lys Thr Trp	
20 25 30	

ctg cta tca gag aag aag ggt gtt tgg ggt gtg ttt tac aaa gcc gct	260
Leu Leu Ser Glu Lys Lys Gly Val Trp Gly Val Phe Tyr Lys Ala Ala	
35 40 45	

gtg att gga acc agg ctg cat gct gct gtg gca att gct tgt gtt gta	308
Val Ile Gly Thr Arg Leu His Ala Ala Val Ala Ile Ala Cys Val Val	
50 55 60 65	

atg gcc ttt tac gtc ctg ttt ata aaa tga a ttccaaagca cccaagtcac	359
Met Ala Phe Tyr Val Leu Phe Ile Lys *	
70 75	

caactgccaa ccaaggggac ggggatgaag aacctgttgg agacctgaac ccagtgtagg	419
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agagttcagc tgaaatcatc ggtccccagg atgacaccac agcatctgcc cctgctatat 479
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ttggccgg 907

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<210> 21
<211> 1329
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (103)..(1116)

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Met Gly Lys Val
1

aag gtc gga gtc aac gga ttt ggt cgt att ggg cgc ctg gtc acc agg 162
Lys Val Gly Val Asn Gly Phe Gly Arg Ile Gly Arg Leu Val Thr Arg
5 10 15 20

gct gct ttt aac tct ggt aaa gtg gat att gtt gcc atc aat gac ccc 210
Ala Ala Phe Asn Ser Gly Lys Val Asp Ile Val Ala Ile Asn Asp Pro
25 30 35

ttc att gac ctc aac tac atg gtt tac atg ttc caa tat gat tcc acc 258
Phe Ile Asp Leu Asn Tyr Met Val Tyr Met Phe Gln Tyr Asp Ser Thr
40 45 50

cat ggc aaa ttc cat ggc acc gtc aag gct gag aac ggg aag ctt gtc 306
His Gly Lys Phe His Gly Thr Val Lys Ala Glu Asn Gly Lys Leu Val
55 60 65

atc aat gga aat ccc atc acc atc ttc cag gag cga gat ccc tcc aaa 354
Ile Asn Gly Asn Pro Ile Thr Ile Phe Gln Glu Arg Asp Pro Ser Lys
70 75 80

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atc aag tgg ggc gat gct ggc gct gag tac gtc gtg gag tcc act ggc	402
Ile Lys Trp Gly Asp Ala Gly Ala Glu Tyr Val Val Glu Ser Thr Gly	
85 90 95 100	
gtc ttc acc acc atg gag aag gct ggg gct cat ttg cag ggg gga gcc	450
Val Phe Thr Thr Met Glu Lys Ala Gly Ala His Leu Gln Gly Gly Ala	
105 110 115	
aaa agg gtc atc atc tct gcc ccc tct gct gat gcc ccc atg ttc gtc	498
Lys Arg Val Ile Ile Ser Ala Pro Ser Ala Asp Ala Pro Met Phe Val	
120 125 130	
atg ggt gtg aac cat gag aag tat gac aac agc ctc aag atc atc agc	546
Met Gly Val Asn His Glu Lys Tyr Asp Asn Ser Leu Lys Ile Ile Ser	
135 140 145	
aat gcc tcc tgc acc acc aac tgc tta gca ccc ctg gcc aag gtc atc	594
Asn Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu Ala Lys Val Ile	
150 155 160	
cat gac aac ttt ggt atc gtg gaa gga ctc atg acc aca gtc cat gcc	642
His Asp Asn Phe Gly Ile Val Glu Gly Leu Met Thr Thr Val His Ala	
165 170 175 180	
atc act gcc acc cag aag act gtg gga tgg ccc ctt ccg gga aac tgt	690
Ile Thr Ala Thr Gln Lys Thr Val Gly Trp Pro Leu Pro Gly Asn Cys	
185 190 195	
ggc gtg atg gcc gcg ggg gcg tct gcc aga aac atc atc cct gcc tct	738
Gly Val Met Ala Ala Gly Ala Ser Ala Arg Asn Ile Ile Pro Ala Ser	
200 205 210	
act ggc gct gcc aag gct gtg ggc aag gtc atc cct gag ctg aac ggg	786
Thr Gly Ala Ala Lys Ala Val Gly Lys Val Ile Pro Glu Leu Asn Gly	
215 220 225	
aag ctc act ggc atg gcc ttc cgt gtc ccc act gcc aac gtg tca gtg	834
Lys Leu Thr Gly Met Ala Phe Arg Val Pro Thr Ala Asn Val Ser Val	
230 235 240	
gtg gac ctg acc tgc cgt cta gaa aaa cct gcc aaa tat gat gac atc	882
Val Asp Leu Thr Cys Arg Leu Glu Lys Pro Ala Lys Tyr Asp Asp Ile	
245 250 255 260	
aag aag gtg gtg aag cag gcg tcg gag ggc ccc ctc aag ggc atc ctg	930
Lys Lys Val Val Lys Gln Ala Ser Glu Gly Pro Leu Lys Gly Ile Leu	
265 270 275	
ggc tac act gag cac cag gtg gtc tcc tct gac ttc aac agc gac acc	978
Gly Tyr Thr Glu His Gln Val Val Ser Ser Asp Phe Asn Ser Asp Thr	
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cac tcc tcc acc ttt gac gct ggg gct ggc att gcc ctc aac gac cac	1026
His Ser Ser Thr Phe Asp Ala Gly Ala Gly Ile Ala Leu Asn Asp His	
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Phe Val Lys Leu Ile Ser Trp Tyr Asp Asn Glu Phe Gly Tyr Ser Asn	
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Arg Val Val Asp Leu Met Ala His Met Ala Ser Lys Glu *	
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cctgccacac tcagtcccc accacactga atctcccctc ctcacagttg ccatgtagac	1243
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ctc ttc act ctg gcc tcg ctg agc ggc tgc ccg agg agg agc tct agg	585
Leu Phe Thr Leu Ala Ser Leu Ser Gly Cys Pro Arg Arg Ser Ser Arg	
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Pro Thr Pro Thr Ala Gly Leu Thr Val Phe Ser Gly Arg Ser Leu Ala	
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gat gca ccg tgg cct ggc ggc gag ccc ccg gtc acc ttc ctc cgc acg	681

Asp	Ala	Pro	Trp	Pro	Gly	Gly	Glu	Pro	Pro	Val	Thr	Phe	Leu	Arg	Thr		
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Glu	Glu	Gly	Pro	Asp	Ala	Thr	Phe	Pro	Arg	Thr	Ile	Pro	Leu	Ile	Gln		
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cag ttg cta aac gcc acg gag ctc acg cag gac ccg gcc gcc tac tcc																	777
Gln	Leu	Leu	Asn	Ala	Thr	Glu	Leu	Thr	Gln	Asp	Pro	Ala	Ala	Tyr	Ser		
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cag ctg gtg gcc gtg ctg gtc tac acc gcc gag cgg gcc aag ttc gcc																	825
Gln	Leu	Val	Ala	Val	Leu	Val	Tyr	Thr	Ala	Glu	Arg	Ala	Lys	Phe	Ala		
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Thr	Gly	Val	Glu	Arg	Gln	Asp	Trp	Met	Glu	Leu	Phe	Ile	Asp	Thr	Phe		
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Lys	Leu	Val	His	Arg	Asp	Ile	Val	Gly	Asp	Pro	Glu	Thr	Ala	Leu	Ala		
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Leu	Cys	*															
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	Met Asn	
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Ala Gly Pro Ser Trp Asn Lys Val Gln His Ser Lys Asn Ser Ser Gly		
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aaa agg cag agt aaa tcc caa gta ccc cac gct tct tcc cag ccg aga		392
Lys Arg Gln Ser Lys Ser Gln Val Pro His Ala Ser Ser Gln Pro Arg		
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Ser Ser Leu Thr Ala Val Thr Gln Pro Thr Glu Glu Lys Leu Lys Glu		
35 40 45 50		
agc att tcc ccg gaa gca aga cgc aaa agg aat cca ctc ggt tcc agg		488
Ser Ile Ser Pro Glu Ala Arg Arg Lys Arg Asn Pro Leu Gly Ser Arg		
55 60 65		
tgt cag ggg gcc tca ggg aat aaa ctg ttt ctt gat ttt cag tca atg		536
Cys Gln Gly Ala Ser Gly Asn Lys Leu Phe Leu Asp Phe Gln Ser Met		
70 75 80		
aaa att att aaa gag aat gct gat gag gac agt gca agt gat ctc tct		584
Lys Ile Ile Lys Glu Asn Ala Asp Glu Asp Ser Ala Ser Asp Leu Ser		
85 90 95		
gat tcg gaa aga att ccc att cct cct tct ccc ctc aca cct cca gat		632
Asp Ser Glu Arg Ile Pro Ile Pro Pro Ser Pro Leu Thr Pro Pro Asp		
100 105 110		
ctc aat ctt cga gct gaa gaa att gat cca gtt tac ttt gat ctt cac		680
Leu Asn Leu Arg Ala Glu Glu Ile Asp Pro Val Tyr Phe Asp Leu His		
115 120 125 130		
cct ggt cag ggc cat aca aaa cct gaa tac tat tat cct aat ttc ctt		728
Pro Gly Gln Gly His Thr Lys Pro Glu Tyr Tyr Tyr Pro Asn Phe Leu		
135 140 145		
cca tcc cct ttc agc tcc tgg gac cta cga gat atg gcc ctg ctt ctg		776
Pro Ser Pro Phe Ser Ser Trp Asp Leu Arg Asp Met Ala Leu Leu Leu		
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Asn Ala Glu Asn Lys Thr Glu Ala Val Pro Arg Val Gly Gly Leu Leu		
165 170 175		
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Gly Lys Tyr Ile Asp Arg Leu Ile Gln Leu Glu Trp Leu Gln Val Gln		
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act gta cag tgt gaa aaa gca aag ggg ggc aaa gca agg ccc ccc act		920
Thr Val Gln Cys Glu Lys Ala Lys Gly Gly Lys Ala Arg Pro Pro Thr		
195 200 205 210		

gcc cct ggg acc tca ggg gca ctg aaa agc cct ggg aga agt aag cta 968
Ala Pro Gly Thr Ser Gly Ala Leu Lys Ser Pro Gly Arg Ser Lys Leu
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Ile Ala Ser Ala Leu Ser Lys Pro Leu Pro His Gln Glu Gly Ala Ser
230 235 240

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Lys Ser Gly Pro Ser Arg Lys Lys Ala Phe His His Glu Glu Ile His
245 250 255

cca tca cat tat gca ttt gag act tcc cct aga ccc att gat gtg ctt 1112
Pro Ser His Tyr Ala Phe Glu Thr Ser Pro Arg Pro Ile Asp Val Leu
260 265 270

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Gly Gly Thr Arg Phe Cys Ser Gln Arg Gln Thr Leu Glu Met Arg Thr
275 280 285 290

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Glu Glu Lys Lys Lys Lys Ser Ser Lys Ser Thr Lys Leu Gln Arg Trp
295 300 305

gat ctg tcc ggc agt gga agc agc tct aag gtg gaa acc agc ggt cac 1256
Asp Leu Ser Gly Ser Gly Ser Ser Ser Lys Val Glu Thr Ser Gly His
310 315 320

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Ile Arg Val Pro Lys Gln Ala Ala Val Ile Leu Asp Ser Ala Asp Ser
325 330 335

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Cys Lys Ala Ser Lys Thr Gln Ala His Ala His Pro Arg Lys Lys Gly
340 345 350

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Lys Ala Glu Ser Cys Gly His Ala Thr Val Ser Ser Glu Lys Lys Leu
355 360 365 370

aaa aca aac gga gta aag caa aac aca tat aaa cta aaa taa atatcta 1449
Lys Thr Asn Gly Val Lys Gln Asn Thr Tyr Lys Leu Lys *
375 380

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cat cag cca ggt agt atc aga ctt gct acc acc cct gta agg gta gat      156
His Gln Pro Gly Ser Ile Arg Leu Ala Thr Thr Pro Val Arg Val Asp
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gaa ttt aaa tat caa atg act cgg act ggc tgg cat gca aca gaa cag      204
Glu Phe Lys Tyr Gln Met Thr Arg Thr Gly Trp His Ala Thr Glu Gln
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tat ctc att gaa cct gaa aaa att caa gag atg ttc cct tta ctc aac      252
Tyr Leu Ile Glu Pro Glu Lys Ile Gln Glu Met Phe Pro Leu Leu Asn
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atg aat aag gtt tta gct gga ttg tat aat cct gga gat ggt cac att      300
Met Asn Lys Val Leu Ala Gly Leu Tyr Asn Pro Gly Asp Gly His Ile
             65             70             75

gat cct tat tct cta act atg gca ctg gct gct ggg gct agg aaa tgt      348
Asp Pro Tyr Ser Leu Thr Met Ala Leu Ala Ala Gly Ala Arg Lys Cys
             80             85             90

ggg gcc ctt tta aaa tat cct gca cca gta act tct ctg aaa gcc agg      396
Gly Ala Leu Leu Lys Tyr Pro Ala Pro Val Thr Ser Leu Lys Ala Arg
             95             100             105

tca gat gga aca tgg gac gtt gaa aca cca cag ggg tct atg aga gca      444
Ser Asp Gly Thr Trp Asp Val Glu Thr Pro Gln Gly Ser Met Arg Ala
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aat aga att gtg aat gct gca gga ttt tgg gct cgt gaa gta ggt aaa      492
Asn Arg Ile Val Asn Ala Ala Gly Phe Trp Ala Arg Glu Val Gly Lys
             130             135             140

atg att gga cta gaa cat cct ctc att ccg gtt caa cat caa tat gtt      540
Met Ile Gly Leu Glu His Pro Leu Ile Pro Val Gln His Gln Tyr Val
             145             150             155

gtt aca tcg act ata tct gaa gtg aaa gct ttg aaa cga gaa ctg cct      588
Val Thr Ser Thr Ile Ser Glu Val Lys Ala Leu Lys Arg Glu Leu Pro
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Val Leu Arg Asp Leu Glu Gly Ser Tyr Tyr Leu Arg Gln Glu Arg Asp
             175             180             185

ggg ctt ttg ttt ggt cca tat gaa agt caa gag aaa atg aaa gtt cag      684
Gly Leu Leu Phe Gly Pro Tyr Glu Ser Gln Glu Lys Met Lys Val Gln
             190             195             200             205

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Phe Glu Ser Asp Leu Asp Arg Ile Met Glu His Ile Lys Ala Ala Met	
225 230 235	
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Glu Met Val Pro Val Leu Lys Lys Ala Asp Ile Ile Asn Val Val Asn	
240 245 250	
ggg cct atc acg tat tct cct gac att ctg cct atg gtg ggg ccc cat	876
Gly Pro Ile Thr Tyr Ser Pro Asp Ile Leu Pro Met Val Gly Pro His	
255 260 265	
cag ggg gtc aga aac tac tgg gtg gct ata ggc ttt gga tat ggc ata	924
Gln Gly Val Arg Asn Tyr Trp Val Ala Ile Gly Phe Gly Tyr Gly Ile	
270 275 280 285	
atc cac gct ggt ggg gta ggg aaa tat ctc agt gac tgg atc ctg cat	972
Ile His Ala Gly Gly Val Gly Lys Tyr Leu Ser Asp Trp Ile Leu His	
290 295 300	
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Gly Glu Pro Pro Phe Asp Leu Ile Glu Leu Asp Pro Asn Arg Tyr Gly	
305 310 315	
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Lys Trp Thr Thr Thr Gln Tyr Thr Glu Ala Lys Ala Arg Glu Ser Tyr	
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Arg Pro Thr Gln Arg Val Ser Gly Leu Tyr Gln Arg Leu Glu Ser Lys	
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370 375 380	
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Lys Pro Gly Gln Asp Thr Gln Tyr Arg Pro Ser Phe Arg His Thr Asn	
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Trp Phe Glu Pro Val Gly Ser Glu Tyr Lys Gln Val Met Gln Arg Val	
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Gly Val Thr Asp Leu Ser Pro Phe Gly Lys Phe Asn Ile Lys Gly Gln	
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430 435 440 445	
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Tyr Ala Glu Leu Thr Val Ser His Gln Ser Pro Gly Glu Phe Leu Leu	
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Ile Thr Gly Ser Gly Ser Glu Leu His Asp Leu Arg Trp Ile Glu Glu	
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Glu Ala Val Lys Gly Gly Tyr Asp Val Glu Ile Lys Asn Ile Thr Asp	
495 500 505	
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Gln Lys Leu Thr Pro Glu Asp Leu Ser Asp Asp Val Phe Lys Phe Leu	
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Ile Ser Tyr Thr Gly Glu Leu Gly Trp Glu Leu Tyr His Arg Arg Glu	
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Ser	Gly	Ser	Tyr	Ser	Tyr	Ser	Ile	Gln	Lys	Ser	Leu	Ala	Phe	Ala	Tyr		
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Leu	Gly	Lys	Asn	Tyr	Pro	Ala	Val	Ile	Ile	Gln	Glu	Pro	Leu	Val	Leu		
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Thr	Glu	Pro	Thr	Arg	Asn	Arg	Leu	Gln	Lys	Lys	Gly	Gly	Lys	Asp	Lys		
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Glu His Ile Ala His Phe Leu Gly Thr Gly Gly Ala Ala Thr Thr Met	
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Gly Asn Ser Cys Ile Cys Arg Asp Asp Ser Gly Thr Asp Asp Ser Val	
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Asp Thr Gln Gln Gln Gln Ala Glu Asn Ser Ala Val Pro Thr Ala Asp	
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Thr Arg Ser Gln Pro Arg Asp Pro Val Arg Pro Pro Arg Arg Gly Arg	
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Gly Pro His Glu Pro Arg Arg Lys Lys Gln Asn Val Asp Gly Leu Val	
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Leu Asp Thr Leu Ala Val Ile Arg Thr Leu Val Asp Asn Asp Gln Glu	
105 110 115 120	
cct ccc tat tca atg ata aca tta cac gaa atg gca gaa aca gat gaa	1037
Pro Pro Tyr Ser Met Ile Thr Leu His Glu Met Ala Glu Thr Asp Glu	
125 130 135	
gga tgg ttg gat gtt gtc cag tct tta att aga gtt att cca ctg gaa	1085
Gly Trp Leu Asp Val Val Gln Ser Leu Ile Arg Val Ile Pro Leu Glu	

140	145	150	
gat cca ctg gga cca gct gtt ata aca ttg tta cta gat gaa tgt cca Asp Pro Leu Gly Pro Ala Val Ile Thr Leu Leu Leu Asp Glu Cys Pro 155 160 165			1133
ttg ccc act aaa gat gca ctc cag aaa ttg act gaa att ctc aat tta Leu Pro Thr Lys Asp Ala Leu Gln Lys Leu Thr Glu Ile Leu Asn Leu 170 175 180			1181
aat gga gaa gta gct tgc cag gac tca agc cat cct gcc aaa cac agg Asn Gly Glu Val Ala Cys Gln Asp Ser Ser His Pro Ala Lys His Arg 185 190 195 200			1229
aac aca tct gca gtc cta ggc tgc ttg gcc gag aaa cta gca ggt cct Asn Thr Ser Ala Val Leu Gly Cys Leu Ala Glu Lys Leu Ala Gly Pro 205 210 215			1277
gca agt ata ggt tta ctt agc cca gga ata ctg gaa tac ttg cta cag Ala Ser Ile Gly Leu Leu Ser Pro Gly Ile Leu Glu Tyr Leu Leu Gln 220 225 230			1325
tgt ctg aag tta cag tcc cac ccc aca gtc atg ctt ttt gca ctt atc Cys Leu Lys Leu Gln Ser His Pro Thr Val Met Leu Phe Ala Leu Ile 235 240 245			1373
gca ctg gaa aag ttt gca cag aca agt gaa aat aaa ttg act att tct Ala Leu Glu Lys Phe Ala Gln Thr Ser Glu Asn Lys Leu Thr Ile Ser 250 255 260			1421
gaa tcc agt att agt gac cgg ctt gtc aca ttg gag tcc tgg gct aat Glu Ser Ser Ile Ser Asp Arg Leu Val Thr Leu Glu Ser Trp Ala Asn 265 270 275 280			1469
gat cct gat tat ctg aaa cgt caa gtt ggt ttc tgt gcc cag tgg agc Asp Pro Asp Tyr Leu Lys Arg Gln Val Gly Phe Cys Ala Gln Trp Ser 285 290 295			1517
tta gac aat ctc ttt tta aaa gaa ggt aga cag ctg acc tat gag aaa Leu Asp Asn Leu Phe Leu Lys Glu Gly Arg Gln Leu Thr Tyr Glu Lys 300 305 310			1565
gtg aac ttg agt agc att agg gcc atg ctg aat agc aat gat gtc agc Val Asn Leu Ser Ser Ile Arg Ala Met Leu Asn Ser Asn Asp Val Ser 315 320 325			1613
gag tac ctg aag atc tca cct cat ggc tta gag gct cgc tgt gat gcc Glu Tyr Leu Lys Ile Ser Pro His Gly Leu Glu Ala Arg Cys Asp Ala 330 335 340			1661
tcc tct ttt gaa agt gtg cgt tgc acc ttt tgt gtg gat gcc ggg gta Ser Ser Phe Glu Ser Val Arg Cys Thr Phe Cys Val Asp Ala Gly Val 345 350 355 360			1709
tgg tac tat gaa gta aca gtg gtc act tct ggc gtc atg cag att ggc Trp Tyr Tyr Glu Val Thr Val Val Thr Ser Gly Val Met Gln Ile Gly 365 370 375			1757

tgg gcc act cga gac agc aaa ttc ctc aat cat gaa ggc tac ggc att	1805
Trp Ala Thr Arg Asp Ser Lys Phe Leu Asn His Glu Gly Tyr Gly Ile	
380 385 390	
ggg gat gat gaa tac tcc tgt gcg tat gat ggc tgc cgg cag ctg att	1853
Gly Asp Asp Glu Tyr Ser Cys Ala Tyr Asp Gly Cys Arg Gln Leu Ile	
395 400 405	
tgg tac aat gcc aga agt aag cct cac ata cac cca tgc tgg aaa gaa	1901
Trp Tyr Asn Ala Arg Ser Lys Pro His Ile His Pro Cys Trp Lys Glu	
410 415 420	
gga gat aca gta gga ttt ctg tta gac ttg aat gaa aag caa atg atc	1949
Gly Asp Thr Val Gly Phe Leu Leu Asp Leu Asn Glu Lys Gln Met Ile	
425 430 435 440	
ttc ttt tta aat ggc aac cag ctg cct cct gaa aag caa gtc ttt tca	1997
Phe Phe Leu Asn Gly Asn Gln Leu Pro Pro Glu Lys Gln Val Phe Ser	
445 450 455	
tct act gta tct gga ttt ttt gct gca gct agt ttc atg tca tat caa	2045
Ser Thr Val Ser Gly Phe Phe Ala Ala Ser Phe Met Ser Tyr Gln	
460 465 470	
caa tgt gag ttc aat ttt gga gca aaa cca ttc aaa tac cca cca tct	2093
Gln Cys Glu Phe Asn Phe Gly Ala Lys Pro Phe Lys Tyr Pro Pro Ser	
475 480 485	
atg aaa ttt agc act ttt aat gac tac gcc ttc cta aca gct gaa gaa	2141
Met Lys Phe Ser Thr Phe Asn Asp Tyr Ala Phe Leu Thr Ala Glu Glu	
490 495 500	
aaa atc att ttg cca agg cac agg cgt ctt gct ctg ttg aag caa gtc	2189
Lys Ile Ile Leu Pro Arg His Arg Arg Leu Ala Leu Leu Lys Gln Val	
505 510 515 520	
agt atc cga gaa aac tgc tgt tcc ctt tgt tgt gat gag gta gca gac	2237
Ser Ile Arg Glu Asn Cys Cys Ser Leu Cys Cys Asp Glu Val Ala Asp	
525 530 535	
aca caa ttg aag cca tgt gga cac agt gac ctg tgc atg gat tgt gcc	2285
Thr Gln Leu Lys Pro Cys Gly His Ser Asp Leu Cys Met Asp Cys Ala	
540 545 550	
ttg cag ctg gag acc tgc cca ttg tgt cgt aaa gaa ata gta tct aga	2333
Leu Gln Leu Glu Thr Cys Pro Leu Cys Arg Lys Glu Ile Val Ser Arg	
555 560 565	
atc aga cag att tct cat att tca tga cacat gtgaagaggc atcgtggact	2385
Ile Arg Gln Ile Ser His Ile Ser *	
570 575	
tttttctact caattccagc caatgttgaa aaaaaaaaaa a	2426

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 <211> 564
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (14)..(475)

<400> 26
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 Met Ala Ser Tyr Phe Asp Glu His Asp Cys Glu Pro
 1 5 10

tcg gac cct gag cag gag acg cga acc aac atg ctg ctg gag ctc gca 97
 Ser Asp Pro Glu Gln Glu Thr Arg Thr Asn Met Leu Leu Glu Leu Ala
 15 20 25

agg tca ctt ttc aat agg atg gac ttt gaa gac ttg ggg ttg gta gta 145
 Arg Ser Leu Phe Asn Arg Met Asp Phe Glu Asp Leu Gly Leu Val Val
 30 35 40

gat tgg gac cac cac ctg cct cca cca gct gcc aag act gtg gtt gag 193
 Asp Trp Asp His His Leu Pro Pro Pro Ala Ala Lys Thr Val Val Glu
 45 50 55 60

aac ctc ccc agg aca gtc atc aga ggc tct cag gct gag ctc aag tgc 241
 Asn Leu Pro Arg Thr Val Ile Arg Gly Ser Gln Ala Glu Leu Lys Cys
 65 70 75

ccc gtg tgt ctt ttg gaa ttt gag gag gag gag act gcc att gag atg 289
 Pro Val Cys Leu Leu Glu Phe Glu Glu Glu Glu Thr Ala Ile Glu Met
 80 85 90

cct tgc cat cac ctt ttc cat tcc agc tgc att ctg ccc tgg cta agc 337
 Pro Cys His His Leu Phe His Ser Ser Cys Ile Leu Pro Trp Leu Ser
 95 100 105

aag aca aat tcc tgt ccc ttg tgc cgc cat gag ctg ccc act gat gac 385
 Lys Thr Asn Ser Cys Pro Leu Cys Arg His Glu Leu Pro Thr Asp Asp
 110 115 120

gac act tat gag gag cac aga cga gat aag gct cga aaa cag cag cag 433
 Asp Thr Tyr Glu Glu His Arg Arg Asp Lys Ala Arg Lys Gln Gln Gln
 125 130 135 140

caa cac cga ctg gag aac ctc cat gga gcc atg tac acg tga ggaggtt 482
 Gln His Arg Leu Glu Asn Leu His Gly Ala Met Tyr Thr *
 145 150

ggggctgagt gctggccctc tgcgtcttcc ttattaacct tgaatcctca ttaaagggtt 542

ctttaccac aaaaaaaaaa aa 564

<210> 27
 <211> 609
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (18)..(581)

<400> 27

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	Met Ala Ser Tyr Phe Asp Glu His Asp Cys Glu	
	1 5 10	
ccg tcg gac cct gag cag gag acg cga acc aac atg ctg ctg gag ctc		98
Pro Ser Asp Pro Glu Gln Glu Thr Arg Thr Asn Met Leu Leu Glu Leu		
	15 20 25	
gca agg tca ctt ttc aat agg atg gac ttt gaa gac ttg ggg ttg gta		146
Ala Arg Ser Leu Phe Asn Arg Met Asp Phe Glu Asp Leu Gly Leu Val		
	30 35 40	
gta gat tgg gac cac cac ctg cct cca cca gct gcc aag act gtg gtt		194
Val Asp Trp Asp His His Leu Pro Pro Pro Ala Ala Lys Thr Val Val		
	45 50 55	
gag aac ctc ccc agg aca gtc atc aga ggc tct cag gct gct ctc acc		242
Glu Asn Leu Pro Arg Thr Val Ile Arg Gly Ser Gln Ala Ala Leu Thr		
	60 65 70 75	
gtg ccc tgg gcc cag tac tca agc ttc ttt ctg ttc atg gac tgc tgg		290
Val Pro Trp Ala Gln Tyr Ser Ser Phe Phe Leu Phe Met Asp Cys Trp		
	80 85 90	
ggg atg gaa gaa gag tgg cag ttg gga gca ggg gag ggt ggt tat cag		338
Gly Met Glu Glu Glu Trp Gln Leu Gly Ala Gly Glu Gly Gly Tyr Gln		
	95 100 105	
ctt atg aag atc aga cca agg cta gaa cac tac tct act ttt ctc aga		386
Leu Met Lys Ile Arg Pro Arg Leu Glu His Tyr Ser Thr Phe Leu Arg		
	110 115 120	
caa att cct gtc cct tgt gcc gct atg agc tgc cca ctg atg acg aca		434
Gln Ile Pro Val Pro Cys Ala Ala Met Ser Cys Pro Leu Met Thr Thr		
	125 130 135	
ctt atg agg agc aca gac gag ata agg ctc gaa aac agc agc agc aac		482
Leu Met Arg Ser Thr Asp Glu Ile Arg Leu Glu Asn Ser Ser Ser Asn		
	140 145 150 155	
acc gac tgg aga acc tcc atg gag cca tgt aca cgt gag gag gtt ggg		530
Thr Asp Trp Arg Thr Ser Met Glu Pro Cys Thr Arg Glu Glu Val Gly		
	160 165 170	
gct gag tgc tgg ccc tct gcg tct tcc tta tta acc ttg aat cct cat		578
Ala Glu Cys Trp Pro Ser Ala Ser Ser Leu Leu Thr Leu Asn Pro His		

175

180

185

taa aggtttcttt acccacaaaa aaaaaaaa

609

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<210> 28

<211> 1291

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (26)..(1057)

<400> 28

tgctggaatt ccccggcgcc gcgcc atg tgg gct gcg gcg ggc ggg ctg tgg 52

Met Trp Ala Ala Ala Gly Gly Leu Trp

1

5

cgc tcc cgc gcg ggt ctc cgg gcc ctg ttc cgt agc cgc gat gct gcg 100

Arg Ser Arg Ala Gly Leu Arg Ala Leu Phe Arg Ser Arg Asp Ala Ala

10

15

20

25

cta ttt cca ggc tgc gag cgg gga ctt cac tgc tct gct gtc tcc tgc 148

Leu Phe Pro Gly Cys Glu Arg Gly Leu His Cys Ser Ala Val Ser Cys

30

35

40

aag aac tgg ctc aag aaa ttt gcc tcg aaa acc aaa aaa aag gtt tgg 196

Lys Asn Trp Leu Lys Lys Phe Ala Ser Lys Thr Lys Lys Lys Val Trp

45

50

55

tat gaa agt cct tcc ttg ggt tct cac tcg act tac aaa cca tcc aag 244

Tyr Glu Ser Pro Ser Leu Gly Ser His Ser Thr Tyr Lys Pro Ser Lys

60

65

70

ttg gaa ttc ctc atg agg agc acc tca aag aaa acc agg aag gaa gac 292

Leu Glu Phe Leu Met Arg Ser Thr Ser Lys Lys Thr Arg Lys Glu Asp

75

80

85

cat gcg cgc ctg agg gcc ctg aac ggc ctc ctc tat aag gca ctg aca 340

His Ala Arg Leu Arg Ala Leu Asn Gly Leu Leu Tyr Lys Ala Leu Thr

90

95

100

105

gac ctg ctg tgt acc cct gaa gtg agt cag gag ctg tat gac ctt aac 388

Asp Leu Leu Cys Thr Pro Glu Val Ser Gln Glu Leu Tyr Asp Leu Asn

110

115

120

gtg gag ctc tcc aag gtt tcc ctg act cca gac ttc tca gcc tgc cga 436

Val Glu Leu Ser Lys Val Ser Leu Thr Pro Asp Phe Ser Ala Cys Arg

125

130

135

gcg tac tgg aag aca acg ctc tct gct gag cag aac gca cac atg gag 484

Ala Tyr Trp Lys Thr Thr Leu Ser Ala Glu Gln Asn Ala His Met Glu	
140 145 150	
gct gtc ctg cag aga agt gcc gcg cac atg agg cac ctt ttg atg tcc	532
Ala Val Leu Gln Arg Ser Ala Ala His Met Arg His Leu Leu Met Ser	
155 160 165	
cag cag acc ctg agg aat gtg cca ccg ata gtg ttt gtt caa gac aag	580
Gln Gln Thr Leu Arg Asn Val Pro Pro Ile Val Phe Val Gln Asp Lys	
170 175 180 185	
gga aat gca gct cta gct gag ctt gat cag tta ctg gca gtc gca gac	628
Gly Asn Ala Ala Leu Ala Glu Leu Asp Gln Leu Leu Ala Val Ala Asp	
190 195 200	
ttt gga ccc cgg gat gaa aga gac aac ttt gta caa aat gat ttc agg	676
Phe Gly Pro Arg Asp Glu Arg Asp Asn Phe Val Gln Asn Asp Phe Arg	
205 210 215	
gac cct gat gcc cca caa ccc tgc ggc acc aca gag ccg acc aca agc	724
Asp Pro Asp Ala Pro Gln Pro Cys Gly Thr Thr Glu Pro Thr Thr Ser	
220 225 230	
tcc agt ctg tgt ggg atc gat cat gag gcg ctc cac aag cag att atg	772
Ser Ser Leu Cys Gly Ile Asp His Glu Ala Leu His Lys Gln Ile Met	
235 240 245	
gag tac aaa agg agg aaa gat aaa ggg ctc ggg ggc ctg gtg tgg cag	820
Glu Tyr Lys Arg Arg Lys Asp Lys Gly Leu Gly Gly Leu Val Trp Gln	
250 255 260 265	
ggg cag gtg gct gag ctg aca acg cag atg aaa aag gga agg aag agg	868
Gly Gln Val Ala Glu Leu Thr Thr Gln Met Lys Lys Gly Arg Lys Arg	
270 275 280	
gcc aag ccc cgc ctg gag cag gac agc tcc ctc aag agt tac ctg tca	916
Ala Lys Pro Arg Leu Glu Gln Asp Ser Ser Leu Lys Ser Tyr Leu Ser	
285 290 295	
ggc gag gag gtt gaa gat gac ctg gac ctg gtt ggt gcc ccg gag tac	964
Gly Glu Glu Val Glu Asp Asp Leu Asp Leu Val Gly Ala Pro Glu Tyr	
300 305 310	
gaa tgc tat gcc ccg gac aca gag gag ttg gag gca gag aga gga ggt	1012
Glu Cys Tyr Ala Pro Asp Thr Glu Glu Leu Glu Ala Glu Arg Gly Gly	
315 320 325	
ggc aga aca gag gat ggc cac agc tgc gga gca agc agg gag tag atg	1060
Gly Arg Thr Glu Asp Gly His Ser Cys Gly Ala Ser Arg Glu *	
330 335 340	
gagaggctct gcccatccca catttgcagg gaaaagcatt ggcacgcaac gcagcatgtg 1120	
gcttcattga ggcagttgat ggagttaaac catctgctct tctgctactt caacattttc 1180	
tagcttttcc gtgtatctaa acacaatttg ctacacaagt cactgttttt ttttccatgc 1240	

actgtgtgta atttaaaaat taaatggcca tcttatcaca aaaaaaaaaa a

1291

<210> 29
 <211> 766
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (103)..(759)

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ggcggctgca ggcttcagcc tgcgctgggtt ggtgaaacag ag atg tca gaa aag 114
 Met Ser Glu Lys
 1

gag aac aac ttc ccg cca ctg ccc aag ttc atc cct gtg aag ccc tgc 162
 Glu Asn Asn Phe Pro Pro Leu Pro Lys Phe Ile Pro Val Lys Pro Cys
 5 10 15 20

ttc tac cag aac ttc tcc gac gag atc cca gtg gag cac cag gtc ctg 210
 Phe Tyr Gln Asn Phe Ser Asp Glu Ile Pro Val Glu His Gln Val Leu
 25 30 35

gtg aag agg atc tac cgg ctg tgg atg ttt tac tgc gcc acc ctc ggc 258
 Val Lys Arg Ile Tyr Arg Leu Trp Met Phe Tyr Cys Ala Thr Leu Gly
 40 45 50

gtc aac ctc att gcc tgc ctg gcc tgg tgg atc ggc gga ggc tcg ggg 306
 Val Asn Leu Ile Ala Cys Leu Ala Trp Trp Ile Gly Gly Gly Ser Gly
 55 60 65

acc aac ttc ggc ctg gcc ttc gtg tgg ctg ctc ctg ttc acg cct tgc 354
 Thr Asn Phe Gly Leu Ala Phe Val Trp Leu Leu Phe Thr Pro Cys
 70 75 80

ggc tac gtg tgc tgg ttc cgg cct gtc tac aag gcc ttc cga gcc gac 402
 Gly Tyr Val Cys Trp Phe Arg Pro Val Tyr Lys Ala Phe Arg Ala Asp
 85 90 95 100

agc tcc ttt aat ttc atg gcg ttt ttc ttc atc ttc gga gcc cag ttt 450
 Ser Ser Phe Asn Phe Met Ala Phe Phe Phe Ile Phe Gly Ala Gln Phe
 105 110 115

gtc ctg acc gtc atc cag gcg att ggc ttc tcc ggc tgg ggc gcg tgc 498
 Val Leu Thr Val Ile Gln Ala Ile Gly Phe Ser Gly Trp Gly Ala Cys
 120 125 130

ggc tgg ctg tcg gca att gga ttc ttc cag tac agc ccg ggc gct gcc 546
 Gly Trp Leu Ser Ala Ile Gly Phe Phe Gln Tyr Ser Pro Gly Ala Ala
 135 140 145

gtg gtc atg ctg ctt cca gcc atc atg ttc tcc gtg tcg gct gcc atg	594
Val Val Met Leu Leu Pro Ala Ile Met Phe Ser Val Ser Ala Ala Met	
150 155 160	
atg gcc atc gcg atc atg aag gtg cac agg atc tac cga ggg ggc tgg	642
Met Ala Ile Ala Ile Met Lys Val His Arg Ile Tyr Arg Gly Gly Trp	
165 170 175 180	
cgg aag ctt cca gaa ggc cag acg gag tgg cac acg ggc ctt ggc gga	690
Arg Lys Leu Pro Glu Gly Gln Thr Glu Trp His Thr Gly Leu Gly Gly	
185 190 195	
acc ccc cgc gac ggg ggc ccc gtc aac atc ttt cgg cga agc ttg ccc	738
Thr Pro Arg Asp Gly Gly Pro Val Asn Ile Phe Arg Arg Ser Leu Pro	
200 205 210	
agt acc ccc ttg tgc ccg taa ccggcgg	766
Ser Thr Pro Leu Cys Pro *	
215	

<210> 30
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 <213> Homo sapiens

<220>
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gacggcaggg gtctcagac cggcgctcgc tcgccggcgc catccctata gagaagaacg	120
gaggtacggc ctgtggtc atg gcg ctg ttc cca gcc ttt gcg ggg ctt agt	171
Met Ala Leu Phe Pro Ala Phe Ala Gly Leu Ser	
1 5 10	
gag gct ccc gat ggc ggg agc tcc agg aaa gag tta gac tgg ctg agc	219
Glu Ala Pro Asp Gly Gly Ser Ser Arg Lys Glu Leu Asp Trp Leu Ser	
15 20 25	
aac cca agc ttt tgt gtt gga tcc ata acg tcc ctg agc caa caa act	267
Asn Pro Ser Phe Cys Val Gly Ser Ile Thr Ser Leu Ser Gln Gln Thr	
30 35 40	
gaa gca gct cca gcc cat gtt tct gaa ggg tta ccg ctg aca agg agt	315
Glu Ala Ala Pro Ala His Val Ser Glu Gly Leu Pro Leu Thr Arg Ser	
45 50 55	
cat ctg aaa tca gag tct tca gat gaa agt gac act aac aaa aag ctc	363
His Leu Lys Ser Glu Ser Ser Asp Glu Ser Asp Thr Asn Lys Lys Leu	
60 65 70 75	

aaa caa aca agt aga aaa aag aag aaa gag aaa aag aaa aaa agg aag Lys Gln Thr Ser Arg Lys Lys Lys Lys Glu Lys Lys Lys Lys Arg Lys	411
80 85 90	
cat cag cat cat aag aaa aca aag agg aag cat ggg ccg tcg agt agc His Gln His His Lys Lys Thr Lys Arg Lys His Gly Pro Ser Ser Ser	459
95 100 105	
agc agg tct gag aca gac acc gat tct gaa aag gac aaa cct tcc aga Ser Arg Ser Glu Thr Asp Thr Asp Ser Glu Lys Asp Lys Pro Ser Arg	507
110 115 120	
ggc gtt gga ggc agt aaa aag gaa tct gag gaa ccg aat caa gga aat Gly Val Gly Gly Ser Lys Lys Glu Ser Glu Glu Pro Asn Gln Gly Asn	555
125 130 135	
aat gct gca gct gat act gga cat cgc ttt gtt tgg ctt gag gac att Asn Ala Ala Ala Asp Thr Gly His Arg Phe Val Trp Leu Glu Asp Ile	603
140 145 150 155	
cag gct gtg acg gga gaa acc ttc aga aca gat aag aaa cca gat cct Gln Ala Val Thr Gly Glu Thr Phe Arg Thr Asp Lys Lys Pro Asp Pro	651
160 165 170	
gcg aac tgg gag tac aag tct ctc tac cga ggg gat ata gca aga tac Ala Asn Trp Glu Tyr Lys Ser Leu Tyr Arg Gly Asp Ile Ala Arg Tyr	699
175 180 185	
aag agg aaa gga gac tcc tgc ctt ggc att aac cct aag aag cag tgc Lys Arg Lys Gly Asp Ser Cys Leu Gly Ile Asn Pro Lys Lys Gln Cys	747
190 195 200	
ata tct tgg gaa ggg act tcc aca gag aag aag cat tca cgc aag cag Ile Ser Trp Glu Gly Thr Ser Thr Glu Lys Lys His Ser Arg Lys Gln	795
205 210 215	
gtt gaa cgc tat ttt act aag aag agt gtg gga tta atg aac atc gat Val Glu Arg Tyr Phe Thr Lys Lys Ser Val Gly Leu Met Asn Ile Asp	843
220 225 230 235	
gga gtt gcc att agc agt aaa act gaa cct ccc tca tct gag ccc atc Gly Val Ala Ile Ser Ser Lys Thr Glu Pro Pro Ser Ser Glu Pro Ile	891
240 245 250	
tcc ttt ata cca gtg aag gac ttg gaa gat gcg gct cct gtt aca acc Ser Phe Ile Pro Val Lys Asp Leu Glu Asp Ala Ala Pro Val Thr Thr	939
255 260 265	
tgg ttg aat cct ctg ggg att tat gat cag tca acc aca cat tgg cta Trp Leu Asn Pro Leu Gly Ile Tyr Asp Gln Ser Thr Thr His Trp Leu	987
270 275 280	
caa gga cag ggt cct cca gag cag gaa tca aag cag cca gac gca cag Gln Gly Gln Gly Pro Pro Glu Gln Glu Ser Lys Gln Pro Asp Ala Gln	1035
285 290 295	

cca gac agc gag agt gcg gct ctc aag gcc aag gtg gag gag ttt aac	1083
Pro Asp Ser Glu Ser Ala Ala Leu Lys Ala Lys Val Glu Glu Phe Asn	
300 305 310 315	
agg agg gtg cgg gag aat cct cgg gat acg cag ctg tgg atg gca ttt	1131
Arg Arg Val Arg Glu Asn Pro Arg Asp Thr Gln Leu Trp Met Ala Phe	
320 325 330	
gtt gct ttt cag gac gag gtc atg aaa agt cct ggc ctg tat gcc atc	1179
Val Ala Phe Gln Asp Glu Val Met Lys Ser Pro Gly Leu Tyr Ala Ile	
335 340 345	
gag gaa gga gag cag gaa aag cga aag agg tcc ctg aag ctc att ctg	1227
Glu Glu Gly Glu Gln Glu Lys Arg Lys Arg Ser Leu Lys Leu Ile Leu	
350 355 360	
gag aag aag ctg gcc att ctg gag cgg gcc att gag agc aac cag agc	1275
Glu Lys Lys Leu Ala Ile Leu Glu Arg Ala Ile Glu Ser Asn Gln Ser	
365 370 375	
agt gtg gat ctg aaa ctg gcc aag ctg aag ctc tgc aca gag ttc tgg	1323
Ser Val Asp Leu Lys Leu Ala Lys Leu Lys Leu Cys Thr Glu Phe Trp	
380 385 390 395	
gag ccc tcc act ctg gtc aaa gag tgg cag aaa ctg ata ttt ttg cat	1371
Glu Pro Ser Thr Leu Val Lys Glu Trp Gln Lys Leu Ile Phe Leu His	
400 405 410	
ccc aat aat aca gcc ctt tgg cag aaa tac ctt tta ttt tgc cag agc	1419
Pro Asn Asn Thr Ala Leu Trp Gln Lys Tyr Leu Leu Phe Cys Gln Ser	
415 420 425	
cag ttt agt acc ttt tcg ata tca aaa att cac agt ctt tat gga aaa	1467
Gln Phe Ser Thr Phe Ser Ile Ser Lys Ile His Ser Leu Tyr Gly Lys	
430 435 440	
tgc ttg agc act ttg tct gct gtt aag gac ggc agc atc tta tct cac	1515
Cys Leu Ser Thr Leu Ser Ala Val Lys Asp Gly Ser Ile Leu Ser His	
445 450 455	
cct gcg ttg cct ggc acg gaa gag gcc atg ttt gca ctc ttt ctt cag	1563
Pro Ala Leu Pro Gly Thr Glu Glu Ala Met Phe Ala Leu Phe Leu Gln	
460 465 470 475	
cag tgc cac ttt ctg cgg cag gct ggc cac tct gag aag gcc atc tca	1611
Gln Cys His Phe Leu Arg Gln Ala Gly His Ser Glu Lys Ala Ile Ser	
480 485 490	
ttg ttc cag gcc atg gtg gac ttc acc ttc ttc aaa ccc gac agc gta	1659
Leu Phe Gln Ala Met Val Asp Phe Thr Phe Phe Lys Pro Asp Ser Val	
495 500 505	
aaa gat ctg cct acc aaa gga cag gtg gaa ttc ttt gaa ccc ttt tgg	1707
Lys Asp Leu Pro Thr Lys Gly Gln Val Glu Phe Phe Glu Pro Phe Trp	
510 515 520	
gac agt gga gag ccc cgg gct ggg gag aag gga gcc cga ggc tgg aag	1755

Asp	Ser	Gly	Glu	Pro	Arg	Ala	Gly	Glu	Lys	Gly	Ala	Arg	Gly	Trp	Lys	
525						530					535					
gcg	tgg	atg	cac	cag	cag	gaa	cga	ggt	ggc	tgg	gtg	gtc	atc	aac	cca	1803
Ala	Trp	Met	His	Gln	Gln	Glu	Arg	Gly	Gly	Trp	Val	Val	Ile	Asn	Pro	
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Lys	Thr	Leu	Pro	Arg	Trp	Gln	Ile	Trp	Leu	Ala	Ala	Glu	Arg	Ser	Arg	
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Asp	Gln	Arg	His	Trp	Arg	Pro	Trp	Arg	Pro	Asp	Lys	Thr	Lys	Lys	Gln	
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acc	gag	gaa	gac	tgt	gag	gat	ccc	gag	aga	cag	ggg	gtg	ttt	gat	gat	1995
Thr	Glu	Glu	Asp	Cys	Glu	Asp	Pro	Glu	Arg	Gln	Gly	Val	Phe	Asp	Asp	
			605			610					615					
att	ggg	caa	tct	tgt	atc	aga	ctt	tcc	agc	cat	gat	ctt	cag	ttc	cag	2043
Ile	Gly	Gln	Ser	Leu	Ile	Arg	Leu	Ser	Ser	His	Asp	Leu	Gln	Phe	Gln	
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Pro	Pro	Ala	Ser	Cys	Leu	Tyr	Leu	Ala	Met	Asp	Glu	Asn	Ser	Ile	Phe	
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Asp	Asn	Gly	Leu	Tyr	Asp	Glu	Lys	Pro	Leu	Thr	Phe	Phe	Asn	Pro	Leu	
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Phe	Ser	Gly	Ala	Ser	Cys	Val	Gly	Arg	Met	Asp	Arg	Leu	Gly	Tyr	Pro	
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Arg	Trp	Thr	Arg	Gly	Gln	Asn	Arg	Glu	Gly	Glu	Glu	Phe	Ile	Arg	Asn	
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gtc	ttc	cac	ctt	gtc	atg	cct	tta	ttt	tca	ggc	aaa	gag	aag	tcc	cag	2331
Val	Phe	His	Leu	Val	Met	Pro	Leu	Phe	Ser	Gly	Lys	Glu	Lys	Ser	Gln	
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ctc	tgc	ttc	tcc	tgg	tta	cag	tat	gag	att	gca	aag	gtc	att	tgg	tgc	2379
Leu	Cys	Phe	Ser	Trp	Leu	Gln	Tyr	Glu	Ile	Ala	Lys	Val	Ile	Trp	Cys	
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Leu	His	Thr	Lys	Asn	Lys	Lys	Arg	Leu	Lys	Ser	Gln	Gly	Lys	Asn	Cys	

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Lys Lys Leu Ala Lys Asn Leu Leu Lys Glu Pro Glu Asn Cys Asn Asn			
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Phe Cys Leu Trp Lys Gln Tyr Ala His Leu Glu Trp Leu Leu Gly Asn			
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acg gag gat gcc aga aaa gtt ttt gac aca gca ctt ggc atg gca gga			2571
Thr Glu Asp Ala Arg Lys Val Phe Asp Thr Ala Leu Gly Met Ala Gly			
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Ser Arg Glu Leu Lys Asp Ser Asp Leu Cys Glu Leu Ser Leu Leu Tyr			
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gct gag ctg gag gtg gag ctg tcg cca gaa gtg aga agg gct gcc aca			2667
Ala Glu Leu Glu Val Glu Leu Ser Pro Glu Val Arg Arg Ala Ala Thr			
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Lys Ala Tyr Glu His Ala Leu Gln Asp Cys Leu Gly Asp Ser Cys Val			
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Lys Cys Phe Met Leu Phe Gln Tyr Leu Thr Ile Gly Ile Asp Ala Ala			
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Ser Val Leu Glu Ala Ile Thr Leu Met His Thr Ser Leu Leu Arg Phe			
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cac atg aaa gtg agt gtt tac ccg ctg gcc cct ctg cga gag gca ctc			3099
His Met Lys Val Ser Val Tyr Pro Leu Ala Pro Leu Arg Glu Ala Leu			
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Tyr Val Gln Ile Gln Asn Lys Ser His Ser Ala Ser Lys Thr Arg Arg	
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Phe Phe Asp Thr Ile Thr Arg Ser Ala Lys Pro Leu Glu Pro Trp Leu	
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Gln Arg Leu Asp Gly Arg Glu Ile His Ala Thr Ile Pro Glu Thr Gly	
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Tyr Phe Pro Asp Glu Met Gln Glu Ile Leu Asp Leu Met Thr Glu Lys	
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Asp *	
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Ala Ala Ala Ala Asn Leu Asn Ala Val Arg Glu Thr Met Asp Val Leu
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ctt gag att tca aga att ttg aat act ggc tta gat atg gaa act ctg      145
Leu Glu Ile Ser Arg Ile Leu Asn Thr Gly Leu Asp Met Glu Thr Leu
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Ser Ile Cys Val Arg Leu Cys Glu Gln Gly Ile Asn Pro Glu Ala Leu
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Ser Ser Val Ile Lys Glu Leu Arg Lys Ala Thr Glu Ala Leu Lys Ala
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Ala Glu Asn Met Thr Ser  *
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cagtggaaag tggcttacag agagaactat cagatgtgtt tacatcacat cttattcact      474

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ccaggttgaa gtatagtgga acccatcagt agtaatgtgt agtagttatg acttgttgac      654

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Met Ser Ser Pro Leu Gln Arg Ala Val Gly Asp Thr Lys Arg
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Ala Phe Ser Ala Ser Ser Ser Ser Ser Ala Ser Leu Pro Phe Asp Asp
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Arg Asp Ser Asn His Thr Ser Glu Gly Asn Gly Asp Ser Leu Leu Ala
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gat gaa gac act gac ttt gaa gac agc ttg aat cgc aat gtg aag aag 433
Asp Glu Asp Thr Asp Phe Glu Asp Ser Leu Asn Arg Asn Val Lys Lys
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Arg Ala Ala Lys Arg Pro Pro Lys Thr Thr Pro Val Ala Lys His Pro
65 70 75
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Lys Lys Gly Ser Arg Val Val His Arg His Ser Arg Lys Lys Ser Glu
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cca cca gcc aat gat ctt ttc aat gct gtg aaa gcc gcc aaa agt gac 577
Pro Pro Ala Asn Asp Leu Phe Asn Ala Val Lys Lys Ala Ala Lys Ser Asp
95 100 105 110

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Met Gln Ser Leu Val Asp Glu Trp Leu Asp Ser Tyr Lys Gln Asp Gln	
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Asp Ala Gly Phe Leu Glu Leu Val Asn Phe Phe Ile Gln Ser Cys Gly	
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Cys Lys Gly Ile Val Thr Pro Glu Met Phe Lys Lys Met Ser Asn Ser	
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Glu Ile Ile Gln His Leu Thr Glu Gln Phe Asn Glu Asp Ser Gly Asp	
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Tyr Pro Leu Ile Ala Pro Gly Pro Ser Trp Lys Lys Phe Gln Gly Ser	
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Ala Met Lys Leu Met Thr Ser Leu Val Lys Val Ala Leu Gln Leu Ser	
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Val His Gln Asp Asn Asn Gln Arg Gln Tyr Glu Ala Glu Arg Asn Lys	
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Glu Ile Arg Ala Ile Cys Ile Glu Glu Ile Gly Cys Trp Met Gln Ser	
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Thr	Leu	His	Asp	Lys	His	Arg	Glu	Val	Arg	Val	Lys	Cys	Val	Lys	Ala		
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Phe	Thr	Ser	Arg	Phe	Lys	Asp	Arg	Met	Val	Ser	Met	Ile	Met	Asp	Arg		
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Glu	Tyr	Ser	Val	Ala	Val	Glu	Ala	Val	Arg	Leu	Leu	Ile	Leu	Ile	Leu		
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Lys	Asn	Met	Glu	Gly	Leu	Leu	Thr	Asp	Ala	Asp	Cys	Glu	Ser	Val	Tyr		
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Pro	Val	Val	Tyr	Pro	Ser	Asn	Arg	Gly	Leu	Ala	Ser	Ala	Ala	Gly	Glu		
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Phe	Leu	Tyr	Trp	Lys	Leu	Phe	Tyr	Pro	Glu	Cys	Glu	Ile	Arg	Thr	Met		
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gct ttt gtc tta tta agt gat cta ctt ctc atc ttt agc cct cag atg	2689
Ala Phe Val Leu Leu Ser Asp Leu Leu Leu Ile Phe Ser Pro Gln Met	
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Ile Val Gly Gly Arg Asp Phe Leu Arg Pro Leu Val Phe Phe Pro Glu	
815 820 825 830	
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Ala Thr Leu Gln Ser Glu Leu Ala Ser Phe Leu Met Asp His Val Phe	
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Ile Gln Pro Gly Asp Leu Gly Ser Gly Asp Ser Gln Glu Asp His Leu	
850 855 860	
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Gln Ile Glu Arg Leu His Gln Arg Arg Arg Leu Leu Ala Gly Phe Cys	
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Lys Leu Leu Leu Tyr Gly Val Leu Glu Met Asp Ala Ala Ser Asp Val	
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Phe Lys His Tyr Asn Lys Phe Tyr Asn Asp Tyr Gly Asp Ile Ile Lys	
895 900 905 910	
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Glu Thr Leu Thr Arg Ala Arg Gln Ile Asp Arg Ser His Cys Ser Arg	
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Ile Leu Leu Leu Ser Leu Lys Gln Leu Tyr Thr Glu Leu Leu Gln Glu	
930 935 940	
cat ggg ccc cag ggc ctg aat gag ctt cct gcc ttc atc gag atg agg	3121
His Gly Pro Gln Gly Leu Asn Glu Leu Pro Ala Phe Ile Glu Met Arg	
945 950 955	
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Asp Leu Ala Arg Arg Phe Ala Leu Ser Phe Gly Pro Gln Gln Leu Gln	
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Asn Arg Asp Leu Val Val Met Leu His Lys Glu Gly Ile Gln Phe Ser	
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Leu Ser Glu Leu Pro Pro Ala Gly Ser Ser Asn Gln Pro Pro Asn Leu	
995 1000 1005	
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Ala Phe Leu Glu Leu Leu Ser Glu Phe Ser Pro Arg Leu Phe His Gln	
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gac aag cag ctt tta ctg tcc tat cta gaa aag tgc ctg cag cat gtc 3361
Asp Lys Gln Leu Leu Leu Ser Tyr Leu Glu Lys Cys Leu Gln His Val
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tcc cag gca cct ggc cat ccc tgg ggc cca gtc acc acc tac tgc cac 3409
Ser Gln Ala Pro Gly His Pro Trp Gly Pro Val Thr Thr Tyr Cys His
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Ser Leu Ser Pro Val Glu Asn Thr Ala Glu Thr Ser Pro Gln Val Leu
1055 1060 1065 1070

ccc agc tcc aag agg agg cgc gtt gaa ggg cct gcc aag cct aac aga 3505
Pro Ser Ser Lys Arg Arg Arg Val Glu Gly Pro Ala Lys Pro Asn Arg
1075 1080 1085

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Asp Met Gln Ala Ser Ser Tyr Ser Ser Thr Ser Glu Arg Gly Leu Asp
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Leu Leu Asp Ser Thr Glu Leu Asp Ile Glu Asp Phe *

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Leu Glu Asn Ala Gln His Val Ala Leu Val Cys Ala Arg Gly Glu Arg
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ttc ctg gcg cgg gat gcg ctg cgc agc ctg gcg gtg ctg gaa ggc gcc      148
Phe Leu Ala Arg Asp Ala Leu Arg Ser Leu Ala Val Leu Glu Gly Ala
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agc ctg gtg gtg ggc aaa gat gga ttt ata aaa gct att ggt cct gct      196
Ser Leu Val Val Gly Lys Asp Gly Phe Ile Lys Ala Ile Gly Pro Ala
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gat gtt att caa aga cag ttt tct gga gaa act ttt gaa gaa tta att      244
Asp Val Ile Gln Arg Gln Phe Ser Gly Glu Thr Phe Glu Glu Leu Ile
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gac tgc tct ggg aaa tgt atc cta cca ggt ttg gtg gat gca cac aca      292
Asp Cys Ser Gly Lys Cys Ile Leu Pro Gly Leu Val Asp Ala His Thr
                                75                               80                               85

cat cca gta tgg gct ggt gaa aga gtt cac gaa ttt gca atg aag ttg      340
His Pro Val Trp Ala Gly Glu Arg Val His Glu Phe Ala Met Lys Leu
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Ala Gly Ala Thr Tyr Met Glu Ile His Gln Ala Gly Gly Gly Ile His
    105                               110                               115                               120

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 Ile Ile Asn Ser Ser Arg Trp Glu His Leu Ile Tyr Gln Phe Gly Gly
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 His His Glu Leu Ile Glu Tyr Val Ile Ala Lys Gly Lys Leu Ile Tyr
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 Lys Thr *
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ccccagaa atg cac aaa tat cac tgt gaa ctc aaa aac tta agg gag 288
 Met His Lys Tyr His Cys Glu Leu Lys Asn Leu Arg Glu
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 Lys Glu Lys Gln Leu Glu Thr Ser Cys Lys Glu Lys Thr Glu Tyr Leu
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Pro	Asp	Pro	Val	Met	Ser	Tyr	Leu	Cys	Cys	Gln	Tyr	His	Ile	His	Glu	
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Val	Lys	Thr	Ser	Phe	Tyr	Ser	Asn	Lys	Val	Ile	Ser	Ser	Asn	Thr	Ser	
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ttc aac atg ctg gag gct ctg ccc gag ggt ctt ttc cag cac ctg gct Phe Asn Met Leu Glu Ala Leu Pro Glu Gly Leu Phe Gln His Leu Ala	489
130 135 140 145	
gcc ctg gag tcc ctc cac ctg cag ggg aac cag ctc cag gcc ctg ccc Ala Leu Glu Ser Leu His Leu Gln Gly Asn Gln Leu Gln Ala Leu Pro	537
150 155 160	
agg agg ctc ttc cag cct ctg acc cat ctg aag aca ctc aac ctg gcc Arg Arg Leu Phe Gln Pro Leu Thr His Leu Lys Thr Leu Asn Leu Ala	585
165 170 175	
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180 185 190	
agc ctg cag acc ctg aag ctg agc aac aac gcg ctc tct ggt ctc ccc Ser Leu Gln Thr Leu Lys Leu Ser Asn Asn Ala Leu Ser Gly Leu Pro	681
195 200 205	
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210 215 220 225	
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230 235 240	
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Cys	Leu	Glu	Arg	Leu	Trp	Leu	Gln	Arg	Asn	Ala	Ile	Thr	His	Leu	Pro	
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Leu	Ser	Ile	Phe	Ala	Ser	Leu	Gly	Asn	Leu	Thr	Phe	Leu	Ser	Leu	Gln	
		260					265				270					
tgg	aac	atg	ctt	cgg	gtc	ctg	cct	gcc	ggc	ctc	ttt	gcc	cac	acc	cca	921
Trp	Asn	Met	Leu	Arg	Val	Leu	Pro	Ala	Gly	Leu	Phe	Ala	His	Thr	Pro	
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Cys	Leu	Val	Gly	Leu	Ser	Leu	Thr	His	Asn	Gln	Leu	Glu	Thr	Val	Ala	
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gag	ggc	acc	ttt	gcc	cac	ctg	tcc	aac	ctg	cgt	tcc	ctc	atg	ctc	tca	1017
Glu	Gly	Thr	Phe	Ala	His	Leu	Ser	Asn	Leu	Arg	Ser	Leu	Met	Leu	Ser	
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tac	aat	gcc	att	acc	cac	ctc	cca	gct	ggc	atc	ttc	aga	gac	ctg	gag	1065
Tyr	Asn	Ala	Ile	Thr	His	Leu	Pro	Ala	Gly	Ile	Phe	Arg	Asp	Leu	Glu	
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gag	ttg	gtc	aaa	ctc	tac	ctg	ggc	agc	aac	aac	ctt	acg	gcg	ctg	cac	1113
Glu	Leu	Val	Lys	Leu	Tyr	Leu	Gly	Ser	Asn	Asn	Leu	Thr	Ala	Leu	His	
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cca	gcc	ctc	ttc	cag	aac	ctg	tcc	aag	ctg	gag	ctg	ctc	agc	ctc	tcc	1161
Pro	Ala	Leu	Phe	Gln	Asn	Leu	Ser	Lys	Leu	Glu	Leu	Leu	Ser	Leu	Ser	
	355					360					365					
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Lys	Asn	Gln	Leu	Thr	Thr	Leu	Pro	Glu	Gly	Ile	Phe	Asp	Thr	Asn	Tyr	
370					375					380					385	
aac	ctg	ttc	aac	ctg	gcc	ctg	cac	ggt	aac	ccc	tgg	cag	tgc	gac	tgc	1257
Asn	Leu	Phe	Asn	Leu	Ala	Leu	His	Gly	Asn	Pro	Trp	Gln	Cys	Asp	Cys	
				390					395					400		
cac	ctg	gcc	tac	ctc	ttc	aac	tgg	ctg	cag	cag	tac	acc	gat	cgg	ctc	1305
His	Leu	Ala	Tyr	Leu	Phe	Asn	Trp	Leu	Gln	Gln	Tyr	Thr	Asp	Arg	Leu	
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ctg	aac	atc	cag	acc	tac	tgc	gct	ggc	cct	gcc	tac	ctc	aaa	ggc	cag	1353
Leu	Asn	Ile	Gln	Thr	Tyr	Cys	Ala	Gly	Pro	Ala	Tyr	Leu	Lys	Gly	Gln	
		420					425					430				
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Val	Val	Pro	Ala	Leu	Asn	Glu	Lys	Gln	Leu	Val	Cys	Pro	Val	Thr	Arg	
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Asp	His	Leu	Gly	Phe	Gln	Val	Thr	Trp	Pro	Asp	Glu	Ser	Lys	Ala	Gly	
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ggc	agc	tgg	gat	ctg	gct	gtg	cag	gaa	agg	gca	gcc	cgg	agc	cag	tgc	1497
Gly	Ser	Trp	Asp	Leu	Ala	Val	Gln	Glu	Arg	Ala	Ala	Arg	Ser	Gln	Cys	

470	475	480	
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cag tgt cgc tgg ctg aac gtc cag ctc tct cct cgg cag ggc tcc ctg			1593
Gln Cys Arg Trp Leu Asn Val Gln Leu Ser Pro Arg Gln Gly Ser Leu			
500	505	510	
gga ctg cag tac aat gct agt cag gag tgg gac ctg agg tcg agc tgc			1641
Gly Leu Gln Tyr Asn Ala Ser Gln Glu Trp Asp Leu Arg Ser Ser Cys			
515	520	525	
ggt tct ctg cgg ctc acc gtg tct atc gag gct cgg gca gca ggg ccc			1689
Gly Ser Leu Arg Leu Thr Val Ser Ile Glu Ala Arg Ala Ala Gly Pro			
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tcccaggtct tcagctaagc tcaaccaatt gtcaaccaga aaatgtttaa atttacctac			2766
agcctggaag caccacccc cgctgcttcg agttgtcctg cttttctgaa ctcaaccaat			2826

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 Met Asn His Ile Val Gln Thr Phe Ser Pro Val Asn Ser Gly
 1 5 10
 cag cct ccc aac tac gag atg ctc aag gag gag cag gaa gtg gct atg 157
 Gln Pro Pro Asn Tyr Glu Met Leu Lys Glu Glu Gln Glu Val Ala Met
 15 20 25 30
 ctg ggg gtg ccc cac aac cct gct ccc ccg atg tcc acc gtg atc cac 205
 Leu Gly Val Pro His Asn Pro Ala Pro Pro Met Ser Thr Val Ile His
 35 40 45
 atc cgc agc gag acc tcc gtg cct gac cat gtg gtc tgg tcc ctg ttc 253
 Ile Arg Ser Glu Thr Ser Val Pro Asp His Val Val Trp Ser Leu Phe
 50 55 60
 aac acc ctc ttc atg aac acc tgc tgc ctg ggc ttc ata gca ttc gcg 301
 Asn Thr Leu Phe Met Asn Thr Cys Cys Leu Gly Phe Ile Ala Phe Ala
 65 70 75
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 Tyr Ser Val Lys Ser Arg Asp Arg Lys Met Val Gly Asp Val Thr Gly
 80 85 90
 gcc cag gcc tat gcc tcc acc gcc aag tgc ctg aac atc tgg gcc ctg 397
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 95 100 105 110
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 Ile Leu Gly Ile Phe Met Thr Ile Leu Leu Ile Ile Ile Pro Val Leu
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 Val Val Gln Ala Gln Arg *
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cccgtagagct gtatccacgt actctatctt ccattcttcg cctgccccca gaggccagag 558
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ggatcccagc gcccgatcc cggcgcccca acccccacgc ccgcctccgc caactttcac 240
gctgcctcgg cggcccggcc cggctcgacg cca atg gtg gag gcc ata gtg gag 294
                               Met Val Glu Ala Ile Val Glu
                               1                               5

ttt gac tac cag gcc cag cac gat gat gag ctg acg atc agc gtg ggt 342
Phe Asp Tyr Gln Ala Gln His Asp Asp Glu Leu Thr Ile Ser Val Gly
          10          15          20

gaa atc atc acc aac atc agg aag gag gat gga ggc tgg tgg gag gga 390
Glu Ile Ile Thr Asn Ile Arg Lys Glu Asp Gly Gly Trp Trp Glu Gly
          25          30          35

cag atc aac ggc agg aga ggt ttg ttc cct gac aac ttt gta aga gaa 438
Gln Ile Asn Gly Arg Arg Gly Leu Phe Pro Asp Asn Phe Val Arg Glu
          40          45          50          55

ata aag aaa gag atg aag aaa gac cct ctc acc aac aaa gct cca gaa 486
Ile Lys Lys Glu Met Lys Lys Asp Pro Leu Thr Asn Lys Ala Pro Glu
          60          65          70

aag ccc ctg cac gaa gtg ccc agt gga aac tct ttg ctg tct tct gaa 534
Lys Pro Leu His Glu Val Pro Ser Gly Asn Ser Leu Leu Ser Ser Glu
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acg att tta aga acc aat aag aga ggc gag cga cgg agg cgc cgg tgc 582
Thr Ile Leu Arg Thr Asn Lys Arg Gly Glu Arg Arg Arg Arg Arg Cys
          90          95          100

cag gtg gca ttc agc tac ctg ccc cag aat gac gat gaa ctt gag ctg 630

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Gln Val Ala Phe Ser Tyr Leu Pro Gln Asn Asp Asp Glu Leu Glu Leu	
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aaa gtt ggc gac atc ata gag gtg gta gga gag gta gag gaa gga tgg	678
Lys Val Gly Asp Ile Ile Glu Val Val Gly Glu Val Glu Glu Gly Trp	
120 125 130 135	
tgg gaa ggt gtt ctc aac ggg aag act gga atg ttt cct tcc aac ttc	726
Trp Glu Gly Val Leu Asn Gly Lys Thr Gly Met Phe Pro Ser Asn Phe	
140 145 150	
atc aag gag ctg tca ggg gag tcg gat gag ctt ggc att tcc cag gat	774
Ile Lys Glu Leu Ser Gly Glu Ser Asp Glu Leu Gly Ile Ser Gln Asp	
155 160 165	
gag cag cta tcc aag tca agt tta agg gaa acc aca ggc tcc gag agt	822
Glu Gln Leu Ser Lys Ser Ser Leu Arg Glu Thr Thr Gly Ser Glu Ser	
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Asp Gly Gly Asp Ser Ser Ser Thr Lys Ser Glu Gly Ala Asn Gly Thr	
185 190 195	
gtg gca act gca gca atc cag ccc aag aaa gtt aag gga gtg ggc ttt	918
Val Ala Thr Ala Ala Ile Gln Pro Lys Lys Val Lys Gly Val Gly Phe	
200 205 210 215	
gga gac att ttc aaa gac aag cca atc aaa cta aga cca agg tca att	966
Gly Asp Ile Phe Lys Asp Lys Pro Ile Lys Leu Arg Pro Arg Ser Ile	
220 225 230	
gaa gta gaa aat gac ttt ctg ccg gta gaa aag act att ggg aag aag	1014
Glu Val Glu Asn Asp Phe Leu Pro Val Glu Lys Thr Ile Gly Lys Lys	
235 240 245	
tta cct gca act aca gca act cca gac tca tca aaa aca gaa atg gac	1062
Leu Pro Ala Thr Thr Ala Thr Pro Asp Ser Ser Lys Thr Glu Met Asp	
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Ser Arg Thr Lys Ser Lys Asp Tyr Cys Lys Val Ile Phe Pro Tyr Glu	
265 270 275	
gca cag aat gat gat gaa ttg aca atc aaa gaa gga gat ata gtc act	1158
Ala Gln Asn Asp Asp Glu Leu Thr Ile Lys Glu Gly Asp Ile Val Thr	
280 285 290 295	
ctc atc aat aag gac tgc atc gac gta ggc tgg tgg gaa gga gag ctg	1206
Leu Ile Asn Lys Asp Cys Ile Asp Val Gly Trp Trp Glu Gly Glu Leu	
300 305 310	
aac ggc aga cga ggc gtg ttc ccc gat aac ttc gtg aag tta ctt cca	1254
Asn Gly Arg Arg Gly Val Phe Pro Asp Asn Phe Val Lys Leu Leu Pro	
315 320 325	
ccg gac ttt gaa aag gaa ggg aat aga ccc aag aag cca ccg cct cca	1302
Pro Asp Phe Glu Lys Glu Gly Asn Arg Pro Lys Lys Pro Pro Pro Pro	

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aca gaa gaa aaa gaa aga cca gag aga gag cca aaa ctg gat tta cag Thr Glu Glu Lys Glu Arg Pro Glu Arg Glu Pro Lys Leu Asp Leu Gln 380 385 390			1446
aag ccc tcc gtt cct gcc ata ccg cca aaa aag cct cgg cca cct aag Lys Pro Ser Val Pro Ala Ile Pro Pro Lys Lys Pro Arg Pro Pro Lys 395 400 405			1494
acc aat tct ctc agc aga cct ggc gca ctg ccc ccg aga agg ccg gag Thr Asn Ser Leu Ser Arg Pro Gly Ala Leu Pro Pro Arg Arg Pro Glu 410 415 420			1542
aga ccg gtg ggt ccg ctg aca cac acc agg ggt gac agt cca aag att Arg Pro Val Gly Pro Leu Thr His Thr Arg Gly Asp Ser Pro Lys Ile 425 430 435			1590
gac ttg gcc ggc agt tcg cta tct ggc atc ctg gac aaa gat ctc tcg Asp Leu Ala Gly Ser Ser Leu Ser Gly Ile Leu Asp Lys Asp Leu Ser 440 445 450 455			1638
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Ser Ala Ala Pro Ser Pro Leu Ser Ser Ser Leu Gly Thr Ala Gly His	
570 575 580	
aga gcc aac tcc ccg tct ctg ttc ggc acg gaa gga aaa cca aag atg	2070
Arg Ala Asn Ser Pro Ser Leu Phe Gly Thr Glu Gly Lys Pro Lys Met	
585 590 595	
gag cct gcg gcc agc agc cag gcg gcc gtg gag gag cta agg aca cag	2118
Glu Pro Ala Ala Ser Ser Gln Ala Ala Val Glu Glu Leu Arg Thr Gln	
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gtc cgc gag ctg agg agc atc atc gag acc atg aag gac cag cag aaa	2166
Val Arg Glu Leu Arg Ser Ile Ile Glu Thr Met Lys Asp Gln Gln Lys	
620 625 630	
cga gag att aaa cag tta ttg tct gag ttg gat gaa gag aag aaa atc	2214
Arg Glu Ile Lys Gln Leu Leu Ser Glu Leu Asp Glu Glu Lys Lys Ile	
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cgccgccgcc actgaggaag aagccggccc agccgccgcc gcgtccggac cctcgcgccct      180
ggatcccagc gccccgatcc cgggcgcccca acccccacgc ccgcctccgc caactttcac      240
gctgcctcgg cggcccggcc cggctcgacg cca atg gtg gag gcc ata gtg gag      294
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                               1                               5

ttt gac tac cag gcc cag cac gat gat gag ctg acg atc agc gtg ggt      342
Phe Asp Tyr Gln Ala Gln His Asp Asp Glu Leu Thr Ile Ser Val Gly
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gaa atc atc acc aac atc agg aag gag gat gga ggc tgg tgg gag gga      390
Glu Ile Ile Thr Asn Ile Arg Lys Glu Asp Gly Gly Trp Trp Glu Gly
                               25                               30                               35

cag atc aac ggc agg aga ggt ttg ttc cct gac aac ttt gta aga gaa      438
Gln Ile Asn Gly Arg Arg Gly Leu Phe Pro Asp Asn Phe Val Arg Glu
                               40                               45                               50                               55

ata aag aaa gag atg aag aaa gac cct ctc acc aac aaa gct cca gaa      486
Ile Lys Lys Glu Met Lys Lys Asp Pro Leu Thr Asn Lys Ala Pro Glu
                               60                               65                               70

aag ccc ctg cac gaa gtg ccc agt gga aac tct ttg ctg tct tct gaa      534
Lys Pro Leu His Glu Val Pro Ser Gly Asn Ser Leu Leu Ser Ser Glu
                               75                               80                               85

acg att tta aga acc aat aag aga ggc gag cga cgg agg cgc cgg tgc      582
Thr Ile Leu Arg Thr Asn Lys Arg Gly Glu Arg Arg Arg Arg Arg Cys
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cag gtg gca ttc agc tac ctg ccc cag aat gac gat gaa ctt gag ctg      630
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                               105                               110                               115

aaa gtt ggc gac atc ata gag gtg gta gga gag gta gag gaa gga tgg      678
Lys Val Gly Asp Ile Ile Glu Val Val Gly Glu Val Glu Glu Gly Trp
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tgg gaa ggt gtt ctc aac ggg aag act gga atg ttt cct tcc aac ttc      726
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Glu Gln Leu Ser Lys Ser Ser Leu Arg Glu Thr Thr Gly Ser Glu Ser	
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gat ggg ggt gac tca agc agc acc aag tct gaa ggt gcc aac ggg aca	870
Asp Gly Gly Asp Ser Ser Ser Thr Lys Ser Glu Gly Ala Asn Gly Thr	
185 190 195	
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Val Ala Thr Ala Ala Ile Gln Pro Lys Lys Val Lys Gly Val Gly Phe	
200 205 210 215	
gga gac att ttc aaa gac aag cca atc aaa cta aga cca agg tca att	966
Gly Asp Ile Phe Lys Asp Lys Pro Ile Lys Leu Arg Pro Arg Ser Ile	
220 225 230	
gaa gta gaa aat gac ttt ctg ccg gta gaa aag act att ggg aag aag	1014
Glu Val Glu Asn Asp Phe Leu Pro Val Glu Lys Thr Ile Gly Lys Lys	
235 240 245	
tta cct gca act aca gca act cca gac tca tca aaa aca gaa atg gac	1062
Leu Pro Ala Thr Thr Ala Thr Pro Asp Ser Ser Lys Thr Glu Met Asp	
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agc agg aca aag agc aag gat tac tgc aaa gta ata ttt cca tat gag	1110
Ser Arg Thr Lys Ser Lys Asp Tyr Cys Lys Val Ile Phe Pro Tyr Glu	
265 270 275	
gca cag aat gat gat gaa ttg aca atc aaa gaa gga gat ata gtc act	1158
Ala Gln Asn Asp Asp Glu Leu Thr Ile Lys Glu Gly Asp Ile Val Thr	
280 285 290 295	
ctc atc aat aag gac tgc atc gac gta ggc tgg tgg gaa gga gag ctg	1206
Leu Ile Asn Lys Asp Cys Ile Asp Val Gly Trp Trp Glu Gly Glu Leu	
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aac ggc aga cga ggc gtg ttc ccc gat aac ttc gtg aag tta ctt cca	1254
Asn Gly Arg Arg Gly Val Phe Pro Asp Asn Phe Val Lys Leu Leu Pro	
315 320 325	
ccg gac ttt gaa aag gaa ggg aat aga ccc aag aag cca ccg cct cca	1302
Pro Asp Phe Glu Lys Glu Gly Asn Arg Pro Lys Lys Pro Pro Pro Pro	
330 335 340	
tcc gct cct gtc atc aaa caa ggg gca ggc acc act gag aga aaa cat	1350
Ser Ala Pro Val Ile Lys Gln Gly Ala Gly Thr Thr Glu Arg Lys His	
345 350 355	
gaa att aaa aag ata cct cct gaa aga cca gaa atg ctt cca aac aga	1398
Glu Ile Lys Lys Ile Pro Pro Glu Arg Pro Glu Met Leu Pro Asn Arg	
360 365 370 375	
aca gaa gaa aaa gaa aga cca gag aga gag cca aaa ctg gat tta cag	1446

Thr	Glu	Glu	Lys	Glu	Arg	Pro	Glu	Arg	Glu	Pro	Lys	Leu	Asp	Leu	Gln		
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aag	ccc	tcc	gtt	cct	gcc	ata	ccg	cca	aaa	aag	cct	cgg	cca	cct	aag		1494
Lys	Pro	Ser	Val	Pro	Ala	Ile	Pro	Pro	Lys	Lys	Pro	Arg	Pro	Pro	Lys		
			395				400					405					
acc	aat	tct	ctc	agc	aga	cct	ggc	gca	ctg	ccc	ccg	aga	agg	ccg	gag		1542
Thr	Asn	Ser	Leu	Ser	Arg	Pro	Gly	Ala	Leu	Pro	Pro	Arg	Arg	Pro	Glu		
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aga	ccg	gtg	ggg	ccg	ctg	aca	cac	acc	agg	ggg	gac	agt	cca	aag	att		1590
Arg	Pro	Val	Gly	Pro	Leu	Thr	His	Thr	Arg	Gly	Asp	Ser	Pro	Lys	Ile		
	425					430					435						
gac	ttg	gcc	ggc	agt	tcg	cta	tct	ggc	atc	ctg	gac	aaa	gat	ctc	tcg		1638
Asp	Leu	Ala	Gly	Ser	Ser	Leu	Ser	Gly	Ile	Leu	Asp	Lys	Asp	Leu	Ser		
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gac	cgc	agc	aat	gac	att	gac	tta	gaa	ggg	ttt	gac	tcc	gtg	gta	tca		1686
Asp	Arg	Ser	Asn	Asp	Ile	Asp	Leu	Glu	Gly	Phe	Asp	Ser	Val	Val	Ser		
			460					465					470				
tct	act	gag	aaa	ctc	agt	cat	ccg	acc	aca	agc	aga	cca	aaa	gct	aca		1734
Ser	Thr	Glu	Lys	Leu	Ser	His	Pro	Thr	Thr	Ser	Arg	Pro	Lys	Ala	Thr		
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ggg	agg	cgg	cct	ccg	tcc	cag	tcc	ctc	aca	tct	gtg	tct	gac	aac	aaa		1782
Gly	Arg	Arg	Pro	Pro	Ser	Gln	Ser	Leu	Thr	Ser	Val	Ser	Asp	Asn	Lys		
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gca	tcc	ctg	ccg	ccc	aag	ccg	ggg	acc	atg	gca	gca	ggg	ggc	ggg	ggg		1830
Ala	Ser	Leu	Pro	Pro	Lys	Pro	Gly	Thr	Met	Ala	Ala	Gly	Gly	Gly	Gly		
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cca	gcc	cct	ctg	tcc	tca	gcg	gcg	ccc	tcc	ccc	ctg	tca	tcc	tct	ttg		1878
Pro	Ala	Pro	Leu	Ser	Ser	Ala	Ala	Pro	Ser	Pro	Leu	Ser	Ser	Ser	Leu		
	520				525				530						535		
gga	aca	gct	gga	cac	aga	gcc	aac	tcc	ccg	tct	ctg	ttc	ggc	acg	gaa		1926
Gly	Thr	Ala	Gly	His	Arg	Ala	Asn	Ser	Pro	Ser	Leu	Phe	Gly	Thr	Glu		
			540					545					550				
gga	aaa	cca	aag	atg	gag	cct	gcg	gcc	agc	agc	cag	gcg	gcc	gtg	gag		1974
Gly	Lys	Pro	Lys	Met	Glu	Pro	Ala	Ala	Ser	Ser	Gln	Ala	Ala	Val	Glu		
		555					560					565					
gag	cta	agg	aca	cag	gtc	cgc	gag	ctg	agg	agc	atc	atc	gag	acc	atg		2022
Glu	Leu	Arg	Thr	Gln	Val	Arg	Glu	Leu	Arg	Ser	Ile	Ile	Glu	Thr	Met		
	570					575					580						
aag	gac	cag	cag	aaa	cga	gag	att	aaa	cag	tta	ttg	tct	gag	ttg	gat		2070
Lys	Asp	Gln	Gln	Lys	Arg	Glu	Ile	Lys	Gln	Leu	Leu	Ser	Glu	Leu	Asp		
	585					590				595							
gaa	gag	aag	aaa	atc	cgg	ctt	cgg	ttg	cag	atg	gaa	gtg	aac	gac	ata		2118
Glu	Glu	Lys	Lys	Ile	Arg	Leu	Arg	Leu	Gln	Met	Glu	Val	Asn	Asp	Ile		

600	605	610	615	
aag aaa gct cta caa tca aaa tga atacttgatc aatgaaatgt cacattattc				2172
Lys Lys Ala Leu Gln Ser Lys *				
	620			

atcctgagtc cgagactcaa attttctgcc ccagccaaaa taatcttgtg ccaaaagatt	2232
aaaggtttgc ctcaaaatgt ccctgtttga aagattagca caaaagtctt gatagcacia	2292
cacaaattcc atccaagagg agaatcttcc ccagggttta gtcctggggc tggcactcgt	2352
tgtgacttac acagagcaaa attgtgctaa aggcttttct actctgagat ctcaatgcga	2412
aatgaaaact caggcagttt agtccatagt ggtactatctt tgatgatatt ttccattaat	2472
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agcagggtga ggagcagctg ccagccccgg caggcccagg ccctgtctgg gtgcacagga	180
cagagacaca gcaagatgcc caggagtgct cgcttcctgg gctagagaca agcaccagcc	240
tgcatggag aacgcaggac cccgctgccc agaaggagca gccacggcct gcggaggact	300
ggcccagcaa ggtcccaggt cttccctctc ctacgcct aagagagagg ccagtgcg	360
gtgaggagtc gcgaggaaga ggcggaaggc gccggaaggc acc atg ttc cgc aag	415
	Met Phe Arg Lys

aaa aag aag aaa cgc cct gag atc tca gcg cca cag aac ttc cag cac	463
Lys Lys Lys Lys Arg Pro Glu Ile Ser Ala Pro Gln Asn Phe Gln His	
5 10 15 20	
cgt gtc cac acc tcc ttc gac ccc aaa gaa ggc aag ttt gtg ggc ctc	511
Arg Val His Thr Ser Phe Asp Pro Lys Glu Gly Lys Phe Val Gly Leu	
25 30 35	
ccc cca caa tgg cag aac atc ctg gac aca ctg cgg cgc ccc aag ccc	559
Pro Pro Gln Trp Gln Asn Ile Leu Asp Thr Leu Arg Arg Pro Lys Pro	
40 45 50	
gtg gtg gac cct tcg cga atc aca cgg gtg cag ctc cag ccc atg aag	607
Val Val Asp Pro Ser Arg Ile Thr Arg Val Gln Leu Gln Pro Met Lys	
55 60 65	
aca gtg gtg cgg ggc agc gcg atg cct gtg gat ggc tac atc tcg ggg	655
Thr Val Val Arg Gly Ser Ala Met Pro Val Asp Gly Tyr Ile Ser Gly	
70 75 80	
ctg ctc aac gac atc cag aag ttg tca gtc atc agc tcc aac acc ctg	703
Leu Leu Asn Asp Ile Gln Lys Leu Ser Val Ile Ser Ser Asn Thr Leu	
85 90 95 100	
cgt ggc cgc agc ccc acc agc cgg cgg cgg gca cag tcc ctg ggg ctg	751
Arg Gly Arg Ser Pro Thr Ser Arg Arg Arg Ala Gln Ser Leu Gly Leu	
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ctg ggg gat gag cac tgg gcc acc gac cca gac atg tac ctc cag agc	799
Leu Gly Asp Glu His Trp Ala Thr Asp Pro Asp Met Tyr Leu Gln Ser	
120 125 130	
ccc cag tct gag cgc act gac ccc cac ggc ctc tac ctc agc tgc aac	847
Pro Gln Ser Glu Arg Thr Asp Pro His Gly Leu Tyr Leu Ser Cys Asn	
135 140 145	
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Gly Gly Thr Pro Ala Gly His Lys Gln Met Pro Trp Pro Glu Pro Gln	
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Ser Pro Arg Val Leu Pro Asn Gly Leu Ala Ala Lys Ala Gln Ser Leu	
165 170 175 180	
ggc ccc gcc gag ttt cag ggt gcc tcg cag cgc tgt ctg cag ctg ggt	991
Gly Pro Ala Glu Phe Gln Gly Ala Ser Gln Arg Cys Leu Gln Leu Gly	
185 190 195	
gcc tgc ctg cag agc tcc cca cca gga gcc tcg ccc ccc acg ggc acc	1039
Ala Cys Leu Gln Ser Ser Pro Pro Gly Ala Ser Pro Pro Thr Gly Thr	
200 205 210	
aat agg cat gga atg aag gct gcc aag cat ggc tct gag gag gcc cgg	1087
Asn Arg His Gly Met Lys Ala Ala Lys His Gly Ser Glu Glu Ala Arg	
215 220 225	

cca cag tcc tgc ctg gtg ggc tca gcc aca ggc agg cca ggt ggg gaa	1135
Pro Gln Ser Cys Leu Val Gly Ser Ala Thr Gly Arg Pro Gly Gly Glu	
230 235 240	
ggc agc cct agc cct aag acc cgg gag agc agc ctg aag cgc agg cta	1183
Gly Ser Pro Ser Pro Lys Thr Arg Glu Ser Ser Leu Lys Arg Arg Leu	
245 250 255 260	
ttc cga agc atg ttc ctg tcc act gct gcc aca gcc cct cca agc agc	1231
Phe Arg Ser Met Phe Leu Ser Thr Ala Ala Thr Ala Pro Pro Ser Ser	
265 270 275	
agc aag cca ggc cct cca cca cag agc aag ccc aac tcc tct ttc cga	1279
Ser Lys Pro Gly Pro Pro Pro Gln Ser Lys Pro Asn Ser Ser Phe Arg	
280 285 290	
ccg ccg cag aaa gac aac ccc cca agc ctg gtg gcc aag gcc cag tcc	1327
Pro Pro Gln Lys Asp Asn Pro Pro Ser Leu Val Ala Lys Ala Gln Ser	
295 300 305	
ttg ccc tcg gac cag ccg gtg ggg acc ttc agc cct ctg acc act tcg	1375
Leu Pro Ser Asp Gln Pro Val Gly Thr Phe Ser Pro Leu Thr Thr Ser	
310 315 320	
gat acc agc agc ccc cag aag tcc ctc cgc aca gcc ccg gcc aca ggc	1423
Asp Thr Ser Ser Pro Gln Lys Ser Leu Arg Thr Ala Pro Ala Thr Gly	
325 330 335 340	
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Gln Leu Pro Gly Arg Ser Ser Pro Ala Gly Ser Pro Arg Thr Trp His	
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Ala Gln Ile Ser Thr Ser Asn Leu Tyr Leu Pro Gln Asp Pro Thr Val	
360 365 370	
gcc aag ggt gcc ctg gct ggt gag gac aca ggt gtt gtg aca cat gag	1567
Ala Lys Gly Ala Leu Ala Gly Glu Asp Thr Gly Val Val Thr His Glu	
375 380 385	
cag ttc aag gct gcg ctc agg atg gtg gtg gac cag ggt gac ccc ccg	1615
Gln Phe Lys Ala Ala Leu Arg Met Val Val Asp Gln Gly Asp Pro Arg	
390 395 400	
ctg ctg ctg gac agc tac gtg aag att ggc gag ggc tcc acc ggc atc	1663
Leu Leu Leu Asp Ser Tyr Val Lys Ile Gly Glu Gly Ser Thr Gly Ile	
405 410 415 420	
gtc tgc ttg gcc ccg gag aag cac tcg ggc cgc cag gtg gcc gtc aag	1711
Val Cys Leu Ala Arg Glu Lys His Ser Gly Arg Gln Val Ala Val Lys	
425 430 435	
atg atg gac ctc agg aag cag cag cgc agg gag ctg ctc ttc aac gag	1759
Met Met Asp Leu Arg Lys Gln Gln Arg Arg Glu Leu Leu Phe Asn Glu	
440 445 450	

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aag agc tac ctg gtg gga gag gag ctg tgg gtg ctc atg gag ttc ctg Lys Ser Tyr Leu Val Gly Glu Glu Leu Trp Val Leu Met Glu Phe Leu 470 475 480	1855
cag gga gga gcc ctc aca gac atc gtc tcc caa gtc agg ctg aat gag Gln Gly Gly Ala Leu Thr Asp Ile Val Ser Gln Val Arg Leu Asn Glu 485 490 495 500	1903
gag cag att gcc act gtg tgt gag gct gtg ctg cag gcc ctg gcc tac Glu Gln Ile Ala Thr Val Cys Glu Ala Val Leu Gln Ala Leu Ala Tyr 505 510 515	1951
ctg cat gct cag ggt gtc atc cac cgg gac atc aag agt gac tcc atc Leu His Ala Gln Gly Val Ile His Arg Asp Ile Lys Ser Asp Ser Ile 520 525 530	1999
ctg ctg acc ctc gat ggc agg gtg aag ctc tcg gac ttc gga ttc tgt Leu Leu Thr Leu Asp Gly Arg Val Lys Leu Ser Asp Phe Gly Phe Cys 535 540 545	2047
gct cag atc agc aaa gac gtc cct aag agg aag tcc ctg gtg gga acc Ala Gln Ile Ser Lys Asp Val Pro Lys Arg Lys Ser Leu Val Gly Thr 550 555 560	2095
ccc tac tgg atg gct cct gaa gtg atc tcc agg tct ttg tat gcc act Pro Tyr Trp Met Ala Pro Glu Val Ile Ser Arg Ser Leu Tyr Ala Thr 565 570 575 580	2143
gag gtg gat atc tgg tct ctg ggc atc atg gtg att gag atg gta gat Glu Val Asp Ile Trp Ser Leu Gly Ile Met Val Ile Glu Met Val Asp 585 590 595	2191
ggg gag cca ccg tac ttc agt gac tcc cca gtg caa gcc atg aag agg Gly Glu Pro Pro Tyr Phe Ser Asp Ser Pro Val Gln Ala Met Lys Arg 600 605 610	2239
ctc cgg gac agc ccc cca ccc aag ctg aaa aac tct cac aag gtc tcc Leu Arg Asp Ser Pro Pro Pro Lys Leu Lys Asn Ser His Lys Val Ser 615 620 625	2287
cca gtg ctg cga gac ttc ctg gag cgg atg ctg gtg cgg gac ccc caa Pro Val Leu Arg Asp Phe Leu Glu Arg Met Leu Val Arg Asp Pro Gln 630 635 640	2335
gag aga gcc aca gcc cag gag ctc cta gac cac ccc ttc ctg ctg cag Glu Arg Ala Thr Ala Gln Glu Leu Leu Asp His Pro Phe Leu Leu Gln 645 650 655 660	2383
aca ggg cta cct gag tgc ctg gtg ccc ctg atc cag ctc tac cga aag Thr Gly Leu Pro Glu Cys Leu Val Pro Leu Ile Gln Leu Tyr Arg Lys 665 670 675	2431
cag acc tcc acc tgc tga gccac cccaagtatg cctgccacct acgcccacag	2485

Gln Thr Ser Thr Cys *

680

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tctctccaaa gattgaaatg tgaagcccca gccccaccct ctgcccttca gcctactggg 2605
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gtccactagt gtcctaggcc actgcagagg gcagactgct ggtctccaca gatacctgct 2845
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cggaatcccg cttcctccct cacgtctgat gtcctgaagg tgcagtccca cctgtacagc 2965
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<211> 1968

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<213> Homo sapiens

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ggtgacaggc gttgagacca ccgaaggga ccc atg gct agg atc agt ttt tcc 174
Met Ala Arg Ile Ser Phe Ser
1 5

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Tyr Leu Cys Pro Ala Ser Trp Tyr Phe Thr Val Pro Thr Val Ser Pro
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Phe Leu Arg Gln Arg Val Ala Phe Leu Gly Leu Phe Phe Ile Ser Cys
25 30 35

ctc ctt tta ctt atg tta atc ata gac ttt cga cat tgg agt gct tca 318
Leu Leu Leu Leu Met Leu Ile Ile Asp Phe Arg His Trp Ser Ala Ser
40 45 50 55

tta cca cga gat agg caa tac gaa agg tat ttg gct cga gta ggg gag	366
Leu Pro Arg Asp Arg Gln Tyr Glu Arg Tyr Leu Ala Arg Val Gly Glu	
60 65 70	
ctt gaa gct act gac act gaa gac cca aat ctg aat tat gga ctt gtt	414
Leu Glu Ala Thr Asp Thr Glu Asp Pro Asn Leu Asn Tyr Gly Leu Val	
75 80 85	
gtt gac tgt ggc agc agt ggt tcc cgg att ttt gtt tat ttc tgg cca	462
Val Asp Cys Gly Ser Ser Gly Ser Arg Ile Phe Val Tyr Phe Trp Pro	
90 95 100	
aga cat aat ggg aac ccc cat gac ttg ctg gac atc aaa cag atg aga	510
Arg His Asn Gly Asn Pro His Asp Leu Leu Asp Ile Lys Gln Met Arg	
105 110 115	
gac cgc aac agc caa cca gtg gtt aaa aaa atc aag cca gga atc tct	558
Asp Arg Asn Ser Gln Pro Val Val Lys Lys Ile Lys Pro Gly Ile Ser	
120 125 130 135	
gca atg gca gac act cca gaa cat gcc agt gat tac ctt cgt cct ctg	606
Ala Met Ala Asp Thr Pro Glu His Ala Ser Asp Tyr Leu Arg Pro Leu	
140 145 150	
ctg agc ttt gct gct gct cat gtg cct gtg aag aag cac aag gag acc	654
Leu Ser Phe Ala Ala Ala His Val Pro Val Lys Lys His Lys Glu Thr	
155 160 165	
cct ctt tac atc ctc tgc aca gca ggc atg agg ctt ctc cct gag agg	702
Pro Leu Tyr Ile Leu Cys Thr Ala Gly Met Arg Leu Leu Pro Glu Arg	
170 175 180	
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Lys Gln Leu Ala Ile Leu Ala Asp Leu Val Lys Asp Leu Pro Leu Glu	
185 190 195	
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Phe Asp Phe Leu Phe Ser Gln Ser Gln Ala Glu Val Ile Ser Gly Lys	
200 205 210 215	
cag gaa ggg gtt tat gca tgg att gga atc aac ttt gtt ttg gga aga	846
Gln Glu Gly Val Tyr Ala Trp Ile Gly Ile Asn Phe Val Leu Gly Arg	
220 225 230	
ttc gac cac gag gat gaa tca gat gct gag gct acc cag gaa ttg gca	894
Phe Asp His Glu Asp Glu Ser Asp Ala Glu Ala Thr Gln Glu Leu Ala	
235 240 245	
gca gga cgg aga agg aca gta ggg ata ctg gat atg gga gga gcc tct	942
Ala Gly Arg Arg Arg Thr Val Gly Ile Leu Asp Met Gly Gly Ala Ser	
250 255 260	
ctc caa att gct tat gaa gtt cct acc tca acc tct gtc ctt cct gca	990
Leu Gln Ile Ala Tyr Glu Val Pro Thr Ser Thr Ser Val Leu Pro Ala	
265 270 275	

aag cag gaa gaa gct gcc aag atc ctg ctg gct gag ttc aac ctg ggc	1038
Lys Gln Glu Glu Ala Ala Lys Ile Leu Leu Ala Glu Phe Asn Leu Gly	
280 285 290 295	
tgt gat gtg caa cac act gaa cac gtg tac agg gtt tat gtc aca act	1086
Cys Asp Val Gln His Thr Glu His Val Tyr Arg Val Tyr Val Thr Thr	
300 305 310	
ttt ctg ggt ttc gga ggc aac ttt gcc cgg cag cgc tac gaa gac ctt	1134
Phe Leu Gly Phe Gly Gly Asn Phe Ala Arg Gln Arg Tyr Glu Asp Leu	
315 320 325	
gtt ctg aat gaa act ctt aac aaa aac aga ttg ctt ggt cag aag aca	1182
Val Leu Asn Glu Thr Leu Asn Lys Asn Arg Leu Leu Gly Gln Lys Thr	
330 335 340	
ggg ctg agt ccc gac aat cca ttt ctg gat ccc tgc ctg cca gtg gga	1230
Gly Leu Ser Pro Asp Asn Pro Phe Leu Asp Pro Cys Leu Pro Val Gly	
345 350 355	
ctc aca gat gtg gtg gag agg aac agc caa gtc tta cat gtc cga gga	1278
Leu Thr Asp Val Val Glu Arg Asn Ser Gln Val Leu His Val Arg Gly	
360 365 370 375	
aga gga gac tgg gtg tct tgt ggg gca atg ctg agc ccc ctg ctg gct	1326
Arg Gly Asp Trp Val Ser Cys Gly Ala Met Leu Ser Pro Leu Leu Ala	
380 385 390	
cgc tcc aac acc agc cag gcc tca ctc aat ggc ata tat caa tcg cct	1374
Arg Ser Asn Thr Ser Gln Ala Ser Leu Asn Gly Ile Tyr Gln Ser Pro	
395 400 405	
att gac ttc aac aac agc gag ttc tac ggc ttc tct gag ttt ttt tat	1422
Ile Asp Phe Asn Asn Ser Glu Phe Tyr Gly Phe Ser Glu Phe Phe Tyr	
410 415 420	
tgt aca gag gat gtg ttg cgc att ggt ggc cgc tac cat ggg cca aca	1470
Cys Thr Glu Asp Val Leu Arg Ile Gly Gly Arg Tyr His Gly Pro Thr	
425 430 435	
ttt gcc aag gct gct cag gat tac tgt ggc atg gct tgg tcg gta cta	1518
Phe Ala Lys Ala Ala Gln Asp Tyr Cys Gly Met Ala Trp Ser Val Leu	
440 445 450 455	
act cag aga ttc aag aat ggc ctc ttt tca tca cat gca gat gag cat	1566
Thr Gln Arg Phe Lys Asn Gly Leu Phe Ser Ser His Ala Asp Glu His	
460 465 470	
cga ctc aaa tat cag tgt ttt aaa tcg gct tgg atg tac caa gtc tta	1614
Arg Leu Lys Tyr Gln Cys Phe Lys Ser Ala Trp Met Tyr Gln Val Leu	
475 480 485	
cat gaa gga ttc cac ttt ccc tat gac tac cca aac ctg cgg aca gcc	1662
His Glu Gly Phe His Phe Pro Tyr Asp Tyr Pro Asn Leu Arg Thr Ala	
490 495 500	
cag ctg gtg tat gac cga gag gtt cag tgg acg ctg gga gcc att cta	1710

cca atc atc act ggt agc aaa gat tta cag aat gtc aat atc aca ctg	513
Pro Ile Ile Thr Gly Ser Lys Asp Leu Gln Asn Val Asn Ile Thr Leu	
20 25 30	
cgc atc atc ttc cag cct gtt gct agc cag ctt cct cgc atc ttc acc	561
Arg Ile Ile Phe Gln Pro Val Ala Ser Gln Leu Pro Arg Ile Phe Thr	
35 40 45	
agc atc gga gag gac tat gat gag cct gtg ctg acg tac atc acg acc	609
Ser Ile Gly Glu Asp Tyr Asp Glu Pro Val Leu Thr Tyr Ile Thr Thr	
50 55 60	
gag atc ctc aag tca gtg gtg gct cgc ttt gat gct gga gaa gtt atc	657
Glu Ile Leu Lys Ser Val Val Ala Arg Phe Asp Ala Gly Glu Val Ile	
65 70 75 80	
act cag aga gag ctg gtc tcc agg cag gtg agc aac gac ctt acg gag	705
Thr Gln Arg Glu Leu Val Ser Arg Gln Val Ser Asn Asp Leu Thr Glu	
85 90 95	
caa gca gcc aca ttt ggg ctc atc ctg gac gac gtg tcc ttg aca tat	753
Gln Ala Ala Thr Phe Gly Leu Ile Leu Asp Asp Val Ser Leu Thr Tyr	
100 105 110	
ctg acc ttt gga aag gag ttc aca gaa gca gtg gaa gcc aaa cag gtg	801
Leu Thr Phe Gly Lys Glu Phe Thr Glu Ala Val Glu Ala Lys Gln Val	
115 120 125	
gct cag cag gaa gca gag agg gcc aga ttt gtg aag gaa aag gct gag	849
Ala Gln Gln Glu Ala Glu Arg Ala Arg Phe Val Lys Glu Lys Ala Glu	
130 135 140	
cag cag aaa aag gct gag cag cag aaa aag gtt gag cag cag aaa aag	897
Gln Gln Lys Lys Ala Glu Gln Gln Lys Lys Val Glu Gln Gln Lys Lys	
145 150 155 160	
gca gcc gtg atc tct gct gag ggc gac tcc aag gca acc gag ctg att	945
Ala Ala Val Ile Ser Ala Glu Gly Asp Ser Lys Ala Thr Glu Leu Ile	
165 170 175	
gcc aac tca ctg gcc acc gcg ggg gac ggc ctg atg gag ctg tgc aag	993
Ala Asn Ser Leu Ala Thr Ala Gly Asp Gly Leu Met Glu Leu Cys Lys	
180 185 190	
ttg gaa gcc gcg gag gct ctc gga aca tga c ctacctgccg gcggggcagt	1044
Leu Glu Ala Ala Glu Ala Leu Gly Thr *	
195 200	
ccgctcctcc ggctgcccc tgagggccca ccctgcctgc acctccgcag gctgactggg	1104
ccacagcccc aatgattctt aacactgcct taccctcccta cccagaaat cactgaaatt	1164
tcataattgg cttaaagtga aggaaataaa agtaaaatca cttcagaact cttaaaaaaa	1224
aaaaa	1229

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 <213> Homo sapiens

<220>
 <221> CDS
 <222> (88)..(1653)

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ggagctgcca atcaaaagtg gcattac      atg aaa aat ata aaa gca ctt gtg      111
                                   Met Lys Asn Ile Lys Ala Leu Val
                                   1                               5

gcc ttt cat agc act gcc ttg gat aag gaa att aca tca gca aat tat      159
Ala Phe His Ser Thr Ala Leu Asp Lys Glu Ile Thr Ser Ala Asn Tyr
    10                               15                               20

gct ggt gtc tgt aca tca tct gtg att aaa gaa gaa aac att gat caa      207
Ala Gly Val Cys Thr Ser Ser Val Ile Lys Glu Glu Asn Ile Asp Gln
    25                               30                               35                               40

cca gga tac tgt tat ctc tca cct gat gga aag aga aaa act atg ctc      255
Pro Gly Tyr Cys Tyr Leu Ser Pro Asp Gly Lys Arg Lys Thr Met Leu
                                45                               50                               55

tgc ttg gct tgt gga caa tcc atg aga aca gag aaa gga ctg aaa caa      303
Cys Leu Ala Cys Gly Gln Ser Met Arg Thr Glu Lys Gly Leu Lys Gln
                                60                               65                               70

ttg ctt cca ggg gtt cca ttc ctc tgt att tca ggc acc aag act cag      351
Leu Leu Pro Gly Val Pro Phe Leu Cys Ile Ser Gly Thr Lys Thr Gln
                                75                               80                               85

aag ccc ttc tta caa ggg ccc ttc aag gtc atc agt gtg gct gag gtt      399
Lys Pro Phe Leu Gln Gly Pro Phe Lys Val Ile Ser Val Ala Glu Val
    90                               95                               100

gat ttg tcg tgt gac aag gct gaa aaa act cta agt tac tac caa gca      447
Asp Leu Ser Cys Asp Lys Ala Glu Lys Thr Leu Ser Tyr Tyr Gln Ala
   105                               110                               115                               120

cgt cta ttg tct tta cgg atg aag acc tgc acg caa gct gca tct cac      495
Arg Leu Leu Ser Leu Arg Met Lys Thr Cys Thr Gln Ala Ala Ser His
                                125                               130                               135

agt ggc atg gca gcc aca cac cag aag gca gtg aaa ata att gca tac      543
Ser Gly Met Ala Ala Thr His Gln Lys Ala Val Lys Ile Ile Ala Tyr
                                140                               145                               150

aaa aat ggg gat ggg tat cgt aat ggg aag tta att gtg gct gga aca      591
Lys Asn Gly Asp Gly Tyr Arg Asn Gly Lys Leu Ile Val Ala Gly Thr

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gtc aag ccg agc aac ctg tat aag cag ccc aac aca aaa cga gtg tgg	1311
Val Lys Pro Ser Asn Leu Tyr Lys Gln Pro Asn Thr Lys Arg Val Trp	
395 400 405	
att tat cta aat gga ggc aga cct gaa gat ggc act tat gcc tgg ggc	1359
Ile Tyr Leu Asn Gly Gly Arg Pro Glu Asp Gly Thr Tyr Ala Trp Gly	
410 415 420	
aaa act att tca gag ctg ctg caa gac tgc tcc tct cgt ctc aaa atg	1407
Lys Thr Ile Ser Glu Leu Leu Gln Asp Cys Ser Ser Arg Leu Lys Met	
425 430 435 440	
acc cac cca gct aga gca ctg tac acc ccc agt gga gag cca att cag	1455
Thr His Pro Ala Arg Ala Leu Tyr Thr Pro Ser Gly Glu Pro Ile Gln	
445 450 455	
tcc tgg gac gac ata gag cga gat atg gtc atc tgt gtg tct atg gga	1503
Ser Trp Asp Asp Ile Glu Arg Asp Met Val Ile Cys Val Ser Met Gly	
460 465 470	
cat ggt ttc aaa acc cca aaa gag tta aaa caa ctg atg gag atc aga	1551
His Gly Phe Lys Thr Pro Lys Glu Leu Lys Gln Leu Met Glu Ile Arg	
475 480 485	
gca aat tat gcc aga atc cga agg cag cag ggc cct caa gcc aca gac	1599
Ala Asn Tyr Ala Arg Ile Arg Arg Gln Gln Gly Pro Gln Ala Thr Asp	
490 495 500	
att gtg gtg tca cca tcc acg aag ctg ctg tct ctg gca cat ctc cac	1647
Ile Val Val Ser Pro Ser Thr Lys Leu Leu Ser Leu Ala His Leu His	
505 510 515 520	
aat taa ctccatcag aaccatcgga tttctgctg ttttttctg gaaagaaaac	1703
Asn *	
tttctttacc cacttataaa cagaagactg tgacaagaag gccattatt tccatcgctg	1763
aagactctaa atttgcaaa tcttctaaat aacaatcctg catagtttat taaaaaaaaat	1823
tagtcgtaaa atttatcctt caaaaatctg catttttaaata aaaccctgac agtgatttct	1883
caagactgta aagatattag tctgagaatg caactctaac agactgctct gggcatcttt	1943
tctctttgcc ttggccaggc ctctcagaat tgagtgagcg tgtgactcca tttgcacagt	2003
gggacagata gtacaactga aataaaaaagt ggaggcctct gcaaaaaata aaaaataaaa	2063
aataaattta tccttcaaaa taactcagtt ttttcaatgg gcctatTTTTT aagaatgaac	2123
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 <213> Homo sapiens

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<220>
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 <222> (1)...(1432)
 <223> n = a,t,c or g

<400> 45

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caacgctggc aagtctcaaa gtcgccacag aaacatgccc ctgattcagt gcctctgctt      120
agctgtaaca tgtaaatcag aactacctgg catcttcctg aacaagactt tcaatagggg      180
ccagt      atg ctt cgc ttc atc cag aag ttt tct caa gca tct tca aag      227
           Met Leu Arg Phe Ile Gln Lys Phe Ser Gln Ala Ser Ser Lys
             1             5             10

ata ctg aag tac tct ttc cca gtg gga cta aga acc agc aga aca gat      275
Ile Leu Lys Tyr Ser Phe Pro Val Gly Leu Arg Thr Ser Arg Thr Asp
  15             20             25             30

ata ctt tct ctc aag atg tct ctc cag caa aac ttt tcc cca tgt cca      323
Ile Leu Ser Leu Lys Met Ser Leu Gln Gln Asn Phe Ser Pro Cys Pro
             35             40             45

agg cct tgg ctt tcc tca tca ttt cca gcg tat atg agc aag aca cag      371
Arg Pro Trp Leu Ser Ser Ser Phe Pro Ala Tyr Met Ser Lys Thr Gln
             50             55             60

tgc tat cat aca tcc ccc tgc agc ttt aaa aag cag cag aag caa gca      419
Cys Tyr His Thr Ser Pro Cys Ser Phe Lys Lys Gln Gln Lys Gln Ala
             65             70             75

ctt cta gcc aga ccc tca agc acc atc act tac cta act gac agc cca      467
Leu Leu Ala Arg Pro Ser Ser Thr Ile Thr Tyr Leu Thr Asp Ser Pro
             80             85             90

aag cca gca tta tgt gta act ctg gca gga cta atc ccc ttc gtt gct      515
Lys Pro Ala Leu Cys Val Thr Leu Ala Gly Leu Ile Pro Phe Val Ala
  95             100             105             110

cca cca ctg gtc atg ctg atg aca aaa act tat att ccc ata tta gct      563
Pro Pro Leu Val Met Leu Met Thr Lys Thr Tyr Ile Pro Ile Leu Ala
             115             120             125

ttt act cag atg gct tat gga gcc agt ttc cta tct ttc ttg ggt ggg      611
Phe Thr Gln Met Ala Tyr Gly Ala Ser Phe Leu Ser Phe Leu Gly Gly
             130             135             140

atc aga tgg ggt ttt gct cta cca gaa ggt agt cca gcc aaa cca gac      659

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Ile Arg Trp Gly Phe Ala Leu Pro Glu Gly Ser Pro Ala Lys Pro Asp
    145                                150                        155

tac ctt aat tta gct agc agt gca gct cct ctt ttc ttt tca tgg ttt    707
Tyr Leu Asn Leu Ala Ser Ser Ala Ala Pro Leu Phe Phe Ser Trp Phe
    160                                165                        170

gcc ttc ctt att tct gaa aga ctt agt gaa gcc ata gtc aca gta ata    755
Ala Phe Leu Ile Ser Glu Arg Leu Ser Glu Ala Ile Val Thr Val Ile
    175                                180                        185                        190

atg ggt atg gga gta gca ttc cac ctt gaa ctt ttt ctc tta cca cat    803
Met Gly Met Gly Val Ala Phe His Leu Glu Leu Phe Leu Leu Pro His
    195                                200                        205

tat ccc aac tgg ttt aaa gcc ctg agg ata gta gtc act tta ttg gcc    851
Tyr Pro Asn Trp Phe Lys Ala Leu Arg Ile Val Val Thr Leu Leu Ala
    210                                215                        220

act ttt tca ttt ata atc act tta gta gtt aaa agt agt ttt cca gaa    899
Thr Phe Ser Phe Ile Ile Thr Leu Val Val Lys Ser Ser Phe Pro Glu
    225                                230                        235

aaa gga cat aag aga cct ggt caa gta taa a aaatataaaa gtctgggaag    950
Lys Gly His Lys Arg Pro Gly Gln Val *
    240                                245

tgaggagcac ctctgcccag ctgctgcccc gtctgggaag tgaggagcgc ctctgcctgg    1010

ccgcctgacc atctgggaag tgtgacaagc gcctctgccc ggccgctgtg caaccttcca    1070

cgtgtgaagt gacagccttg tgtgtgatct tttctgtctt ccccaagttt gcattttcga    1130

cattaaagtt tacttttttag ttaaaagttt aaaaaatata tataaataca ctgtagagan    1190

aacatgtgtn tgccagctac acctttctcn acttctgttt ggcttttttt cccacacca    1250

atggtaatth atcttcacag atngttcttc atttctagaa attgttactt catggtaatt    1310

acttgagcaa aagcttgaaa atccctgaca agtacttntc atctcatagt atattagttt    1370

tcactcagtc attttatgaa taatanagtt atccacttaa acatttcaat aatgtaacca    1430

gc                                                                    1432

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 <211> 2047
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 <213> Homo sapiens

<220>
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 <222> (269) .. (1372)

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cctctctcag tccaaaagcg gcttttgggtt cggcgcagag agaccggggg gtctagcttt 180
tcctcgaaaa gcgccgcctt gcccttggcc ccgagaacag acaaagagca ccgcagggcc 240
gatcacgctg ggggcgctga ggccggcc atg gtc atg gaa gtg ggc acc ctg 292
Met Val Met Glu Val Gly Thr Leu
1 5
gac gct gga ggc ctg cgg gcg ctg ctg ggg gag cga gcg gcg caa tgc 340
Asp Ala Gly Gly Leu Arg Ala Leu Leu Gly Glu Arg Ala Ala Gln Cys
10 15 20
ctg ctg ctg gac tgc cgc tcc ttc ttc gct ttc aac gcc ggc cac atc 388
Leu Leu Leu Asp Cys Arg Ser Phe Phe Ala Phe Asn Ala Gly His Ile
25 30 35 40
gcc ggc tct gtc aac gtg cgc ttc agc acc atc gtg cgg cgc cgg gcc 436
Ala Gly Ser Val Asn Val Arg Phe Ser Thr Ile Val Arg Arg Arg Ala
45 50 55
aag ggc gcc atg ggc ctg gag cac atc gtg ccc aac gcc gag ctc cgc 484
Lys Gly Ala Met Gly Leu Glu His Ile Val Pro Asn Ala Glu Leu Arg
60 65 70
ggc cgc ctg ctg gcc ggc gcc tac cac gcc gtg gtg ttg ctg gac gag 532
Gly Arg Leu Leu Ala Gly Ala Tyr His Ala Val Val Leu Leu Asp Glu
75 80 85
cgc agc gcc gcc ctg gac ggc gcc aag cgc gac ggc acc ctg gcc ctg 580
Arg Ser Ala Ala Leu Asp Gly Ala Lys Arg Asp Gly Thr Leu Ala Leu
90 95 100
gcg gcc ggc gcg ctc tgc cgc gag gcg cgc gcc gcg caa gtc ttc ttc 628
Ala Ala Gly Ala Leu Cys Arg Glu Ala Arg Ala Ala Gln Val Phe Phe
105 110 115 120
ctc aaa gga gga tac gaa gcg ttt tcg gct tcc tgc ccg gag ctg tgc 676
Leu Lys Gly Gly Tyr Glu Ala Phe Ser Ala Ser Cys Pro Glu Leu Cys
125 130 135
agc aaa cag tcg acc ccc atg ggg ctc agc ctt ccc ctg agt act agc 724
Ser Lys Gln Ser Thr Pro Met Gly Leu Ser Leu Pro Leu Ser Thr Ser
140 145 150
gtc cct gac agc gcg gaa tct ggg tgc agt tcc tgc agt acc cca ctc 772
Val Pro Asp Ser Ala Glu Ser Gly Cys Ser Ser Cys Ser Thr Pro Leu
155 160 165
tac gat cag ggt ggc ccg gtg gaa atc ctg ccc ttt ctg tac ctg ggc 820
Tyr Asp Gln Gly Gly Pro Val Glu Ile Leu Pro Phe Leu Tyr Leu Gly
170 175 180

agt gcg tat cac gct tcc cgc aag gac atg ctg gat gcc ttg ggc ata	868
Ser Ala Tyr His Ala Ser Arg Lys Asp Met Leu Asp Ala Leu Gly Ile	
185 190 195 200	
act gcc ttg atc aac gtc tca gcc aat tgt ccc aac cat ttt gag ggt	916
Thr Ala Leu Ile Asn Val Ser Ala Asn Cys Pro Asn His Phe Glu Gly	
205 210 215	
cac tac cag tac aag agc atc cct gtg gag gac aac cac aag gca gac	964
His Tyr Gln Tyr Lys Ser Ile Pro Val Glu Asp Asn His Lys Ala Asp	
220 225 230	
atc agc tcc tgg ttc aac gag gcc att gac ttc ata gac tcc atc aag	1012
Ile Ser Ser Trp Phe Asn Glu Ala Ile Asp Phe Ile Asp Ser Ile Lys	
235 240 245	
aat gct gga gga agg gtg ttt gtc cac tgc cag gca ggc att tcc cgg	1060
Asn Ala Gly Gly Arg Val Phe Val His Cys Gln Ala Gly Ile Ser Arg	
250 255 260	
tca gcc acc atc tgc ctt gct tac ctt atg agg act aat cga gtc aag	1108
Ser Ala Thr Ile Cys Leu Ala Tyr Leu Met Arg Thr Asn Arg Val Lys	
265 270 275 280	
ctg gac gag gcc ttt gag ttt gtg aag cag agg cga agc atc atc tct	1156
Leu Asp Glu Ala Phe Glu Phe Val Lys Gln Arg Arg Ser Ile Ile Ser	
285 290 295	
ccc aac ttc agc ttc atg ggc cag ctg ctg cag ttt gag tcc cag gtg	1204
Pro Asn Phe Ser Phe Met Gly Gln Leu Leu Gln Phe Glu Ser Gln Val	
300 305 310	
ctg gct ccg cac tgt tcg gca gag gct ggg agc ccc gcc atg gct gtg	1252
Leu Ala Pro His Cys Ser Ala Glu Ala Gly Ser Pro Ala Met Ala Val	
315 320 325	
ctc gac cga ggc acc tcc acc acc acc gtg ttc aac ttc ccc gtc tcc	1300
Leu Asp Arg Gly Thr Ser Thr Thr Thr Val Phe Asn Phe Pro Val Ser	
330 335 340	
atc cct gtc cac tcc acg aac agt gcg ctg agc tac ctt cag agc ccc	1348
Ile Pro Val His Ser Thr Asn Ser Ala Leu Ser Tyr Leu Gln Ser Pro	
345 350 355 360	
att acg acc tct ccc agc tgc tga aaggccacgg gaggtgaggc tcttcacatc	1402
Ile Thr Thr Ser Pro Ser Cys *	
365	
ccattggggac tccatgctcc ttgagaggag aaatgcaata actctgggag gggctcgaga	1462
gggctgggtcc ttatttatatt aacttcaccc gagttcctct gggtttctaa gcagttatgg	1522
tgatgactta gcgtcaagac atttgctgaa ctgagcacat tcgggaccaa tatatagtgg	1582
gtacatcaag tccatctgac aaaatggggc agaagagaaa ggactcagtg tgtgatccgg	1642
tttttttttg ctgcgccctg ttttttgtag aatctcttca tgcttgacat acctaccagt	1702

attattcccg acgacacata tacatatgag aatatacctt atttattttt gtgtaggtgt 1762
 ctgccttcac aaatgtcatt gtctactcct agaagaacca aatacctcaa tttttgtttt 1822
 tgagtactgt actatcctgt aaatatatct taagcaggtt tgttttcagc actgatggaa 1882
 aataccagtgt ttgggttttt ttttagttgc caacagttgt atgtttgctg attatttatg 1942
 acctgaaata atatatttct tcttctaaga agacattttg ttacataagg atgacttttt 2002
 tatacaatgg aataaattat ggcatattcta ttgaaaaaaa aaaaa 2047

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 ccctgcgcgt aagcttccta taagactgtt ttctctgatt gacttctggg ggcttggcctt 120
 cattatgatg tgtttatgtt cacagaaatt tttgtaattt ctctatggta acaacttttt 180
 atgccttaag agtgtctctg aggcaggatt ctaagagatt ctctttgact caatcccaga 240
 tagaggataa atctcctggc aaagcccaga atg acc aca gcc ctg gaa cct 291
 Met Thr Thr Ala Leu Glu Pro
 1 5
 gag gac caa aaa gga ctt ctg ata att aag gca gag gac cat tac tgg 339
 Glu Asp Gln Lys Gly Leu Leu Ile Ile Lys Ala Glu Asp His Tyr Trp
 10 15 20
 gga cag gat tcc agc tca caa aag tgc agt cct cac agg agg gaa ctc 387
 Gly Gln Asp Ser Ser Ser Gln Lys Cys Ser Pro His Arg Arg Glu Leu
 25 30 35
 tat aga caa cac ttc agg aag ctc tgc tat cag gat gca cct gga ccc 435
 Tyr Arg Gln His Phe Arg Lys Leu Cys Tyr Gln Asp Ala Pro Gly Pro
 40 45 50 55
 cgt gaa gct ctt acc cag ctg tgg gag ctc tgc cgt cag tgg ctg agg 483
 Arg Glu Ala Leu Thr Gln Leu Trp Glu Leu Cys Arg Gln Trp Leu Arg
 60 65 70
 cca gaa tgc cac acc aag gag cag att tta gac ctg ctg gtg cta gaa 531
 Pro Glu Cys His Thr Lys Glu Gln Ile Leu Asp Leu Leu Val Leu Glu
 75 80 85

cag ttc ctg agc att ctt cct aaa gac ctg caa gca tgg gtg cgt gca Gln Phe Leu Ser Ile Leu Pro Lys Asp Leu Gln Ala Trp Val Arg Ala 90 95 100	579
cac cat cca gag act gga gag gag gca gtg acg gta ctg gag gat ctg His His Pro Glu Thr Gly Glu Glu Ala Val Thr Val Leu Glu Asp Leu 105 110 115	627
gag aga gag ctt gat gaa cct gga aag cag gtc cca ggc aat tca gaa Glu Arg Glu Leu Asp Glu Pro Gly Lys Gln Val Pro Gly Asn Ser Glu 120 125 130 135	675
aga cgg gac ata ctc atg gac aag ttg gcc ccc ttg gga agg cca tat Arg Arg Asp Ile Leu Met Asp Lys Leu Ala Pro Leu Gly Arg Pro Tyr 140 145 150	723
gaa tca ctg act gtc cag ctc cat ccc aaa aag acc cag ctg gag cag Glu Ser Leu Thr Val Gln Leu His Pro Lys Lys Thr Gln Leu Glu Gln 155 160 165	771
gaa gct ggg aaa cca caa agg aat ggt gat aaa act agg act aag aat Glu Ala Gly Lys Pro Gln Arg Asn Gly Asp Lys Thr Arg Thr Lys Asn 170 175 180	819
gaa gag ttg ttc cag aag gaa gat atg ccc aaa gac aag gaa ttc ctt Glu Glu Leu Phe Gln Lys Glu Asp Met Pro Lys Asp Lys Glu Phe Leu 185 190 195	867
ggg gag ata aat gac aga ctg aac aaa gat act cct cag cat cct aag Gly Glu Ile Asn Asp Arg Leu Asn Lys Asp Thr Pro Gln His Pro Lys 200 205 210 215	915
tcc aaa gat att att gaa aat gag ggc aga tca gaa tgg caa cag agg Ser Lys Asp Ile Ile Glu Asn Glu Gly Arg Ser Glu Trp Gln Gln Arg 220 225 230	963
gaa aga aga cga tat aaa tgt gat gaa tgt ggg aaa agt ttc agt cat Glu Arg Arg Arg Tyr Lys Cys Asp Glu Cys Gly Lys Ser Phe Ser His 235 240 245	1011
agc tca gac ctt agt aaa cac agg aga act cac acg gga gag aag ccc Ser Ser Asp Leu Ser Lys His Arg Arg Thr His Thr Gly Glu Lys Pro 250 255 260	1059
tat aaa tgt gat gag tgt gga aaa gcc ttc att cag cgc tca cat ctc Tyr Lys Cys Asp Glu Cys Gly Lys Ala Phe Ile Gln Arg Ser His Leu 265 270 275	1107
att gga cat cat aga gta cac acg gga gta aaa ccc tat aaa tgt aaa Ile Gly His His Arg Val His Thr Gly Val Lys Pro Tyr Lys Cys Lys 280 285 290 295	1155
gaa tgt ggg aaa gac ttc agt ggg cgc aca ggt ctt att cag cat cag Glu Cys Gly Lys Asp Phe Ser Gly Arg Thr Gly Leu Ile Gln His Gln 300 305 310	1203

aga atc cac aca ggt gaa aaa ccc tat gaa tgt gat gag tgt gga agg 1251
 Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Asp Glu Cys Gly Arg
 315 320 325

cct ttc cga gta agt tca gct ctt att aga cat caa aga att cat acc 1299
 Pro Phe Arg Val Ser Ser Ala Leu Ile Arg His Gln Arg Ile His Thr
 330 335 340

gca aat aaa ctc tac taa tatagc agtaatatca aaagttcttt ggacactcag 1353
 Ala Asn Lys Leu Tyr *
 345

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gcttcagtca tcattaaact tctctggacc aaaaaaaaa 1451

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 aatgtcctgg ctgagattca gtcttttcgaa ctgcctattg aagctacttt aagtcaacag 180
 gaagagatac ctctttgggtc aggaatgtaa aaacaggaag gaggaagtct attgcaaadc 240
 tgtgctggct gattatgaat tcagggttca ccatggagga tggtcatta atg atc 295
 Met Ile
 1

atc agt gtg ctg tgc tgt tat tca aaa tta cag tct gtg tat gat gac 343
 Ile Ser Val Leu Cys Cys Tyr Ser Lys Leu Gln Ser Val Tyr Asp Asp
 5 10 15

caa cca aat gcg cac aag aag ttt atg gaa aag tta gat gct tgt atc 391
 Gln Pro Asn Ala His Lys Lys Phe Met Glu Lys Leu Asp Ala Cys Ile
 20 25 30

cgt aat cat gac aag gaa att gaa aag atg tgt aat ttt cat cat cag 439
 Arg Asn His Asp Lys Glu Ile Glu Lys Met Cys Asn Phe His His Gln
 35 40 45 50

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 Gly Phe Val Asp Ala Ile Thr Glu Leu Leu Lys Val Arg Thr Asp Ala
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Glu Lys Leu Lys Val Gln Val Thr Asp Thr Asn Arg Arg Phe Gln Asp	
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Ala Gly Lys Glu Val Ile Val His Thr Glu Asp Ile Ile Arg Cys Arg	
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Ile Gln Gln Arg Asn Ile Thr Thr Val Val Glu Lys Leu Gln Leu Cys	
100 105 110	
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Leu Pro Val Leu Glu Met Tyr Ser Lys Leu Lys Glu Gln Met Ser Ala	
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Lys Arg Tyr Tyr Ser Ala Leu Lys Thr Met Glu Gln Leu Glu Asn Val	
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Tyr Phe Pro Trp Val Ser Gln Tyr Arg Phe Cys Gln Leu Met Ile Glu	
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Asn Leu Pro Lys Leu Arg Glu Asp Ile Lys Glu Ile Ser Met Ser Asp	
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Leu Lys Asp Phe Leu Glu Ser Ile Arg Lys His Ser Asp Lys Ile Gly	
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Glu Thr Ala Met Lys Gln Ala Gln His Gln Lys Thr Phe Ser Val Ser	
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Leu Gln Lys Gln Asn Lys Met Lys Phe Gly Lys Asn Met Tyr Ile Asn	
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Arg Asp Arg Ile Pro Glu Glu Arg Asn Glu Thr Val Leu Lys His Ser	
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Leu Glu Glu Glu Asp Glu Asn Glu Glu Glu Ile Leu Thr Val Gln Asp	
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260 265 270	
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Leu Gly Asp Glu Glu Thr Phe Glu Asn Tyr Tyr Arg Lys Gln Arg Lys	
275 280 285 290	
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Lys	Gln	Ala	Arg	Leu	Val	Leu	Gln	Pro	Gln	Ser	Asn	Met	His	Glu	Thr		
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Val	Asp	Gly	Tyr	Arg	Arg	Tyr	Phe	Thr	Gln	Ile	Val	Gly	Phe	Phe	Val		
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Val	Glu	Asp	His	Ile	Leu	His	Val	Thr	Gln	Gly	Leu	Val	Thr	Arg	Ala		
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Tyr	Thr	Asp	Glu	Leu	Trp	Asn	Met	Ala	Leu	Ser	Lys	Ile	Ile	Ala	Val		
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Leu	Arg	Ala	His	Ser	Ser	Tyr	Cys	Thr	Asp	Pro	Asp	Leu	Val	Leu	Glu		
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Leu	Lys	Asn	Leu	Thr	Val	Ile	Phe	Ala	Asp	Thr	Leu	Gln	Gly	Tyr	Gly		
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Phe	Pro	Val	Asn	Arg	Leu	Phe	Asp	Leu	Leu	Phe	Glu	Ile	Arg	Asp	Gln		
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Tyr	Asn	Glu	Thr	Leu	Leu	Lys	Lys	Trp	Ala	Gly	Val	Phe	Arg	Asp	Ile		
		405					410					415					
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Phe	Glu	Glu	Asp	Asn	Tyr	Ser	Pro	Ile	Pro	Val	Val	Asn	Glu	Glu	Glu		
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tat	aaa	att	gtc	atc	agc	aaa	ttt	ccc	ttt	caa	gat	cca	gac	ctt	gaa		1639
Tyr	Lys	Ile	Val	Ile	Ser	Lys	Phe	Pro	Phe	Gln	Asp	Pro	Asp	Leu	Glu		
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Lys	Gln	Ser	Phe	Pro	Lys	Lys	Phe	Pro	Met	Ser	Gln	Ser	Val	Pro	His		
				455				460						465			
att	tac	att	caa	gtt	aaa	gaa	ttt	att	tat	gcc	agc	ctt	aaa	ttt	tca		1735
Ile	Tyr	Ile	Gln	Val	Lys	Glu	Phe	Ile	Tyr	Ala	Ser	Leu	Lys	Phe	Ser		
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gag	tca	cta	cac	cgg	agc	tca	aca	gaa	ata	gac	gat	atg	ctt	aga	aaa		1783
Glu	Ser	Leu	His	Arg	Ser	Ser	Thr	Glu	Ile	Asp	Asp	Met	Leu	Arg	Lys		
		485					490					495					
tca	aca	aat	ctg	ctg	ctg	acc	aga	act	ttg	agt	agc	tgt	tta	ctg	aac		1831
Ser	Thr	Asn	Leu	Leu	Leu	Thr	Arg	Thr	Leu	Ser	Ser	Cys	Leu	Leu	Asn		
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ctt	att	aga	aaa	cct	cat	ata	ggg	ttg	aca	gag	ctg	gta	caa	atc	atc		1879
Leu	Ile	Arg	Lys	Pro	His	Ile	Gly	Leu	Thr	Glu	Leu	Val	Gln	Ile	Ile		

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Ile Asn Thr Thr His Leu Glu Gln Ala Cys Lys Tyr Leu Glu Asp Phe				
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ata act aac att aca aat att tcc caa gaa act gtt cat act aca aga				1975
Ile Thr Asn Ile Thr Asn Ile Ser Gln Glu Thr Val His Thr Thr Arg				
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ctt tat gga ctt tct act ttc aag gat gct cga cat gca gca gaa gga				2023
Leu Tyr Gly Leu Ser Thr Phe Lys Asp Ala Arg His Ala Ala Glu Gly				
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Glu Ile Tyr Thr Lys Leu Asn Gln Lys Ile Asp Glu Phe Val Gln Leu				
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Ala Asp Tyr Asp Trp Thr Met Ser Glu Pro Asp Gly Arg Ala Ser Gly				
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tat tta atg gac ctt ata aat ttt ttg aga agc atc ttt caa gtg ttt				2167
Tyr Leu Met Asp Leu Ile Asn Phe Leu Arg Ser Ile Phe Gln Val Phe				
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act cat ttg cct ggg aaa gtt gct cag aca gct tgc atg tca gcc tgc				2215
Thr His Leu Pro Gly Lys Val Ala Gln Thr Ala Cys Met Ser Ala Cys				
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Gln His Leu Ser Thr Ser Leu Met Gln Met Leu Leu Asp Ser Glu Leu				
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aaa caa ata agc atg gga gct gtt cag cag ttt aac tta gat gtc ata				2311
Lys Gln Ile Ser Met Gly Ala Val Gln Gln Phe Asn Leu Asp Val Ile				
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Gln Cys Glu Leu Phe Ala Ser Ser Glu Pro Val Pro Gly Phe Gln Gly				
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gat acc ctg cag cta gca ttc att gac ctc aga caa ctc ctt gac ctg				2407
Asp Thr Leu Gln Leu Ala Phe Ile Asp Leu Arg Gln Leu Leu Asp Leu				
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Phe Met Val Trp Asp Trp Ser Thr Tyr Leu Ala Asp Tyr Gly Gln Pro				
	710	715	720	
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Ala Ser Lys Tyr Leu Arg Val Asn Pro Asn Thr Ala Leu Thr Leu Leu				
	725	730	735	
gag aag atg aag gat act agc aaa aag aac aat ata ttt gct cag ttc				2551
Glu Lys Met Lys Asp Thr Ser Lys Lys Asn Asn Ile Phe Ala Gln Phe				
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Arg Lys Asn Asp Arg Asp Lys Gln Lys Leu Ile Glu Thr Val Val Lys
755                               760                               765                               770

cag ctg aga agt ttg gtg aat ggt atg tcc cag cac atg tag acctcac      2648
Gln Leu Arg Ser Leu Val Asn Gly Met Ser Gln His Met  *
                               775                               780

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tatggcctttg gaattcaatc atgtctgata tggtagtatt tcactaccat tttctgactt      3068

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ggcctgtaag aaactatgcc tgattctgta aaataagtgt aaagaattat atgtacatct      3728

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Lys Lys Glu Ala Pro Ala Pro Pro Lys Ala Glu Ala Lys Ala Lys Ala
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Leu Gln Gly Gln Glu Gly Ser Val Glu Arg Cys Pro Gln Pro Gln Lys
25 30 35

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Lys Gln Asp Pro His Val Thr His Leu Pro Ala Ala Gln Asp Thr Val
40 45 50

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Thr Pro Glu Ala Ala Gln Ile Ser Leu Glu Glu His Pro Gln Glu Lys
55 60 65

taa gctt gaccaccatg ttatcatcaa gtttccgctg accactgagt aggctgtgaa 304
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70

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gatcaaacag gctgtgaaga agtttgtgac attgatgtgg ccaaagtcaa cactctgatt 424

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cggccccgga gccctcggc ggcgccacc atg tac tcg gga gcc ggc ccc gca 173
Met Tyr Ser Gly Ala Gly Pro Ala
1 5

ctt gca cct cct gcg ccg ccg ccc ccc atc caa gga tat gcc ttc aag	221
Leu Ala Pro Pro Ala Pro Pro Pro Pro Ile Gln Gly Tyr Ala Phe Lys	
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Pro Pro Pro Arg Pro Asp Phe Gly Thr Ser Gly Arg Thr Ile Lys Leu	
25 30 35 40	
cag gcc aat ttc ttc gaa atg gac atc ccc aaa att gac atc tat cat	317
Gln Ala Asn Phe Phe Glu Met Asp Ile Pro Lys Ile Asp Ile Tyr His	
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Tyr Glu Leu Asp Ile Lys Pro Glu Lys Cys Pro Arg Arg Val Asn Arg	
60 65 70	
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Glu Ile Val Glu His Met Val Gln His Phe Lys Thr Gln Ile Phe Gly	
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Asp Arg Lys Pro Val Phe Asp Gly Arg Lys Asn Leu Tyr Thr Ala Met	
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Pro Leu Pro Ile Gly Arg Asp Lys Val Glu Leu Glu Val Thr Leu Pro	
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Gly Glu Gly Lys Asp Arg Ile Phe Lys Val Ser Ile Lys Trp Val Ser	
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Cys Val Ser Leu Gln Ala Leu His Asp Ala Leu Ser Gly Arg Leu Pro	
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Ser Val Pro Phe Glu Thr Ile Gln Ala Leu Asp Val Val Met Arg His	
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Leu Pro Ser Met Arg Tyr Thr Pro Val Gly Arg Ser Phe Phe Thr Ala	
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Gly Phe His Gln Ser Val Arg Pro Ser Leu Trp Lys Met Met Leu Asn	
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Ile Asp Val Ser Ala Thr Ala Phe Tyr Lys Ala Gln Pro Val Ile Glu	
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Phe Val Cys Glu Val Leu Asp Phe Lys Ser Ile Glu Glu Gln Gln Lys	
235 240 245	
cct ctg aca gat tcc caa agg gta aag ttt acc aaa gaa att aaa ggt	941
Pro Leu Thr Asp Ser Gln Arg Val Lys Phe Thr Lys Glu Ile Lys Gly	
250 255 260	
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Leu Lys Val Glu Ile Thr His Cys Gly Gln Met Lys Arg Lys Tyr Arg	
265 270 275 280	
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Val Cys Asn Val Thr Arg Arg Pro Ala Ser His Gln Thr Phe Pro Leu	
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Lys Asp Arg His Lys Leu Val Leu Arg Tyr Pro His Leu Pro Cys Leu	
315 320 325	
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Thr Ser Thr Met Ile Arg Ala Thr Ala Arg Ser Ala Pro Asp Arg Gln	
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Glu Glu Ile Ser Lys Leu Met Arg Ser Ala Ser Phe Asn Thr Asp Pro	
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Tyr Val Arg Glu Phe Gly Ile Met Val Lys Asp Glu Met Thr Asp Val	
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Lys Ala Ile Ala Thr Pro Val Gln Gly Val Trp Asp Met Arg Asn Lys	
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Gln	Leu	Arg	Lys	Ile	Ser	Arg	Asp	Ala	Gly	Met	Pro	Ile	Gln	Gly	Gln		
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Pro	Cys	Phe	Cys	Lys	Tyr	Ala	Gln	Gly	Ala	Asp	Ser	Val	Glu	Pro	Met		
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Phe	Arg	His	Leu	Lys	Asn	Thr	Tyr	Ala	Gly	Leu	Gln	Leu	Val	Val	Val		
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Ile	Leu	Pro	Gly	Lys	Thr	Pro	Val	Tyr	Ala	Glu	Val	Lys	Arg	Val	Gly		
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Gln	Arg	Thr	Thr	Pro	Gln	Thr	Leu	Ser	Asn	Leu	Cys	Leu	Lys	Ile	Asn		
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Gln	His	Arg	Gln	Glu	Ile	Ile	Gln	Asp	Leu	Ala	Ala	Met	Val	Arg	Glu		
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Leu	Leu	Ile	Gln	Phe	Tyr	Lys	Ser	Thr	Arg	Phe	Lys	Pro	Thr	Arg	Ile		
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atc	ttc	tac	cgc	gac	ggc	gtc	tct	gaa	ggc	cag	ttc	cag	cag	gtt	ctc	2189	
Ile	Phe	Tyr	Arg	Asp	Gly	Val	Ser	Glu	Gly	Gln	Phe	Gln	Gln	Val	Leu		
665					670					675					680		
cac	cac	gag	ttg	ctg	gcc	atc	cgt	gag	gcc	tgt	atc	aag	cta	gaa	aaa	2237	
His	His	Glu	Leu	Leu	Ala	Ile	Arg	Glu	Ala	Cys	Ile	Lys	Leu	Glu	Lys		

685	690	695	
gac tac cag ccc ggg atc acc ttc atc gtg gtg cag aag agg cac cac Asp Tyr Gln Pro Gly Ile Thr Phe Ile Val Val Gln Lys Arg His His 700 705 710			2285
acc cgg ctc ttc tgc act gac aag aac gag cgg gtt ggg aaa agt gga Thr Arg Leu Phe Cys Thr Asp Lys Asn Glu Arg Val Gly Lys Ser Gly 715 720 725			2333
aac att cca gca ggc acg act gtg gac acg aaa atc acc cac ccc acc Asn Ile Pro Ala Gly Thr Thr Val Asp Thr Lys Ile Thr His Pro Thr 730 735 740			2381
gag ttc gac ttc tac ctg tgt agt cac gct ggc atc cag ggg aca agc Glu Phe Asp Phe Tyr Leu Cys Ser His Ala Gly Ile Gln Gly Thr Ser 745 750 755 760			2429
agg cct tcg cac tat cac gtc ctc tgg gac gac aat cgt ttc tcc tct Arg Pro Ser His Tyr His Val Leu Trp Asp Asp Asn Arg Phe Ser Ser 765 770 775			2477
gat gag ctg cag atc cta acc tac cag ctg tgt cac acc tac gtg cgc Asp Glu Leu Gln Ile Leu Thr Tyr Gln Leu Cys His Thr Tyr Val Arg 780 785 790			2525
tgc aca cgc tcc gtg tcc atc cca gcg cca gca tac tac gct cac ctg Cys Thr Arg Ser Val Ser Ile Pro Ala Pro Ala Tyr Tyr Ala His Leu 795 800 805			2573
gtg gcc ttc cgg gcc agg tac cac ctg gtg gat aag gaa cat gac agt Val Ala Phe Arg Ala Arg Tyr His Leu Val Asp Lys Glu His Asp Ser 810 815 820			2621
gct gaa gga agc cat acc tct ggg cag agt aac ggg cga gac cac caa Ala Glu Gly Ser His Thr Ser Gly Gln Ser Asn Gly Arg Asp His Gln 825 830 835 840			2669
gca ctg gcc aag gcg gtc cag gtt cac caa gac act ctg cgc acc atg Ala Leu Ala Lys Ala Val Gln Val His Gln Asp Thr Leu Arg Thr Met 845 850 855			2717
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caaacttggga ttttgaactg cagacctgta tgagaaccca atgtcatagg aaatatggtt			2952
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cattgacctt ggtctactgc tttgcttttc taacagag      atg gtt cac ttc att      653
                                   Met Val His Phe Ile
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ttg ggt cga ctc tac aac ttc cag ccc ttc ctc act cgc act gaa gtt      701
Leu Gly Arg Leu Tyr Asn Phe Gln Pro Phe Leu Thr Arg Thr Glu Val
                                   10                               15                               20

tac aaa act ggt gtc aca cat tat ttt agc tta gag aaa gcc aag aaa      749
Tyr Lys Thr Gly Val Thr His Tyr Phe Ser Leu Glu Lys Ala Lys Lys
                                   25                               30                               35

gag cta ggt tat aag gct cag cca ttt gac ctc cag gaa gca gtg gaa      797
Glu Leu Gly Tyr Lys Ala Gln Pro Phe Asp Leu Gln Glu Ala Val Glu
                                   40                               45                               50

tgg ttt aaa gcc cat ggt cat ggc aga agt tct gga agt cgt gac tcg      845
Trp Phe Lys Ala His Gly His Gly Arg Ser Ser Gly Ser Arg Asp Ser
                                   55                               60                               65

gag tgt ttt gtt tgg gat ggg cta ttg gtc ttc ctc ctg att ata gca      893
Glu Cys Phe Val Trp Asp Gly Leu Leu Val Phe Leu Leu Ile Ile Ala
                                   70                               75                               80                               85

gtt ctc atg tgg ctg cct tct tct gtg att ctg tca ctg tga aggaggg      942
Val Leu Met Trp Leu Pro Ser Ser Val Ile Leu Ser Leu *
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Ala	Thr	Cys	Ile	Ile	Ser	Gly	Asn	Thr	Val	Ile	Trp	Asp	Asn	Lys	Thr		
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Pro	Val	Cys	Asp	Ser	Glu	Leu	Lys	Tyr	Ala	Phe	Leu	Phe	Leu	Leu	Pro		
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ata	cat	tct	aat	ttt	tct	ctg	gaa	taa	taaaa	atctattccg	aaaaaaaaaa					707	
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						Met											
						1											
gtg	ggg	aga	tcc	cgg	cgg	cgc	gga	gca	gct	aag	tgg	gca	gct	gtg	cga	224	
Val	Gly	Arg	Ser	Arg	Arg	Arg	Gly	Ala	Ala	Lys	Trp	Ala	Ala	Val	Arg		
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gcc	aag	gca	ggt	ccc	acg	ctc	acc	gac	gaa	aat	gga	gat	gat	tta	gga	272	
Ala	Lys	Ala	Gly	Pro	Thr	Leu	Thr	Asp	Glu	Asn	Gly	Asp	Asp	Leu	Gly		
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Leu	Pro	Pro	Ser	Pro	Gly	Asp	Thr	Ser	Tyr	Tyr	Gln	Asp	Gln	Val	Asp		
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gac	ttt	cat	gag	gca	cga	tcc	cgg	gcc	gcc	tta	gct	aag	ggc	tgg	aat	368	
Asp	Phe	His	Glu	Ala	Arg	Ser	Arg	Ala	Ala	Leu	Ala	Lys	Gly	Trp	Asn		
	50				55					60					65		
gaa	gta	cag	agt	gga	gac	gag	gag	gat	ggc	gag	gag	gag	gag	gag	gag	416	
Glu	Val	Gln	Ser	Gly	Asp	Glu	Glu	Asp	Gly	Glu	Glu	Glu	Glu	Glu	Glu		
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Val Leu Ala Leu Asp Met Asp Asp Glu Asp Asp Glu Asp Gly Gly Asn	
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gcg ggg gag gag gag gag gag gag aat gcc gat gat gat ggt ggg agc	512
Ala Gly Glu Glu Glu Glu Glu Glu Asn Ala Asp Asp Asp Gly Gly Ser	
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Ser Val Gln Ser Glu Ala Glu Ala Ser Val Asp Pro Ser Leu Ser Trp	
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ggt cag agg aaa aaa ctt tac tat gac acg gac tat ggt tcc aag tcc	608
Gly Gln Arg Lys Lys Leu Tyr Tyr Asp Thr Asp Tyr Gly Ser Lys Ser	
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Arg Gly Arg Gln Ser Gln Gln Glu Ala Glu Glu Glu Glu Arg Glu Glu	
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Glu Glu Glu Ala Gln Ile Ile Gln Arg Arg Leu Ala Gln Ala Leu Gln	
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Glu Asp Asp Phe Gly Val Ala Trp Val Glu Ala Phe Ala Lys Pro Val	
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Pro Gln Val Asp Glu Ala Glu Thr Arg Val Val Lys Asp Leu Ala Lys	
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Val Ser Val Lys Glu Lys Leu Lys Met Leu Arg Lys Glu Ser Pro Glu	
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230 235 240	
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Asp Glu Leu Glu Pro Leu Leu Glu Leu Val Glu Gln Gly Ile Ile Pro	
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Pro Gly Lys Gly Ser Gln Tyr Leu Arg Thr Lys Tyr Asn Leu Tyr Leu	
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Asn Tyr Cys Ser Asn Ile Ser Phe Tyr Leu Ile Leu Lys Ala Arg Arg	
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Val Pro Ala His Gly His Pro Val Ile Glu Arg Leu Val Thr Tyr Arg	
290 295 300 305	

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Asn Leu Ile Asn Lys Leu Ser Val Val Asp Gln Lys Leu Ser Ser Glu	
310 315 320	
att cgt cat ctg ttg aca ctt aag gat gat gct gta aag aaa gaa ctg	1184
Ile Arg His Leu Leu Thr Leu Lys Asp Asp Ala Val Lys Lys Glu Leu	
325 330 335	
att cca aaa gca aaa tcc acc aag ccc aaa cca aag tct gtt tca aag	1232
Ile Pro Lys Ala Lys Ser Thr Lys Pro Lys Pro Lys Ser Val Ser Lys	
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act tct gct gct gcc tgt gct gtt aca gat ctt tct gat gat tct gat	1280
Thr Ser Ala Ala Ala Cys Ala Val Thr Asp Leu Ser Asp Asp Ser Asp	
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Phe Asp Glu Lys Ala Lys Leu Lys Tyr Tyr Lys Glu Ile Glu Asp Arg	
370 375 380 385	
caa aag cta aag aga aag aaa gaa gaa aat agc act gaa gaa cag gct	1376
Gln Lys Leu Lys Arg Lys Lys Glu Glu Asn Ser Thr Glu Glu Gln Ala	
390 395 400	
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Leu Glu Asp Gln Asn Ala Lys Arg Ala Ile Thr Tyr Gln Ile Ala Lys	
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Asn Arg Gly Leu Thr Pro Arg Arg Lys Lys Ile Asp Arg Asn Pro Arg	
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Val Lys His Arg Glu Lys Phe Arg Arg Ala Lys Ile Arg Arg Arg Gly	
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Gln Val Arg Glu Val Arg Lys Glu Glu Gln Arg Tyr Ser Gly Glu Leu	
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Ser Gly Ile Arg Ala Gly Val Lys Lys Ser Ile Lys Leu Lys *	
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Met Phe Phe	
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Cys Asp Val Asp Ile Tyr Phe Ser Ala Glu Phe Leu Asn Ser Cys Arg	
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Leu Asn Ala Glu Pro Gly Lys Lys Val Phe Tyr Pro Val Val Phe Ser	
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ctt tac aat cct gcc att gtt tat gcc aac cag gaa gtg cca cca cct	441
Leu Tyr Asn Pro Ala Ile Val Tyr Ala Asn Gln Glu Val Pro Pro Pro	
40 45 50	
gtg gag cag cag ctg gtt cac aaa aag gat tct ggc ttt tgg cga gat	489
Val Glu Gln Gln Leu Val His Lys Lys Asp Ser Gly Phe Trp Arg Asp	
55 60 65	
ttt ggc ttt gga atg act tgt cag tat cgt tca gat ttc ctg acc att	537
Phe Gly Phe Gly Met Thr Cys Gln Tyr Arg Ser Asp Phe Leu Thr Ile	
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Gly Gly Phe Asp Met Glu Val Lys Gly Trp Gly Gly Glu Asp Val His	
85 90 95	
ctt tat cga aaa tac tta cat ggt gac ctc att gtg att cgg act ccg	633
Leu Tyr Arg Lys Tyr Leu His Gly Asp Leu Ile Val Ile Arg Thr Pro	
100 105 110 115	
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Val Pro Gly Leu Phe His Leu Trp His Glu Lys Arg Cys Ala Asp Glu	
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Leu Thr Pro Glu Gln Tyr Arg Met Cys Ile Gln Ser Lys Ala Met Asn	
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Glu Ala Ser His Ser His Leu Gly Met Leu Val Phe Arg Glu Glu Ile	
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Gly *																
180																
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Trp Gln Ser Phe Cys Thr Gln Lys Asn Phe Ala Trp Lys Glu Glu Tyr	
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Asp Thr Arg Gln Ala Ser Asn Arg Trp Glu Lys Arg Ala Met Glu Lys	
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Glu Asn Lys Lys Ile Arg Asp Lys Ala Arg Lys Glu Lys Asn Glu Leu	
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205 210 215	
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Tyr Cys Pro Ala Cys Asp Lys Ser Phe Lys Thr Glu Lys Ala Met Lys	
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Asn His Glu Lys Ser Lys Lys His Arg Glu Met Val Ala Leu Leu Lys	
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Gln Gln Leu Glu Glu Glu Glu Glu Asn Phe Ser Arg Pro Gln Ile Asp	
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Lys Gln Lys Leu Ser Lys Lys Gln Lys Thr Gln Glu Thr Val Asn Gln	
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His Arg Met Tyr Leu Ala Lys Ile His Ile Cys Leu Gln Leu Thr Phe	
395 400 405 410	
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Met Met Thr Ile Ser Met *	
445	
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 <213> Homo sapiens

<220>
 <221> CDS
 <222> (23) .. (1618)

<400> 56	
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	Met	Lys	Cys	His	Tyr	Glu	Ala	Leu	Gly	Val	
	1				5					10	
cgg cgc gac gcc agc gag gag gag ctc aag aag gcc tat cgg aag ctg											100
Arg Arg Asp Ala Ser Glu Glu Glu Leu Lys Lys Ala Tyr Arg Lys Leu											
			15						20		25
gcc ctg aaa tgg cac ccg gat aaa aat ctg gat aat gcc gca gaa gca											148
Ala Leu Lys Trp His Pro Asp Lys Asn Leu Asp Asn Ala Ala Glu Ala											
			30						35		40
gct gaa caa ttt aaa tta atc caa gca gca tat gat gtg ttg agt gac											196
Ala Glu Gln Phe Lys Leu Ile Gln Ala Ala Tyr Asp Val Leu Ser Asp											
			45						50		55
cct cag gaa aga gca tgg tat gat aat cat aga gag gcc cta ctt aaa											244
Pro Gln Glu Arg Ala Trp Tyr Asp Asn His Arg Glu Ala Leu Leu Lys											
			60						65		70
ggg ggg ttt gat ggc gaa tat caa gat gac agc tta gat ttg cta cgc											292
Gly Gly Phe Asp Gly Glu Tyr Gln Asp Asp Ser Leu Asp Leu Leu Arg											
			75						80		85
tat ttc acc gtt acc tgt tat tct ggt tat gga gat gat gaa aag gga											340
Tyr Phe Thr Val Thr Cys Tyr Ser Gly Tyr Gly Asp Asp Glu Lys Gly											
									95		100
ttt tac acg gtg tat cgt aat gtt ttt gaa atg att gcc aag gaa gaa											388
Phe Tyr Thr Val Tyr Arg Asn Val Phe Glu Met Ile Ala Lys Glu Glu											
			110						115		120
cta gaa tct gtg tta gag gaa gag gtt gat gat ttc cca act ttt gga											436
Leu Glu Ser Val Leu Glu Glu Glu Val Asp Asp Phe Pro Thr Phe Gly											
			125						130		135
gac tcc cag agt gac tat gat acg gta gtc cat cct ttc tac gct tat											484
Asp Ser Gln Ser Asp Tyr Asp Thr Val Val His Pro Phe Tyr Ala Tyr											
			140						145		150
tgg cag agt ttc tgc act caa aag aat ttt gca tgg aag gaa gaa tat											532
Trp Gln Ser Phe Cys Thr Gln Lys Asn Phe Ala Trp Lys Glu Glu Tyr											
			155						160		165
gat aca cga cag gct tca aac cgc tgg gaa aaa cga gcc atg gaa aaa											580
Asp Thr Arg Gln Ala Ser Asn Arg Trp Glu Lys Arg Ala Met Glu Lys											
									175		180
gaa aac aaa aag att cgg gac aaa gca agg aaa gag aag aat gag ctt											628
Glu Asn Lys Lys Ile Arg Asp Lys Ala Arg Lys Glu Lys Asn Glu Leu											
			190						195		200
gtc cgt cag ctg gta gct ttc att cgt aaa aga gat aaa aga gtg cag											676
Val Arg Gln Leu Val Ala Phe Ile Arg Lys Arg Asp Lys Arg Val Gln											
			205						210		215
gcg cat cga aaa ctt gtg gaa gaa cag aat gca gag aag gcg agg aaa											724
Ala His Arg Lys Leu Val Glu Glu Gln Asn Ala Glu Lys Ala Arg Lys											

220	225	230	
gcc gaa gag atg agg cgg cag cag aag cta aag cag gcc aaa ctg gtg			772
Ala Glu Glu Met Arg Arg Gln Gln Lys Leu Lys Gln Ala Lys Leu Val			
235	240	245	250
gag cag tac aga gaa cag agc tgg atg act atg gcc aat ttg gag aaa			820
Glu Gln Tyr Arg Glu Gln Ser Trp Met Thr Met Ala Asn Leu Glu Lys			
	255	260	265
gag ctc cag gag atg gag gca cgg tac gag aag gag ttt gga gat gga			868
Glu Leu Gln Glu Met Glu Ala Arg Tyr Glu Lys Glu Phe Gly Asp Gly			
	270	275	280
tcg gat gaa aat gaa atg gaa gaa cat gaa ctc aaa gat gag gag gat			916
Ser Asp Glu Asn Glu Met Glu Glu His Glu Leu Lys Asp Glu Glu Asp			
	285	290	295
ggt aaa gac agt gat gag gcc gag gac gct gag ctc tat gat gac ctt			964
Gly Lys Asp Ser Asp Glu Ala Glu Asp Ala Glu Leu Tyr Asp Asp Leu			
	300	305	310
tac tgc cca gca tgt gac aaa tcg ttc aag aca gaa aag gcc atg aag			1012
Tyr Cys Pro Ala Cys Asp Lys Ser Phe Lys Thr Glu Lys Ala Met Lys			
	315	320	330
aat cac gag aag tca aag aag cat cgg gaa atg gtg gcc ttg cta aaa			1060
Asn His Glu Lys Ser Lys Lys His Arg Glu Met Val Ala Leu Leu Lys			
	335	340	345
caa cag ctg gag gag gaa gaa gaa aat ttt tca aga cct caa att gat			1108
Gln Gln Leu Glu Glu Glu Glu Asn Phe Ser Arg Pro Gln Ile Asp			
	350	355	360
gaa aat cca tta gat gac aat tct gag gaa gaa atg gaa gat gca cca			1156
Glu Asn Pro Leu Asp Asp Asn Ser Glu Glu Glu Met Glu Asp Ala Pro			
	365	370	375
aaa caa aag ctt tct aaa aaa cag aag aaa aag aaa cag aaa cca gca			1204
Lys Gln Lys Leu Ser Lys Lys Gln Lys Lys Lys Lys Gln Lys Pro Ala			
	380	385	390
cag aat tat gat gac aat ttc aat gta aat gga cct gga gaa gga gta			1252
Gln Asn Tyr Asp Asp Asn Phe Asn Val Asn Gly Pro Gly Glu Gly Val			
	395	400	410
aag gtt gat cca gaa gat act aac tta aat caa gac agt gcc aaa gaa			1300
Lys Val Asp Pro Glu Asp Thr Asn Leu Asn Gln Asp Ser Ala Lys Glu			
	415	420	425
ttg gaa gat agt ccc cag gaa aat gtc agt gtc aca gag atc att aaa			1348
Leu Glu Asp Ser Pro Gln Glu Asn Val Ser Val Thr Glu Ile Ile Lys			
	430	435	440
cca tgt gat gat cca aaa agt gaa gct aaa agt gtt cct aaa ccc aaa			1396
Pro Cys Asp Asp Pro Lys Ser Glu Ala Lys Ser Val Pro Lys Pro Lys			
	445	450	455

gga aag aaa acc aaa gat atg aaa aaa cct gtc aga gta cct gct gaa	1444
Gly Lys Lys Thr Lys Asp Met Lys Lys Pro Val Arg Val Pro Ala Glu	
460 465 470	
cca caa aca atg agt gtt ctt atc agc tgt aca acc tgc cat agt gaa	1492
Pro Gln Thr Met Ser Val Leu Ile Ser Cys Thr Thr Cys His Ser Glu	
475 480 485 490	
ttt cca tct cgg aat aaa ctt ttt gac cat cta aag gcc aca ggt cat	1540
Phe Pro Ser Arg Asn Lys Leu Phe Asp His Leu Lys Ala Thr Gly His	
495 500 505	
gca aga gca cct tca tca tgc tct tta aac agc gca aca agt agt caa	1588
Ala Arg Ala Pro Ser Ser Ser Ser Leu Asn Ser Ala Thr Ser Ser Gln	
510 515 520	
agc aag aaa gag aaa cgt aaa aac aga tag a gattctgcct gtgcttttgt	1639
Ser Lys Lys Glu Lys Arg Lys Asn Arg *	
525 530	
ttgactgtct ctagattttg aaaccaaaaa actgaactga aatcatctaa agagttaaaa	1699
tttcagtgat ctgcaattaa ttacattgtg gaagattatt ttttatcttg taaaaacact	1759
tttttggttt aatatatatt tttaaaacat ttcactagtgt attgaattct acttttgcca	1819
tctgaattga cttgaatgtc ttaaaacagg taaatactgt aaagtgtgta ttcttgatgt	1879
ttattggctc atgtggacag aaatgtacag ggagaattac attatttttaa cacacagaag	1939
tgcaactttc tgctttatatt tctgaatttc acattacttt tacttaatgc ttttgtgttt	1999
tgtaataact tcataatatg tgaaaaactc ggatctttta aaaagcatca tagatcattt	2059
ttccatatga cactgggtcc gatttttaaaa attattttta aataaccgat tattgattac	2119
tgtatttttt ttctcaagaa cagtgatagg tagaaactaa ttgaacattt ggtagtcttt	2179
caagaatagt gtctcttcaa ggttttactt gatttaattt gatattttac tggtttacca	2239
gtaagggtgta ttgttcagtt ttttgctccg atttgaattg tggaggtgga agcaaattag	2299
tttacatggc atgtcctccc taggcacagt gacagctgta aagtatgacg gaacaaggta	2359
gcagatggta cagaatttat actattttaag aagagatgtg gcgttcttca ttgagttttt	2419
ttcttcacta ttttcagaag	2439

<210> 57
 <211> 2331
 <212> DNA
 <213> Homo sapiens

[illegible]

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Gln Gly Val Ala Val Tyr Ile Leu Leu Asp Gln Ala Leu Leu Ser Gln
190 195 200

ttt ctg gat atg tgc atg gat ctg aaa gtt cat cct gaa cag gaa aag Phe Leu Asp Met Cys Met Asp Leu Lys Val His Pro Glu Gln Glu Lys 205 210 215	677
tta atg aca gtt cgg act atc aca gga aat atc tac tat gca agg tca Leu Met Thr Val Arg Thr Ile Thr Gly Asn Ile Tyr Tyr Ala Arg Ser 220 225 230	725
gga act aag att att ggg aag gtt cac gaa aag ttc acg ttg att gat Gly Thr Lys Ile Ile Gly Lys Val His Glu Lys Phe Thr Leu Ile Asp 235 240 245	773
ggc atc cgc gtg gca aca ggc tcc tac agt ttt aca tgg acg gat ggc Gly Ile Arg Val Ala Thr Gly Ser Tyr Ser Phe Thr Trp Thr Asp Gly 250 255 260 265	821
aaa tta aac agc agt aac ttg gta att ctg tct ggc caa gtg gtt gaa Lys Leu Asn Ser Ser Asn Leu Val Ile Leu Ser Gly Gln Val Val Glu 270 275 280	869
cac ttt gat ctg gag ttc cga atc ctg tat gcc cag tcc aag ccc atc His Phe Asp Leu Glu Phe Arg Ile Leu Tyr Ala Gln Ser Lys Pro Ile 285 290 295	917
agc ccc aaa ctc ctg tct cac ttc cag agc agc aac aag ttt gat cac Ser Pro Lys Leu Leu Ser His Phe Gln Ser Ser Asn Lys Phe Asp His 300 305 310	965
ctc acc aac cga aaa cca cag tcc aag gag ctc acc ctg ggc aac ctg Leu Thr Asn Arg Lys Pro Gln Ser Lys Glu Leu Thr Leu Gly Asn Leu 315 320 325	1013
ctg cgg atg cgg ctg gct agg ctg tca agt act ccc agg aag gcg gac Leu Arg Met Arg Leu Ala Arg Leu Ser Ser Thr Pro Arg Lys Ala Asp 330 335 340 345	1061
ctg gac cca gag atg ccc gca gag ggc aag gca gag cgc aag ccc cat Leu Asp Pro Glu Met Pro Ala Glu Gly Lys Ala Glu Arg Lys Pro His 350 355 360	1109
gac tgt gag tcc tct act gtt agt gag gaa gac tac ttc agc agc cac Asp Cys Glu Ser Ser Thr Val Ser Glu Glu Asp Tyr Phe Ser Ser His 365 370 375	1157
agg gac gag ctc cag agc aga aag gcc att gac gct gcc act caa aca Arg Asp Glu Leu Gln Ser Arg Lys Ala Ile Asp Ala Ala Thr Gln Thr 380 385 390	1205
gag cca gga gag gag atg cca ggg ctg agt gtg agt gag gtg gga aca Glu Pro Gly Glu Glu Met Pro Gly Leu Ser Val Ser Glu Val Gly Thr 395 400 405	1253
caa acc agc atc acc aca gca tgt gct ggt acc cag act gca gtc atc Gln Thr Ser Ile Thr Thr Ala Cys Ala Gly Thr Gln Thr Ala Val Ile 410 415 420 425	1301
acc agg ata gca agc tct caa acc acg att tgg tcc aga tcg acc act	1349

Thr Arg Ile Ala Ser Ser Gln Thr Thr Ile Trp Ser Arg Ser Thr Thr	
430 435 440	
act cag act gac atg gat gag aac att ctc ttt cct cga gga act caa	1397
Thr Gln Thr Asp Met Asp Glu Asn Ile Leu Phe Pro Arg Gly Thr Gln	
445 450 455	
tct aca gaa ggg tca cca gtc tca aaa atg tct gta tcg aga tct tcc	1445
Ser Thr Glu Gly Ser Pro Val Ser Lys Met Ser Val Ser Arg Ser Ser	
460 465 470	
agt ttg aag tct tcc tcc tct gtg tct tcc caa ggc tct gtg gca agc	1493
Ser Leu Lys Ser Ser Ser Ser Val Ser Ser Gln Gly Ser Val Ala Ser	
475 480 485	
tcc act ggt tct ccc gct tcc atc aga acc act gac ttc cac aat cct	1541
Ser Thr Gly Ser Pro Ala Ser Ile Arg Thr Thr Asp Phe His Asn Pro	
490 495 500 505	
ggc tat ccc aag tac ctg ggc acc ccc cac ctg gaa ctg tac ttg agt	1589
Gly Tyr Pro Lys Tyr Leu Gly Thr Pro His Leu Glu Leu Tyr Leu Ser	
510 515 520	
gac tca ctt aga aac ttg aac aaa gag cgg caa ttc cac ttc gct ggt	1637
Asp Ser Leu Arg Asn Leu Asn Lys Glu Arg Gln Phe His Phe Ala Gly	
525 530 535	
atc agg tcc cgg ctc aac cac atg ctg gct atg ctg tca agg aga aca	1685
Ile Arg Ser Arg Leu Asn His Met Leu Ala Met Leu Ser Arg Arg Thr	
540 545 550	
ctc ttt act gaa aac cac ctt ggc ctt cat tct ggc aat ttc agc aga	1733
Leu Phe Thr Glu Asn His Leu Gly Leu His Ser Gly Asn Phe Ser Arg	
555 560 565	
gtt aat ttg ctt gct gtt aga gat gta gca ctt tat cct tcc tat cag	1781
Val Asn Leu Leu Ala Val Arg Asp Val Ala Leu Tyr Pro Ser Tyr Gln	
570 575 580 585	
taa ctgc tccgtgttca gactcctggg ttcttccagg cttacagtgg acatcatcag	1838
*	
cttcctgctt taaaaaatat cttatgtccc taattgcctt tcttttacct gactttgtca	1898
cctttgtttgt ctttgaattc tttaggctgc atattatttt acatgctttg ttttgtcatg	1958
tatataccag gtattggttt tatggtttaa acactatgga tacaggggtt tgttttgcac	2018
aattttaata gtcatgcact acataatgat gttttgggtca atgacagacc acgtatatgt	2078
tggcagtctc ataagattat aatactgtat ttttactata ccttttctgt gtttagatac	2138
aaataccatt atgttacagt tgccctacagt attcagtgcg gtaacatgat gtacaggttt	2198
gtagcctggt ttgcattttt cttagggttg atgctcttct gttttaagg tttgaatcac	2258

cagcattttt gtgatcaaaa tcctatttag aaaaaataaa actactttct gtttatctct 2318
 ttaaaaaaaaa aaa 2331

<210> 58
 <211> 1762
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (685)..(1380)

<400> 58
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 accagagatt atttctgaca acccaggata tcccgaagc ttggaggcat atggctggaa 180
 aatgaaacga cccaggacat cgtttctggc tgcattcatta tttgtgtcg cgtagtacca 240
 gatgggcagt cagtgagcgg cgcagggatg tgaacggacg gttttataat gtgaaaattt 300
 tcccttggtg aagctaaaac agatttaatt tccctctctt tcttttact acttccccct 360
 ctttattccc cctctgtctg caatatcagt gaactcaact ttgcagtgag gtggccaaaa 420
 agagagagaa tgaggagatc ttgatcatct tagtgtcaga ggagtcgcag cggactggga 480
 actgcagctg cgaccccccg cgtcctgtgc ggatttcagg gctgataccg cataggcggg 540
 tatggaaagg acggtacacc ggagcggcgg aggatagaga ccctggcccc cggagaggtc 600
 tgctgatttc gcagcagcct tcgaagccgt ggctgccttt catctgctgc gttttattac 660
 tattatcgcc gttccgaaa agtc atg gaa gac agc ccg ctg cca gac ctc 711
 Met Glu Asp Ser Pro Leu Pro Asp Leu
 1 5
 aga gac atc gag ctg aag ctg ggg cgc aaa gta ccc gag agt cta gtg 759
 Arg Asp Ile Glu Leu Lys Leu Gly Arg Lys Val Pro Glu Ser Leu Val
 10 15 20 25
 cgc tct ctc cgt ggg gag gag ccg gtt ccc agg gaa agg gac agg gac 807
 Arg Ser Leu Arg Gly Glu Glu Pro Val Pro Arg Glu Arg Asp Arg Asp
 30 35 40
 ccc tgc ggg ggg agc ggt ggt ggt ggc ggc ggc ggc ggc ggc ggc 855
 Pro Cys Gly Gly Ser Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
 45 50 55
 ggc tgc agt agc agc agc agc tac tgc agc ttc cct ccc tcc ttg tgc 903
 Gly Cys Ser Ser Ser Ser Ser Tyr Cys Ser Phe Pro Pro Ser Leu Ser

60	65	70	
tcc tcc tct tcg tcc tcc cca acc tct ggc tcc cca cga ggt agc cac			951
Ser Ser Ser Ser Ser Ser Pro Thr Ser Gly Ser Pro Arg Gly Ser His			
75	80	85	
tct agc gcc ctg gag agg cta gaa acc aag ctt cac ctc ctc agg caa			999
Ser Ser Ala Leu Glu Arg Leu Glu Thr Lys Leu His Leu Leu Arg Gln			
90	95	100	105
gag atg gtt aac ctc aga gcc aca gac gtc agg ctc atg cgc cag ttg			1047
Glu Met Val Asn Leu Arg Ala Thr Asp Val Arg Leu Met Arg Gln Leu			
110	115	120	
ctt gta atc aat gag agc atc gag tcc atc aag tgg atg atc gaa gaa			1095
Leu Val Ile Asn Glu Ser Ile Glu Ser Ile Lys Trp Met Ile Glu Glu			
125	130	135	
aaa gcc acc att acc agc aga ggc agc agc ctc agt ggc agc ctg tgc			1143
Lys Ala Thr Ile Thr Ser Arg Gly Ser Ser Leu Ser Gly Ser Leu Cys			
140	145	150	
agt ttg ttg gag agt cag agc acc tcc tta cgt ggc agc tac aac agc			1191
Ser Leu Leu Glu Ser Gln Ser Thr Ser Leu Arg Gly Ser Tyr Asn Ser			
155	160	165	
cta cac gat ggc agt gat ggg ctg gat ggc att tcc gtg gga agt tat			1239
Leu His Asp Gly Ser Asp Gly Leu Asp Gly Ile Ser Val Gly Ser Tyr			
170	175	180	185
ctg gac acg ttg gcg gat gat gtc cca ggc cat cag acc cct tca gac			1287
Leu Asp Thr Leu Ala Asp Asp Val Pro Gly His Gln Thr Pro Ser Asp			
190	195	200	
ttg gac caa ttc agt gac agc tcc ctc ata gag gac tca cag gca cta			1335
Leu Asp Gln Phe Ser Asp Ser Ser Leu Ile Glu Asp Ser Gln Ala Leu			
205	210	215	
cac aag cgt cct aaa ttg gat tct gaa tac tac tgc ttt ggc tag tga			1383
His Lys Arg Pro Lys Leu Asp Ser Glu Tyr Tyr Cys Phe Gly *			
220	225	230	
cagttttttg catgggactg gtgtgcaatg aacttgtatt tatccttctt ctccgctgct			1443
atattttttgg tgtgattttt attttaataa gatgaccttt ttaaaagaag ctgattttga			1503
aactgcttaa tgggtattgct gttgctccta atactttctca tctgagctga tttatttttc			1563
tctgttacat ctctattttt tatttattac aatgattttc tcccttcttt tacagtagca			1623
caaacaaagt agggggaaaa gaataagcaa taattatggt tttgcttttg ttttcagagc			1683
aatgggtcag ggattacaag aaaaactttg ctaaatttta caataaacca aagtctgata			1743
acagttaaaa aaaaaaaaaa			1762

<210> 59
 <211> 2860
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (116)..(2488)

<400> 59
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 ctttctcctg gacattgaag atatggccct ttggaggtga cccaggagag aaggg atg 118
 Met
 1
 aag gcc ttt ggt cct cca cat gag ggc ccc ctc caa gga ctc gtg gcc 166
 Lys Ala Phe Gly Pro Pro His Glu Gly Pro Leu Gln Gly Leu Val Ala
 5 10 15
 tcc cgc att gag act tat ggg ggc cgg cat cga gcc tct gct cag agc 214
 Ser Arg Ile Glu Thr Tyr Gly Gly Arg His Arg Ala Ser Ala Gln Ser
 20 25 30
 act act ggc aga ctc tat ccc cga gga tac cct gtg ctg gat ccc agt 262
 Thr Thr Gly Arg Leu Tyr Pro Arg Gly Tyr Pro Val Leu Asp Pro Ser
 35 40 45
 cgc cga cgc ctc cag cag tat gtc ccc ttt gcc agg ggt tct ggc cag 310
 Arg Arg Arg Leu Gln Gln Tyr Val Pro Phe Ala Arg Gly Ser Gly Gln
 50 55 60 65
 gcc cga ggc ctg tca ccc atg aga ctg cga gat cca gag ccc gag aag 358
 Ala Arg Gly Leu Ser Pro Met Arg Leu Arg Asp Pro Glu Pro Glu Lys
 70 75 80
 agg cac ggg ggc cat gtg ggg gct ggc ctg ctt cac tcc ccc aaa ctc 406
 Arg His Gly Gly His Val Gly Ala Gly Leu Leu His Ser Pro Lys Leu
 85 90 95
 aag gaa ctc acc aag gcc cat gag ctg gag gtg agg ctg cac act ttc 454
 Lys Glu Leu Thr Lys Ala His Glu Leu Glu Val Arg Leu His Thr Phe
 100 105 110
 agc atg ttt ggg atg ccc cgg ctg ccc cct gag gac cgg cgg cac tgg 502
 Ser Met Phe Gly Met Pro Arg Leu Pro Pro Glu Asp Arg Arg His Trp
 115 120 125
 gag ata gga gag ggt ggc gac agt ggc ctg acc atc gag aag tcc tgg 550
 Glu Ile Gly Glu Gly Gly Asp Ser Gly Leu Thr Ile Glu Lys Ser Trp
 130 135 140 145
 agg gag ctg gtg cct ggg cac aag gag atg agc cag gag ctc tgc cac 598
 Arg Glu Leu Val Pro Gly His Lys Glu Met Ser Gln Glu Leu Cys His
 150 155 160

caa Gln	cag Gln	gag Glu	gcc Ala 165	ctg Leu	tgg Trp	gag Glu	ctc Leu	ctg Leu	acc Thr	acc Thr	gag Glu	ctg Leu	atc Ile 175	tac Tyr	gtg Val	646
aga Arg	aag Lys	ctc Leu 180	aag Lys	atc Ile	atg Met	act Thr	gat Asp 185	ctg Leu	cta Leu	gcc Ala	gcc Ala	ggc Gly 190	ctg Leu	ctg Leu	aac Asn	694
ctg Leu	cag Gln	cga Arg	gtg Val	gga Gly	ctg Leu	ctg Leu	atg Met 200	gaa Glu	gtg Val	tca Ser	gct Ala 205	gag Glu	acc Thr	ctg Leu	ttt Phe	742
gga Gly 210	aat Asn	gtc Val	ccc Pro	agc Ser	ctg Leu 215	att Ile	cga Arg	acc Thr	cac His	cgg Arg 220	agc Ser	ttt Phe	tgg Trp	gat Asp	gag Glu 225	790
gtg Val	ctg Leu	ggg Gly	ccc Pro	acc Thr 230	ctg Leu	gag Glu	gag Glu	act Thr	cgg Arg 235	gcc Ala	tcg Ser	ggc Gly	cag Gln	cct Pro 240	ctg Leu	838
gac Asp	ccc Pro	att Ile	ggg Gly 245	ctg Leu	caa Gln	agt Ser	ggc Gly	ttc Phe 250	ctg Leu	acg Thr	ttt Phe	ggc Gly	cag Gln 255	cgg Arg	ttc Phe	886
cac His	ccc Pro	tat Tyr 260	gtc Val	cag Gln	tac Tyr	tgc Cys	ctc Leu 265	cga Arg	gtg Val	aag Lys	cag Gln	acc Thr 270	atg Met	gct Ala	tac Tyr	934
gcc Ala 275	cga Arg	gaa Glu	cag Gln	caa Gln	gaa Glu	act Thr 280	aac Asn	cct Pro	ctc Leu	ttc Phe	cat His 285	gcc Ala	ttc Phe	gtg Val	cag Gln	982
tgg Trp 290	tgt Cys	gag Glu	aag Lys	cac His	aag Lys 295	cgc Arg	tct Ser	ggg Gly	agg Arg	cag Gln 300	atg Met	ctc Leu	tgt Cys	gac Asp	ttg Leu 305	1030
ctt Leu	atc Ile	aag Lys	ccc Pro	cac His 310	cag Gln	cgc Arg	atc Ile	acc Thr	aag Lys 315	tac Tyr	cca Pro	ctg Leu	ctg Leu	ctc Leu 320	cat His	1078
gct Ala	gtg Val	ctc Leu	aag Lys 325	agg Arg	agc Ser	ccc Pro	gag Glu	gca Ala 330	cga Arg	gcc Ala	caa Gln	gag Glu 335	gcc Ala	ctg Leu	aat Asn	1126
gcc Ala	atg Met	att Ile 340	gaa Glu	gcc Ala	gtg Val	gag Glu	tca Ser 345	ttc Phe	ctg Leu	cga Arg	cat His 350	atc Ile	aat Asn	ggg Gly	cag Gln	1174
gtc Val	cgc Arg	cag Gln	ggc Gly	gaa Glu	gag Glu	caa Gln 360	gag Glu	agc Ser	ttg Leu	gcg Ala	gct Ala 365	gca Ala	gca Ala	caa Gln	cgc Arg	1222
atc Ile 370	ggg Gly	ccc Pro	tac Tyr	gag Glu	gtg Val 375	ctg Leu	gag Glu	cca Pro	ccc Pro	agt Ser 380	gat Asp	gag Glu	gtg Val	gag Glu	aag Lys 385	1270

aac Asn	ctg Leu	cgc Arg	cca Pro	ttc Phe 390	tcc Ser	acc Thr	ctg Leu	gac Asp	ctg Leu 395	acg Thr	tcc Ser	ccc Pro	atg Met	ctg Leu 400	ggg Gly	1318
gtt Val	gca Ala	tct Ser	gag Glu 405	cac His	acc Thr	aga Arg	cag Gln	ctg Leu 410	ctg Leu	ctg Leu	gag Glu	ggg Gly 415	cct Pro	gtg Val	cga Arg	1366
gtg Val	aag Lys	gag Glu 420	gga Gly	cga Arg	gaa Glu	ggg Gly	aag Lys 425	ctg Leu	gac Asp	gtg Val	tac Tyr	ctg Leu 430	ttc Phe	ctc Leu	ttc Phe	1414
tct Ser	gat Asp 435	gtg Val	ctc Leu	ctt Leu	gtg Val	acc Thr 440	aag Lys	ccc Pro	cag Gln	cgc Arg	aag Lys 445	gcg Ala	gac Asp	aaa Lys	gcc Ala	1462
aag Lys 450	gtc Val	atc Ile	cga Arg	ccc Pro	cct Pro 455	ctc Leu	atg Met	ctg Leu	gag Glu	aag Lys 460	ctc Leu	gtg Val	tgc Cys	caa Gln	ccc Pro 465	1510
ctg Leu	cga Arg	gac Asp	ccc Pro	aac Asn 470	agc Ser	ttc Phe	ctg Leu	ctg Leu	atc Ile 475	cac His	ctc Leu	act Thr	gaa Glu	ttc Phe 480	cag Gln	1558
tgt Cys	gtc Val	tcc Ser	agc Ser 485	gcc Ala	ctc Leu	ctt Leu	gtg Val	cac His 490	tgt Cys	ccc Pro	agt Ser	cct Pro	aca Thr 495	gac Asp	cgt Arg	1606
gcc Ala	cag Gln	tgg Trp 500	ctg Leu	gag Glu	aag Lys	acc Thr	cag Gln 505	cag Gln	gcc Ala	cag Gln	gcc Ala 510	gcc Ala	cta Leu	cag Gln	aag Lys	1654
ctg Leu	aag Lys 515	gca Ala	gag Glu	gag Glu	tat Tyr	gtt Val 520	caa Gln	cag Gln	aag Lys	agg Arg	gag Glu 525	ctc Leu	ctg Leu	acc Thr	ctc Leu	1702
tat Tyr 530	cgg Arg	gac Asp	cag Gln	gac Asp	agg Arg 535	gag Glu	tcc Ser	ccc Pro	agc Ser	acc Thr 540	agg Arg	ccc Pro	tcc Ser	acg Thr	cct Pro 545	1750
tcc Ser	ctg Leu	gag Glu	ggc Gly	tct Ser 550	cag Gln	agc Ser	agc Ser	gca Ala 555	gag Glu	ggg Gly	agg Arg	act Thr	cct Pro	gag Glu 560	ttc Phe	1798
tcg Ser	acc Thr	att Ile	atc Ile 565	ccc Pro	cac His	ctg Leu	gtg Val	gtg Val 570	aca Thr	gaa Glu	gac Asp	aca Thr	gat Asp 575	gaa Glu	gat Asp	1846
gct Ala	ccc Pro	ctt Leu 580	gtg Val	cca Pro	gat Asp	gat Asp	acc Thr 585	tca Ser	gac Asp	tct Ser	ggc Gly 590	tac Tyr	ggc Gly	act Thr	ttg Leu	1894
atc Ile	cca Pro 595	ggc Gly	acc Thr	ccc Pro	acg Thr	ggg Gly 600	tcc Ser	cgc Arg	tcc Ser	cca Pro	ctg Leu 605	agc Ser	cgt Arg	cta Leu	cgc Arg	1942
caa	aga	gcc	ctt	cgg	cgg	gac	cct	cgc	ctc	acc	ttc	tcc	acc	ctg	gaa	1990

Gln Arg Ala Leu Arg Arg Asp Pro Arg Leu Thr Phe Ser Thr Leu Glu	
610 615 620 625	
ctc cgg gac atc cct ctg cgt ccc cac cct ccc gac ccc caa gct cct	2038
Leu Arg Asp Ile Pro Leu Arg Pro His Pro Pro Asp Pro Gln Ala Pro	
630 635 640	
caa cgc cga agc gcc ccc gaa ctg ccg gaa gga atc cta aaa gga ggc	2086
Gln Arg Arg Ser Ala Pro Glu Leu Pro Glu Gly Ile Leu Lys Gly Gly	
645 650 655	
agt ctt ccc cag gaa gac cca cca acc tgg tct gag gaa gaa gat ggg	2134
Ser Leu Pro Gln Glu Asp Pro Pro Thr Trp Ser Glu Glu Glu Asp Gly	
660 665 670	
gcc tcc gag cga ggg aat gtg gtg gtg gaa aca ctc cac agg gcc cgg	2182
Ala Ser Glu Arg Gly Asn Val Val Val Glu Thr Leu His Arg Ala Arg	
675 680 685	
ctt cgg ggc cag ctt ccc tcc tcc cca acc cat gct gac tct gcc ggg	2230
Leu Arg Gly Gln Leu Pro Ser Ser Pro Thr His Ala Asp Ser Ala Gly	
690 695 700 705	
gaa agc ccc tgg gag tcc tca ggg gag gag gaa gaa gag ggg cct ctg	2278
Glu Ser Pro Trp Glu Ser Ser Gly Glu Glu Glu Glu Gly Pro Leu	
710 715 720	
ttc ctg aaa gct ggc cac aca tcc ctg cgc cca atg cgg gct gag gac	2326
Phe Leu Lys Ala Gly His Thr Ser Leu Arg Pro Met Arg Ala Glu Asp	
725 730 735	
atg ctc aga gag atc cgg gag gag ctg gcc agc caa agg att gag ggg	2374
Met Leu Arg Glu Ile Arg Glu Glu Leu Ala Ser Gln Arg Ile Glu Gly	
740 745 750	
gcc gag gag ccc cgg gac agc agg cca cgg aag ctg act cgg gcc cag	2422
Ala Glu Glu Pro Arg Asp Ser Arg Pro Arg Lys Leu Thr Arg Ala Gln	
755 760 765	
ctg cag agg atg cgg ggg ccc cac atc att cag ctg gac acc cct ctg	2470
Leu Gln Arg Met Arg Gly Pro His Ile Ile Gln Leu Asp Thr Pro Leu	
770 775 780 785	
tcc gca tca gag gta tga ggaatg cagaggacct ttggcatgca tctctcccag	2524
Ser Ala Ser Glu Val *	
790	
aggagatctc tccccagtag tgctggtcac cctccggcat ctgtgactct acctcaagga	2584
ccacatttcc caaaggaagc ctggcccagg caccctgcct cctgctctgt ttggggatca	2644
agaactgtaa atttatgtat cataggtgca cctgagcccc acagaaagtt gtgcataaaa	2704
atgactgccc tggctgggca tggctgcctg taatcccagc actttgggag gctgaggtgg	2764
gaggatccct tgagcccagg agttccagac cagcctgggc aatataggga aaccctgtct	2824

ttacaaaaaa aaatttttaa aattaaaaaa aaaaaa

2860

<210> 60
<211> 1676
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> (173)..(1561)

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tgaaatggca acgataatac tgcactctat gtgaacagtt tctgtttcct tcactctgggg 120
cacgtgcata tgatcaactt tggacttctt ttgagattgc caggcgtttg ca atg 175
Met
1
gct gct act gtg aac ttg gaa ctt gat ccc att ttt ttg aaa gca cta 223
Ala Ala Thr Val Asn Leu Glu Leu Asp Pro Ile Phe Leu Lys Ala Leu
5 10 15
ggg ttc ttg cat tca aag agt aaa gat tct gct gaa aag cta aaa gca 271
Gly Phe Leu His Ser Lys Ser Lys Asp Ser Ala Glu Lys Leu Lys Ala
20 25 30
ctg ctt gat gaa tct ttg gct cgg ggc att gat tcc agt tac cgt cca 319
Leu Leu Asp Glu Ser Leu Ala Arg Gly Ile Asp Ser Ser Tyr Arg Pro
35 40 45
tct caa aag gat gtg gag cca ccc aaa att tca agc aca aaa aac att 367
Ser Gln Lys Asp Val Glu Pro Pro Lys Ile Ser Ser Thr Lys Asn Ile
50 55 60 65
tcc att aag caa gag ccc aaa ata tca tcc agt ctt cct tct ggt aat 415
Ser Ile Lys Gln Glu Pro Lys Ile Ser Ser Ser Leu Pro Ser Gly Asn
70 75 80
aat aat ggc aag gtc ctc aca act gaa aag gta aag aag gaa gct gaa 463
Asn Asn Gly Lys Val Leu Thr Thr Glu Lys Val Lys Lys Glu Ala Glu
85 90 95
aag aga cct gct gat aaa atg aaa tca gac atc act gaa gga gtt gat 511
Lys Arg Pro Ala Asp Lys Met Lys Ser Asp Ile Thr Glu Gly Val Asp
100 105 110
att cca aag aaa cct aga ttg gag aaa cca gaa aca cag tca tct ccc 559
Ile Pro Lys Lys Pro Arg Leu Glu Lys Pro Glu Thr Gln Ser Ser Pro
115 120 125
att act gtc caa agt agc aag gat tta cct atg gct gac ctt tcc agt 607
Ile Thr Val Gln Ser Ser Lys Asp Leu Pro Met Ala Asp Leu Ser Ser

130	135	140	145	
ttt gag gag acc agt gct gat gat ttt gcc atg gag atg gga ttg gcc				655
Phe Glu Glu Thr Ser Ala Asp Asp Phe Ala Met Glu Met Gly Leu Ala	150	155	160	
tgc gtt gtt tgt agg caa atg atg gtg gca tct ggc aat caa tta gta				703
Cys Val Val Cys Arg Gln Met Met Val Ala Ser Gly Asn Gln Leu Val	165	170	175	
gaa tgt cag gag tgc cat aat ctc tac cac cga gat tgt cat aaa ccc				751
Glu Cys Gln Glu Cys His Asn Leu Tyr His Arg Asp Cys His Lys Pro	180	185	190	
cag gtg aca gac aag gaa gcg aat gac cct cgc ctg gtg tgg tat tgt				799
Gln Val Thr Asp Lys Glu Ala Asn Asp Pro Arg Leu Val Trp Tyr Cys	195	200	205	
gcc cga tgt acc aga caa atg aaa aga atg gct caa aaa act cag aaa				847
Ala Arg Cys Thr Arg Gln Met Lys Arg Met Ala Gln Lys Thr Gln Lys	210	215	220	225
cca ccg cag aaa cca gcc cct gca gtt gtt tct gta act cca gct gtc				895
Pro Pro Gln Lys Pro Ala Pro Ala Val Val Ser Val Thr Pro Ala Val	230	235	240	
aaa gat cca ttg gtt aag aaa cca gaa act aaa ctg aaa caa gag aca				943
Lys Asp Pro Leu Val Lys Lys Pro Glu Thr Lys Leu Lys Gln Glu Thr	245	250	255	
act ttt cta gcg ttt aag aga aca gaa gtc aag aca tcc aca gtt att				991
Thr Phe Leu Ala Phe Lys Arg Thr Glu Val Lys Thr Ser Thr Val Ile	260	265	270	
tca gga aat tct tct agt gcc agc gtt tcc tcg tca gta act agt ggc				1039
Ser Gly Asn Ser Ser Ser Ala Ser Val Ser Ser Ser Val Thr Ser Gly	275	280	285	
tta act gga tgg gca gct ttt gca gcc aaa act tcc tct gct ggt cct				1087
Leu Thr Gly Trp Ala Ala Phe Ala Ala Lys Thr Ser Ser Ala Gly Pro	290	295	300	305
tca aca gca aaa ttg agt tca aca aca caa aac aat act ggg aaa cct				1135
Ser Thr Ala Lys Leu Ser Ser Thr Thr Gln Asn Asn Thr Gly Lys Pro	310	315	320	
gct act tcg tca gct aac cag aaa cct gtg ggt ttg act ggt ctg gca				1183
Ala Thr Ser Ser Ala Asn Gln Lys Pro Val Gly Leu Thr Gly Leu Ala	325	330	335	
aca tca tcc aaa ggt gga ata ggt tcc aaa ata ggt tcc aat aac agc				1231
Thr Ser Ser Lys Gly Gly Ile Gly Ser Lys Ile Gly Ser Asn Asn Ser	340	345	350	
act acg ccc act gta cct tta aaa cca cct cca cct cta acc ttg ggt				1279
Thr Thr Pro Thr Val Pro Leu Lys Pro Pro Pro Pro Leu Thr Leu Gly	355	360	365	

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aaa act ggc ctt agt cgc tca gtt agt tgt gac aat gtc agc aaa gta      1327
Lys Thr Gly Leu Ser Arg Ser Val Ser Cys Asp Asn Val Ser Lys Val
370                               375                               380                               385

ggt ctt cct agt cca agt agt tta gtt cca gga agc agc agc caa cta      1375
Gly Leu Pro Ser Pro Ser Ser Leu Val Pro Gly Ser Ser Ser Gln Leu
                               390                               395                               400

agt ggg aat gga aat agt gga aca tca gga cct agt gga agt act acc      1423
Ser Gly Asn Gly Asn Ser Gly Thr Ser Gly Pro Ser Gly Ser Thr Thr
                               405                               410                               415

agc aaa act act tca gaa tcc agc agc tct ccc tca gca tcc ctt aaa      1471
Ser Lys Thr Thr Ser Glu Ser Ser Ser Ser Pro Ser Ala Ser Leu Lys
                               420                               425                               430

ggc cca act tca caa gaa tca cag ctc aat gct atg aag cga tta cag      1519
Gly Pro Thr Ser Gln Glu Ser Gln Leu Asn Ala Met Lys Arg Leu Gln
                               435                               440                               445

atg gtc aag aag aaa gct gcc caa aag aaa ctc aag aag taa tgtggcc      1568
Met Val Lys Lys Lys Ala Ala Gln Lys Lys Leu Lys Lys *
450                               455                               460

aagtaggttt ttgtatcata ttagcctaaa gatgaaaggc ttattattat gatataatct      1628

gtaatacact gtaatttaat aaaagtcttc ataatcaaaa aaaaaaaaaa      1676

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<210> 61
<211> 1110
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (158)..(1051)

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gcgagactcg caggcgcaaa gagccccatt cacgccggcc caggtggcct caggtgaggg      60

ggggcgagac gcacctgtgg ggacgggacg acgagttcaa gcctccgtgg gtgcagttgg      120

tcgccagcga gggatgcgga gacgcccttg aacgacc atg gca tcg gcc gac gag      175
                               Met Ala Ser Ala Asp Glu
                               1                               5

ctg acc ttc cat gaa ttc gag gag gcc act aat ctt ctg gct gac acc      223
Leu Thr Phe His Glu Phe Glu Glu Ala Thr Asn Leu Leu Ala Asp Thr
                               10                               15                               20

cca gat gca gcc acc acc agc aga agc gat cag ctg acc cca caa ggg      271
Pro Asp Ala Ala Thr Thr Ser Arg Ser Asp Gln Leu Thr Pro Gln Gly
                               25                               30                               35

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cac	gtg	gct	gtg	gcc	gtg	ggc	tca	ggt	ggc	agc	tat	gga	gcc	gag	gat	319
His	Val	Ala	Val	Ala	Val	Gly	Ser	Gly	Gly	Ser	Tyr	Gly	Ala	Glu	Asp	
	40					45					50					
gag	gtg	gag	gag	gag	agt	gac	aag	gcc	gcg	ctc	ctg	cag	gag	cag	cag	367
Glu	Val	Glu	Glu	Glu	Ser	Asp	Lys	Ala	Ala	Leu	Leu	Gln	Glu	Gln	Gln	
	55				60					65					70	
cag	cag	cag	cag	ccg	gga	ttc	tgg	acc	ttc	agc	tac	tat	cag	agc	ttc	415
Gln	Gln	Gln	Gln	Pro	Gly	Phe	Trp	Thr	Phe	Ser	Tyr	Tyr	Gln	Ser	Phe	
				75					80					85		
ttt	gac	gtg	gac	acc	tca	cag	gtc	ctg	gac	cgg	atc	aaa	ggc	tca	ctg	463
Phe	Asp	Val	Asp	Thr	Ser	Gln	Val	Leu	Asp	Arg	Ile	Lys	Gly	Ser	Leu	
			90					95					100			
ctg	ccc	cgg	cct	ggc	cac	aac	ttt	gtg	cgg	cac	cat	ctg	cgg	aat	cgg	511
Leu	Pro	Arg	Pro	Gly	His	Asn	Phe	Val	Arg	His	His	Leu	Arg	Asn	Arg	
		105					110					115				
ccg	gat	ctg	tat	ggc	ccc	ttc	tgg	atc	tgt	gcc	acg	ttg	gcc	ttt	gtc	559
Pro	Asp	Leu	Tyr	Gly	Pro	Phe	Trp	Ile	Cys	Ala	Thr	Leu	Ala	Phe	Val	
	120					125					130					
ctg	gcc	gtc	act	ggc	aac	ctg	acg	ctg	gtg	ctg	gcc	cag	agg	agg	gac	607
Leu	Ala	Val	Thr	Gly	Asn	Leu	Thr	Leu	Val	Leu	Ala	Gln	Arg	Arg	Asp	
	135				140					145					150	
ccc	tcc	atc	cac	tac	agc	ccc	cag	ttc	cac	aag	gtg	acc	gtg	gca	ggc	655
Pro	Ser	Ile	His	Tyr	Ser	Pro	Gln	Phe	His	Lys	Val	Thr	Val	Ala	Gly	
			155						160					165		
atc	agc	atc	tac	tgc	tat	gcg	tgg	ctg	gtg	ccc	ctg	gcc	ctg	tgg	ggc	703
Ile	Ser	Ile	Tyr	Cys	Tyr	Ala	Trp	Leu	Val	Pro	Leu	Ala	Leu	Trp	Gly	
			170					175					180			
ttc	ctg	cgg	tgg	cgc	aag	ggt	gtc	cag	gag	cgc	atg	ggg	ccc	tac	acc	751
Phe	Leu	Arg	Trp	Arg	Lys	Gly	Val	Gln	Glu	Arg	Met	Gly	Pro	Tyr	Thr	
		185				190						195				
ttc	ctg	gag	act	gtg	tgc	atc	tac	ggc	tac	tcc	ctc	ttt	gtc	ttc	atc	799
Phe	Leu	Glu	Thr	Val	Cys	Ile	Tyr	Gly	Tyr	Ser	Leu	Phe	Val	Phe	Ile	
	200					205					210					
ccc	atg	gtg	gtc	ctg	tgg	ctc	atc	cct	gtg	cct	tgg	ctg	cag	tgg	ctc	847
Pro	Met	Val	Val	Leu	Trp	Leu	Ile	Pro	Val	Pro	Trp	Leu	Gln	Trp	Leu	
	215				220					225					230	
ttt	ggg	gcg	ctg	gcc	ctg	ggc	ctg	tca	gcc	gcc	ggg	ctg	gta	ttc	acc	895
Phe	Gly	Ala	Leu	Ala	Leu	Gly	Leu	Ser	Ala	Ala	Gly	Leu	Val	Phe	Thr	
			235						240					245		
ctc	tgg	ccc	gtg	gtc	cgt	gag	gac	acc	agg	ctg	gtg	gcc	aca	gtg	ctg	943
Leu	Trp	Pro	Val	Val	Arg	Glu	Asp	Thr	Arg	Leu	Val	Ala	Thr	Val	Leu	
			250				255						260			

ctg tcc gtg gtc gtg ctg ctc cag gcc ctc ctg gcc atg ggc tgt gaa	991
Leu Ser Val Val Val Leu Leu Gln Ala Leu Leu Ala Met Gly Cys Glu	
265 270 275	
gtt gga ctt ctt ccg gtg tgc ctc ggg gac gtg gtc ctc ccc cca ttc	1039
Val Gly Leu Leu Pro Val Cys Leu Gly Asp Val Val Leu Pro Pro Phe	
280 285 290	
att ttg ccc taa att gggggcctac tgtcggggccg ggcccctcag aggcggggccg	1094
Ile Leu Pro *	
295	
gcccttggac ccttgg	1110

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 <212> DNA
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 <222> (51)..(716)

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atg gcc	
Met Ala	
1	
ggg act ggg ctg ctg gcg ctg cgg acg ctg cca ggg ccc agc tgg gtg	104
Gly Thr Gly Leu Leu Ala Leu Arg Thr Leu Pro Gly Pro Ser Trp Val	
5 10 15	
cga ggc tcg ggc cct tcc gtg ctg agc cgc ctg cag gac gcg gcc gtg	152
Arg Gly Ser Gly Pro Ser Val Leu Ser Arg Leu Gln Asp Ala Ala Val	
20 25 30	
gtg cgg cct ggc ttc ctg agc acg gca gag gag gag acg ctg agc cga	200
Val Arg Pro Gly Phe Leu Ser Thr Ala Glu Glu Glu Thr Leu Ser Arg	
35 40 45 50	
gaa ctg gag ccc gag ctg cgc cgc cgc cgc tac gaa tac gat cac tgg	248
Glu Leu Glu Pro Glu Leu Arg Arg Arg Arg Tyr Glu Tyr Asp His Trp	
55 60 65	
gac gcg gcc atc cac ggc ttc cga gag aca gag aag tcg cgc tgg tca	296
Asp Ala Ala Ile His Gly Phe Arg Glu Thr Glu Lys Ser Arg Trp Ser	
70 75 80	
gaa gcc agc cgg gcc atc ctg cag cgc gtg cag gcg gcc gcc ttt ggc	344
Glu Ala Ser Arg Ala Ile Leu Gln Arg Val Gln Ala Ala Ala Phe Gly	
85 90 95	
ccc ggc cag acc ctg ctc tcc tcc gtg cac gtg ctg gac ctg gaa gcc	392
Pro Gly Gln Thr Leu Leu Ser Ser Val His Val Leu Asp Leu Glu Ala	

100	105	110	
cgc ggc tac atc aag ccc cac gtg gac agc atc aag ttc tgc ggg gcc			440
Arg Gly Tyr Ile Lys Pro His Val Asp Ser Ile Lys Phe Cys Gly Ala			
115	120	125	130
acc atc gcc ggc ctg tct ctc ctg tct ccc agc gtt atg cgg ctg gtg			488
Thr Ile Ala Gly Leu Ser Leu Leu Ser Pro Ser Val Met Arg Leu Val			
	135	140	145
cac acc cag gag ccg ggg gag tgg ctg gaa ctc ttg ctg gag ccg ggc			536
His Thr Gln Glu Pro Gly Glu Trp Leu Glu Leu Leu Glu Pro Gly			
	150	155	160
tcc ctc tac atc ctt agg ggc tca gcc cgt tat gac ttc tcc cat gag			584
Ser Leu Tyr Ile Leu Arg Gly Ser Ala Arg Tyr Asp Phe Ser His Glu			
	165	170	175
atc ctt cgg gat gaa gag tcc ttc ttt ggg gaa cgc cag att ccc cgg			632
Ile Leu Arg Asp Glu Glu Ser Phe Phe Gly Glu Arg Gln Ile Pro Arg			
	180	185	190
ggc cgg cgc atc tcc gtg atc tgc cgc tcc ctc cct gag ggc atg ggg			680
Gly Arg Arg Ile Ser Val Ile Cys Arg Ser Leu Pro Glu Gly Met Gly			
195	200	205	210
cca ggg gag tct gga cag ccg ccc cca gcc tgc tga cccc cagctttcta			730
Pro Gly Glu Ser Gly Gln Pro Pro Pro Ala Cys *			
	215	220	
cagacaccag atttgtgaat aaagttgggg aatggacagc ctaactggga cattgcagtg			790
gctgcttgct ggggccggga tttgcagggg aaccaggat ggcaactggcc catagggagc			850
tccaggtgtg gctggctgga cacatgggtca aagtcacaag gccgggagag tgggtgtcctt			910
tattgcactc actgctgggc gccccagccc actccccctcc tcgttgtctc tgcattccagg			970
tctccaataa ataagtcagc cgagaaaaag aaaaaaaaaa a			1011

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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (194)..(736)

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caccaaacc aaaaaagag atctctcgag gatccgaatt cgcggccgcg tcgacatcgc	120

agggagccgg tccgccgccg gaacgggagc ctgggtgtgc gtgtggagtc cggactcgtg 180
 ggagacgata gcg atg aac acg gtg ctg tgc cgg gcg aac tca ctg ttc 229
 Met Asn Thr Val Leu Ser Arg Ala Asn Ser Leu Phe
 1 5 10
 gcc ttc tgc ctg agc gtg atg gcg gcg ctc acc ttc ggc tgc ttc atc 277
 Ala Phe Ser Leu Ser Val Met Ala Ala Leu Thr Phe Gly Cys Phe Ile
 15 20 25
 acc acc gcc ttc aaa gac agg agc gtc ccg gtg cgg ctg cac gtc tgc 325
 Thr Thr Ala Phe Lys Asp Arg Ser Val Pro Val Arg Leu His Val Ser
 30 35 40
 cgg atc ata cta aaa aat gta gaa gat ttc act gga cct aga gaa aga 373
 Arg Ile Ile Leu Lys Asn Val Glu Asp Phe Thr Gly Pro Arg Glu Arg
 45 50 55 60
 agt gat ctg gga ttt atc aca ttt gat ata act gct gat cta gag aat 421
 Ser Asp Leu Gly Phe Ile Thr Phe Asp Ile Thr Ala Asp Leu Glu Asn
 65 70 75
 ata ttt gat tgg aat gtt aag cag ttg ttt ctt tat tta tca gca gaa 469
 Ile Phe Asp Trp Asn Val Lys Gln Leu Phe Leu Tyr Leu Ser Ala Glu
 80 85 90
 tat tca aca aaa aat aat gct ctg aac caa gtt gtc cta tgg gac aag 517
 Tyr Ser Thr Lys Asn Asn Ala Leu Asn Gln Val Val Leu Trp Asp Lys
 95 100 105
 att gtt ttg aga ggt gat aat ccg aag ctg ctg ctg aaa gat atg aaa 565
 Ile Val Leu Arg Gly Asp Asn Pro Lys Leu Leu Leu Lys Asp Met Lys
 110 115 120
 aca aaa tat ttt ttc ttt gac gat gga aat ggt ctc aag gga aac agg 613
 Thr Lys Tyr Phe Phe Phe Asp Asp Gly Asn Gly Leu Lys Gly Asn Arg
 125 130 135 140
 aat gtc act ttg acc ctg tct tgg aac gtc gta cca aat gct gga att 661
 Asn Val Thr Leu Thr Leu Ser Trp Asn Val Val Pro Asn Ala Gly Ile
 145 150 155
 cta cct ctt gtg aca gga tca gga cac gta tct gtc cca ttt cca gat 709
 Leu Pro Leu Val Thr Gly Ser Gly His Val Ser Val Pro Phe Pro Asp
 160 165 170
 aca tat gaa ata acg aag agt tat taa attat tctgaatttg aaacaacata 761
 Thr Tyr Glu Ile Thr Lys Ser Tyr *
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Arg	Lys	His	Val	Val	Lys	Glu	Val	Leu	Gly	Glu	His	
	10							15				
gac	cag	cag	cag	att	gtc	agg	gta	ctc	agg	acc	cca	208
Asp	Gln	Gln	Gln	Ile	Val	Arg	Val	Leu	Arg	Thr	Pro	
	25							30				
cat	gag	gtg	gag	aca	gcc	caa	ggg	cag	cgc	ttc	ctg	256
His	Glu	Val	Glu	Thr	Ala	Gln	Gly	Gln	Arg	Phe	Leu	
	40							45				
tcc	aaa	tac	cgc	aag	aac	atc	tgg	atc	aag	aga	ggg	304

Ser Lys Tyr Arg Lys Asn Ile Trp Ile Lys Arg Gly Asp Phe Leu Ile
55 60 65 70

gtt gac ccc att gaa gag gga gaa aag gtg aag gct gaa atc tcg ttt 352
Val Asp Pro Ile Glu Glu Gly Glu Lys Val Lys Ala Glu Ile Ser Phe
75 80 85

gtg ctc tgc aag gac cac gtg cgc tct ctg cag aag gag ggg ttt tgg 400
Val Leu Cys Lys Asp His Val Arg Ser Leu Gln Lys Glu Gly Phe Trp
90 95 100

cct gag gcc ttc tct gaa gtg gct gag aaa cac aac aac agg aac aga 448
Pro Glu Ala Phe Ser Glu Val Ala Glu Lys His Asn Asn Arg Asn Arg
105 110 115

caa act caa cca gaa ctc cca gct gag cca cag tta tca gga gag gag 496
Gln Thr Gln Pro Glu Leu Pro Ala Glu Pro Gln Leu Ser Gly Glu Glu
120 125 130

tcc agc tca gaa gat gat tct gac ctg ttt gtt aac aca aac cgc aga 544
Ser Ser Ser Glu Asp Asp Ser Asp Leu Phe Val Asn Thr Asn Arg Arg
135 140 145 150

cag tat cat gag agt gag gag gag agt gaa gag gag gag gca gcc tga 592
Gln Tyr His Glu Ser Glu Glu Glu Ser Glu Glu Glu Glu Ala Ala *
155 160 165

gactccagga cccaattctc cacttgctca gggactggcc cctggctctt ctgggcttgg 652

acattcccag ggtgctctgc acatcttcac ccctgcatga ggacaaagca gggctcctct 712

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<212> DNA
<213> Homo sapiens

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<222> (66)..(725)

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aggag atg gcg gag tcg ttg agg tct ccg cgc cgc tcc ctg tac aaa 107
Met Ala Glu Ser Leu Arg Ser Pro Arg Arg Ser Leu Tyr Lys
1 5 10

ctg gtg ggc tcg ccg cct tgg aaa gag gct ttc cgg cag aga tgc ctg 155
Leu Val Gly Ser Pro Trp Lys Glu Ala Phe Arg Gln Arg Cys Leu
15 20 25 30

gag aga atg aga aac agc cgg gac agg ctc cta aac agg tac cgc cag 203

Glu Arg Met Arg Asn Ser Arg Asp Arg Leu Leu Asn Arg Tyr Arg Gln	
35 40 45	
gct gga agc agt ggg cca ggg aat tct cag aac agc ttt cta gtt caa	251
Ala Gly Ser Ser Gly Pro Gly Asn Ser Gln Asn Ser Phe Leu Val Gln	
50 55 60	
gag gtg atg gaa gaa gag tgg aat gct ttg cag tca gtg gag aat tgt	299
Glu Val Met Glu Glu Glu Trp Asn Ala Leu Gln Ser Val Glu Asn Cys	
65 70 75	
cca gaa gac ttg gct cag ctg gag gag ctg ata gac atg gct gtg ctg	347
Pro Glu Asp Leu Ala Gln Leu Glu Glu Leu Ile Asp Met Ala Val Leu	
80 85 90	
gag gaa att caa cag gag ctg atc aac caa gag cag tcc atc atc agc	395
Glu Glu Ile Gln Gln Glu Leu Ile Asn Gln Glu Gln Ser Ile Ile Ser	
95 100 105 110	
gag tat gag aag agc ttg cag ttt gat gaa aag tgt ctc agc atc atg	443
Glu Tyr Glu Lys Ser Leu Gln Phe Asp Glu Lys Cys Leu Ser Ile Met	
115 120 125	
ctg gct gag tgg gag gca aac cca ctc atc tgt cct gta tgt aca aag	491
Leu Ala Glu Trp Glu Ala Asn Pro Leu Ile Cys Pro Val Cys Thr Lys	
130 135 140	
tac aac ctg aga atc aca agc ggt gtg gtg gtg tgt cag tgt ggc ctg	539
Tyr Asn Leu Arg Ile Thr Ser Gly Val Val Val Cys Gln Cys Gly Leu	
145 150 155	
tcc atc cca tct cat tct tct gag ttg aca gag cag aag ctt cgt gcc	587
Ser Ile Pro Ser His Ser Ser Glu Leu Thr Glu Gln Lys Leu Arg Ala	
160 165 170	
tgt tta gag ggt agt ata aat gag cac agt gca cat tgt ccc cac aca	635
Cys Leu Glu Gly Ser Ile Asn Glu His Ser Ala His Cys Pro His Thr	
175 180 185 190	
cct gaa ttt tca gtc act gga gga aca gaa gaa aag tcc agt ctt ctc	683
Pro Glu Phe Ser Val Thr Gly Gly Thr Glu Glu Lys Ser Ser Leu Leu	
195 200 205	
atg agc tgt ctg gcc tgt gat act tgg gct gtg atc ctc tag agccagc	732
Met Ser Cys Leu Ala Cys Asp Thr Trp Ala Val Ile Leu *	
210 215 220	
tgggactcac atcattctat gggcgttgaa gacaactcat tcctctgagg agccttgtac	792
atacaagcct tttatttata acttattttg tattgaaact tttacaccat tctggagaaa	852
aaaaa	857

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<400> 71

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cgctgggacg tatgtgccga gggccgcggc gtctgacctc atggcgtaga gcctagcaac      180
agcgcaggct cccagccgag tccggtt atg gcc gct gcc gtc ccg aag agg atg      233
                Met Ala Ala Ala Val Pro Lys Arg Met
                  1                5

agg ggg cca gca caa gcg aaa ctg ctg ccc ggg tgc gcc atc caa gcc      281
Arg Gly Pro Ala Gln Ala Lys Leu Leu Pro Gly Ser Ala Ile Gln Ala
  10                15                20                25

ctt gtg ggg ttg gcg cgg ccg ctg gtc ttg gcg ctc ctg ctt gtg tcc      329
Leu Val Gly Leu Ala Arg Pro Leu Val Leu Ala Leu Leu Leu Val Ser
                30                35                40

gcc gct cta tcc agt gtt gta tca cgg act gat tca ccg agc cca acc      377
Ala Ala Leu Ser Ser Val Val Ser Arg Thr Asp Ser Pro Ser Pro Thr
                45                50                55

gta ctc aac tca cat att tct acc cca aat gtg aat gct tta aca cat      425
Val Leu Asn Ser His Ile Ser Thr Pro Asn Val Asn Ala Leu Thr His
                60                65                70

gaa aac caa acc aaa cct tct att tcc caa atc agc acc acc ctc cct      473
Glu Asn Gln Thr Lys Pro Ser Ile Ser Gln Ile Ser Thr Thr Leu Pro
                75                80                85

ccc acg acg agt acc aag aaa agt gga gga gca tct gtg gtc cct cat      521
Pro Thr Thr Ser Thr Lys Lys Ser Gly Gly Ala Ser Val Val Pro His
  90                95                100                105

ccc tcg cct act cct ctg tct caa gag gaa gct gat aac aat gaa gat      569
Pro Ser Pro Thr Pro Leu Ser Gln Glu Glu Ala Asp Asn Asn Glu Asp
                110                115                120

cct agt ata gag gag gag gat ctt ctc atg ctg aac agt tct cca tcc      617
Pro Ser Ile Glu Glu Glu Asp Leu Leu Met Leu Asn Ser Ser Pro Ser
                125                130                135

aca gcc aaa gac act cta gac aat ggc gat tat gga gaa cca gac tat      665
Thr Ala Lys Asp Thr Leu Asp Asn Gly Asp Tyr Gly Glu Pro Asp Tyr
                140                145                150

gac tgg acc acg ggc ccc agg gac gac gac gag tct gat gac acc ttg      713
Asp Trp Thr Thr Gly Pro Arg Asp Asp Asp Glu Ser Asp Asp Thr Leu

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155	160	165	
gaa gaa aac agg ggt tac atg gaa att gaa cag tca gtg aaa tct ttt			761
Glu Glu Asn Arg Gly Tyr Met Glu Ile Glu Gln Ser Val Lys Ser Phe			
170	175	180	185
aag atg cca tcc tca aat ata gaa gag gaa gac agc cat ttc ttt ttt			809
Lys Met Pro Ser Ser Asn Ile Glu Glu Glu Asp Ser His Phe Phe Phe			
	190	195	200
cat ctt att att ttt gct ttt tgc att gct gtt gtt tac att aca tat			857
His Leu Ile Ile Phe Ala Phe Cys Ile Ala Val Val Tyr Ile Thr Tyr			
	205	210	215
cac aac aaa agg aag att ttt ctt ctg gtt caa agc agg aaa tgg cgt			905
His Asn Lys Arg Lys Ile Phe Leu Leu Val Gln Ser Arg Lys Trp Arg			
	220	225	230
gat ggc ctt tgt tcc aaa aca gtg gaa tac cat cgc cta gat cag aat			953
Asp Gly Leu Cys Ser Lys Thr Val Glu Tyr His Arg Leu Asp Gln Asn			
	235	240	245
gtt aat gag gca atg cct tct ttg aag att acc aat gat tat att ttt			1001
Val Asn Glu Ala Met Pro Ser Leu Lys Ile Thr Asn Asp Tyr Ile Phe			
	250	255	260
taa			1004
*			

<210> 72
 <211> 1562
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1244)..(1399)

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aagggaagat aaaccaaatt cttagcttggtg ttttaccac agaaggatac aggacaaagg	120
aatagtaact ggcctgtttg gatactaaaa ttgaaaataa ctttttagcct cctccttatg	180
atagccgcca gagtaaatgt tgagcattac tacagaaaag ccacaaacca agaattctacc	240
tgtttggaag gatcttttgc atctctgaag gtgcttaaag catacttagt gccttttcctt	300
ttaactggga agataaaaga agtatctgtc caagatatta atatgtaaga taacattgta	360
gacatgttct tctgataata caaggtttat tctatttgca ttaggatatt tgtggacatg	420

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ttagaaaact tctaaagata attggatgag aatatacata ttgacctgta tattatgact 540
aatcatgact cagatcttaa tacagggatg atctcatagc atttagatat cagaaaaggt 600
tttgacctat atgtctttaa tattgtttga atacatgtat aatctttatc attcctcagt 660
gtttcatttc tcaaattctg taaaaggaat ataaggaggaa agacaattca tatacaaaga 720
caacgagatt aaaaatatgc agtaggaaaa ataattactt aaggggagat tttttttaca 780
tgaaatctgg gctttggatg tgtgtgtgtg tgtgtgtgtg cacatatgca ctgtgggtggg 840
agtggggcaa cttggggaat atgttacatg tgtgactttg ttttgccctg gcgaagttaa 900
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attaaccaca gaattatagc aggtattcat aacttaagtt tgaaaatcaa tagcgtctgc 1080
aatggatta acagattaga gaatcaacag catcgaaaaa taggttaatg catattgctt 1140
ctaacaagtg catgaagaaa tagaagaagc tatgtagctt tcagttctga cagaaaaggg 1200
tgaaggaggg tatcatttca agaaaaaaaa tagctatcac gca atg gtt atc tct 1255
                                     Met Val Ile Ser
                                     1
gaa aat att tgt att aag atg tgt ata cat ggc cag gca tgg tgg ctc 1303
Glu Asn Ile Cys Ile Lys Met Cys Ile His Gly Gln Ala Trp Trp Leu
  5                10                15                20
atg cct gta atc cca gca ctt tgg gag gca ggt gga tca cga ggt cag 1351
Met Pro Val Ile Pro Ala Leu Trp Glu Ala Gly Gly Ser Arg Gly Gln
          25                30                35
gag atc aag acc atc ctg gcc aac atg gtg aaa cct cat ctc tac taa 1399
Glu Ile Lys Thr Ile Leu Ala Asn Met Val Lys Pro His Leu Tyr *
          40                45                50
aaatacaaaa atgagcgggg tgtggtggcc catgcctgta gtcccagctg ctcgaggagac 1459
tgaatctctt gagcctggga agcagaggtt gcagtgaact gagatcgctg cactgcactc 1519
cagcccgggt gacagagcga gattccatct caaaaaaaaa aaa 1562

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<210> 73
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 <212> DNA
 <213> Homo sapiens

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 <222> (1229) .. (1432)

<220>
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 <222> (1) ... (2100)
 <223> n = a,t,c or g

<400> 73

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aacaagaaac	aataattcta	agttagccag	ccaatcaaac	tacttcagta	aatgatcata		180
ctacagcctg	gaatcactca	aacaaaaaat	tcttctagtt	ctcttttaaag	atatttatcg		240
tttatttttt	catgaaacca	aagtaattga	ttcaacaata	ctaacagttc	tagcatgcaa		300
caaaccatct	actatcta	atgtttaa	cttaacatgt	atattttcat	tcctataaag		360
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catgggggat	tgggttctgg	accgtcccc	caaccacag	ataccaaaa	tccaagtata		480
ctcaagtc	ttacataaaa	tgacatattt	gtatataacc	aacgcacatc	cgctgtata		540
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tatttttatt	tgtattattt	ttattttttc	taatattttt	gatctgcaat	tggtttaatc		660
cacagatgca	gagtacatgg	atacagaggg	ccaactgttt	tgttacaggt	acttcaaata		720
gcactacagt	acatctttga	caaaattttt	acaatatctc	acctttcaat	atgaaacagc		780
ttaaaaaggc	atgggtcaaa	aataaagtat	agtagtatca	cttacgcaaa	taaagtctca		840
gaatcataca	agcacaacac	tgttaggact	ctccctgttt	aggctgggaa	aaacattata		900
caaaacattt	tcttcaaata	aaattacata	aattgcttag	aaaaatgcc	aatcaataa		960
tttcaa	acattattaagg	gaga	aaaccttgaa	cattattgga	aatataaac	tagttattcc	1020
ttgcttttaa	cagatgagtt	cttgacaagt	tttgtgtaaa	gcaaattctg	taaaccatta		1080
tcttgcttgc	actggaggaa	catatctcaa	ggaaacctaa	gagaaagtgt	tctttaaagc		1140
atgtgattct	cctgtttttg	ctggatgtct	gtatctacat	aataaacagg	cacacttcta		1200
catcactggg	tattttactc	agactgtc	atg ttt cat ctc tgt aaa tta aac			1252	
			Met Phe His Leu Cys Lys Leu Asn				
			1 5				
cca agt tac tta aaa atc acc tgt ggt aaa aga agc aag cag atc acc						1300	
Pro Ser Tyr Leu Lys Ile Thr Cys Gly Lys Arg Ser Lys Gln Ile Thr							
10 15 20							

ccc atc tac tat ccc tcc cgc ctc ccc cct gtc aaa aga aag ttc tca 1348
Pro Ile Tyr Tyr Pro Ser Arg Leu Pro Pro Val Lys Arg Lys Phe Ser
25 30 35 40

gtt tat gat gca aaa ctt aca att gtt cat tta tcc aca ttc tca ata 1396
Val Tyr Asp Ala Lys Leu Thr Ile Val His Leu Ser Thr Phe Ser Ile
45 50 55

gag gat ttt cca cta tat tta agt atg gca gga taa ttac ccacctgttc 1446
Glu Asp Phe Pro Leu Tyr Leu Ser Met Ala Gly *
60 65

ctcttttcag cttagaaaca taacgggttca ttccttttat tgctagagaa tgtcattcct 1506

gaagatttta taaacaaagg caaatatgaa ggaaaatttg taattatgaa ataagtcctt 1566

tgtagtaaag aatatttccc aaatcataac agttctatctt ggaatgatac ccacaactct 1626

acaagcatct tatccctcta caggaatgac taccttatta attaaaataa aaatttaaca 1686

aggatcaaaa taaaattctt tagcaataga ctcttgcaaa aataaaaaact aaaactagac 1746

ctagtcattg ccatttgatc aaacttagaa caggcttaaa taacagaacc actccattaa 1806

agaggcatag aaagaaaagt ttactaaaat aaatgtaaaa gtcttatgga gatgaagatc 1866

tctagaatag tcttaagtct atgactactg ctatcattaa tgagcaaata aatgacttga 1926

aattattccn cctggaaaag gtaaactcat acgtattatg gaaaangcct atggggcactt 1986

agaaaaatat tcctgggtaa gtaaaccatg gnaaatatag ggtacatcct aagcctctcc 2046

gccctaactt ttaaaattat tnttggagaa aggatagcac tagccgggga ggaa 2100

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<211> 933

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (267) .. (866)

<400> 74

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agcgaccttg gccgttgccc tgaccatctt agtgctgtct gtcgtcacta tcatcatctg 180

cttcacctgc tcctgctgct gcctttacaa gacgtgccgc cgaccacgtc cggttgtcac 240

caccaccaca tccaccactg tgggtgc atg ccc ctt atc ctc agc ctc caa gtg 293

Met Pro Leu Ile Leu Ser Leu Gln Val																
1								5								
tgc	cgc	cca	gct	acc	cgt	gga	cca	agc	tac	cag	ggc	tac	cac	acc	atg	341
Cys	Arg	Pro	Ala	Thr	Arg	Gly	Pro	Ser	Tyr	Gln	Gly	Tyr	His	Thr	Met	
10					15					20					25	
ccg	cct	cag	cca	ggg	atg	cca	gca	gcg	acc	cta	ccc	aat	gca	ggg	aag	389
Pro	Pro	Gln	Pro	Gly	Met	Pro	Ala	Ala	Thr	Leu	Pro	Asn	Ala	Gly	Lys	
				30					35					40		
atg	gcg	gac	att	cag	act	gag	cgt	gcc	tac	caa	aag	cag	ccg	acc	atc	437
Met	Ala	Asp	Ile	Gln	Thr	Glu	Arg	Ala	Tyr	Gln	Lys	Gln	Pro	Thr	Ile	
			45					50					55			
ttt	caa	aac	aag	aag	agg	gtc	ctg	ctg	gga	gaa	act	ggc	aag	gag	aag	485
Phe	Gln	Asn	Lys	Lys	Arg	Val	Leu	Leu	Gly	Glu	Thr	Gly	Lys	Glu	Lys	
		60					65					70				
ctc	ccg	cgg	tac	tac	aag	aac	atc	ggt	ctg	ggc	ttc	aag	aca	ccc	aag	533
Leu	Pro	Arg	Tyr	Tyr	Lys	Asn	Ile	Gly	Leu	Gly	Phe	Lys	Thr	Pro	Lys	
	75					80					85					
gag	gct	att	gag	ggc	acc	tac	att	gac	aag	aaa	tgc	ccc	ttc	act	ggt	581
Glu	Ala	Ile	Glu	Gly	Thr	Tyr	Ile	Asp	Lys	Lys	Cys	Pro	Phe	Thr	Gly	
90				95					100						105	
aat	gtg	tcc	att	cga	ggg	cgg	atc	ctc	tct	ggc	gtg	gtg	acc	aag	atg	629
Asn	Val	Ser	Ile	Arg	Gly	Arg	Ile	Leu	Ser	Gly	Val	Val	Thr	Lys	Met	
				110					115					120		
aag	atg	cag	agg	acc	att	gtc	atc	cgc	cga	gac	tat	ctg	cac	tac	atc	677
Lys	Met	Gln	Arg	Thr	Ile	Val	Ile	Arg	Arg	Asp	Tyr	Leu	His	Tyr	Ile	
			125					130					135			
cgc	aag	tac	aac	cgc	ttc	gag	aag	cgc	cac	aag	aac	atg	tct	gta	cac	725
Arg	Lys	Tyr	Asn	Arg	Phe	Glu	Lys	Arg	His	Lys	Asn	Met	Ser	Val	His	
	140						145					150				
ctg	tcc	ccc	tgc	ttc	agg	gac	gtc	cag	atc	ggt	gac	atc	gtc	aca	gtg	773
Leu	Ser	Pro	Cys	Phe	Arg	Asp	Val	Gln	Ile	Gly	Asp	Ile	Val	Thr	Val	
	155					160					165					
ggc	gag	tgc	cgg	cct	ctg	agc	aag	aca	gtg	cgc	ttc	aac	gtg	ctc	aag	821
Gly	Glu	Cys	Arg	Pro	Leu	Ser	Lys	Thr	Val	Arg	Phe	Asn	Val	Leu	Lys	
170					175					180					185	
gtc	acc	aag	gct	gcc	ggc	acc	aag	aag	cag	ttc	cag	aag	ttc	tga	ggc	869
Val	Thr	Lys	Ala	Ala	Gly	Thr	Lys	Lys	Gln	Phe	Gln	Lys	Phe	*		
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aaaa																933

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 <212> DNA
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<220>
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 <222> (446)..(2956)

<400> 75

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cgtgctccac ctctggccct tcaccatcca cgacctgcgg gcactcgggtg ctaagaagtt    180
ctacggggcgc ttctgcaccg gcaccctgga ccacatcagc atcaggcagc tccagctgct    240
tctgctgaag gtagcattgc tgctgggggt ggaaattcac tgggggtgtca ctttacttgg    300
cctccagccc cctcctagga aggggagtggt ctggcgtgcc cagctccaac ccaaccccc    360
tgcccagctg gccaaactatg aatttgacgt ctttatctcg gctgcaggag gtaaattcgt    420
ccctgaaggc ttcaaagttc gagaa  atg cga ggc aaa ctg gcc att ggc atc      472
                               Met Arg Gly Lys Leu Ala Ile Gly Ile
                               1               5

aca gcc aac ttt gtg aat gga cgc acc gtg gag gag aca cag gtg ccg      520
Thr Ala Asn Phe Val Asn Gly Arg Thr Val Glu Glu Thr Gln Val Pro
 10               15               20               25

gag atc agt ggt gta gcc agg atc tac aac cag agc ttc ttc cag agc      568
Glu Ile Ser Gly Val Ala Arg Ile Tyr Asn Gln Ser Phe Phe Gln Ser
               30               35               40

ctt ctc aaa gcc aca ggc att gat ctg gag aac att gtg tac tac aag      616
Leu Leu Lys Ala Thr Gly Ile Asp Leu Glu Asn Ile Val Tyr Tyr Lys
               45               50               55

gac gac acc cac tac ttt gtg atg aca gcc aag aag cag tgc ctg ctg      664
Asp Asp Thr His Tyr Phe Val Met Thr Ala Lys Lys Gln Cys Leu Leu
               60               65               70

cgg ctg ggg gtg ctg cgc cag gac tgg cca gac acc aat cgg ctg ctg      712
Arg Leu Gly Val Leu Arg Gln Asp Trp Pro Asp Thr Asn Arg Leu Leu
               75               80               85

ggc agt gcc aat gtg gtg ccc gag gct ctg cag cgc ttt acc cgg gca      760
Gly Ser Ala Asn Val Val Pro Glu Ala Leu Gln Arg Phe Thr Arg Ala
               90               95              100              105

gct gct gac ttt gcc acc cat ggc aag ctc ggg aaa cta gag ttt gcc      808
Ala Ala Asp Phe Ala Thr His Gly Lys Leu Gly Lys Leu Glu Phe Ala
               110              115              120
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Asp Leu Tyr Asp Val Leu Ala Lys Glu Pro Val Gln Arg Asn Asn Asp	
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Lys Thr Asp Thr Gly Met Pro Ala Thr Gly Ser Ala Gly Thr Gln Glu	
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Thr Leu Gln Arg Ser Arg Ala Lys Glu Asn Ala Glu Asp Ala Gly Gly	
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Pro Pro Asp Pro Glu Pro Gly Val Pro Leu Thr Pro Pro Ser Gln His	
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Gln Glu Ala Gly Ala Gly Asp Leu Cys Ala Leu Cys Gly Glu His Leu	
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Tyr Val Leu Glu Arg Leu Cys Val Asn Gly His Phe Phe His Arg Ser	
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Gln Thr Asp His Lys Glu Glu Gly Ser Asp Arg Gly Pro Glu Ser Pro	
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Glu Leu Pro Thr Pro Ser Glu Asn Ser Met Pro Pro Gly Leu Ser Thr	
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Pro Thr Arg Arg Gln Ile Arg Leu Ser Ser Pro Glu Arg Gln Arg Leu	

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Pro Pro Arg Ser Cys Ser Ala Leu Ala Arg His Ala Leu Glu Ser Ser	605	610	615	
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Met Glu Lys Glu Glu Lys Glu Ser Pro Phe Ser Ser Glu Glu Glu Glu	635	640	645	
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Glu Asp Val Pro Leu Asp Ser Asp Val Glu Gln Ala Leu Gln Thr Phe	650	655	660	665
gcc aag acc tca ggc acc atg aat aac tac cca aca tgg cgt cgg act				2488
Ala Lys Thr Ser Gly Thr Met Asn Asn Tyr Pro Thr Trp Arg Arg Thr	670	675	680	
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Leu Leu Arg Arg Ala Lys Glu Glu Glu Met Lys Arg Phe Cys Lys Ala	685	690	695	
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Gln Thr Ile Gln Arg Arg Leu Asn Glu Ile Glu Ala Ala Leu Arg Glu	700	705	710	
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Leu Glu Ala Glu Gly Val Lys Leu Glu Leu Ala Leu Arg Arg Gln Ser	715	720	725	
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Lys Ala Gly Lys Trp Glu Val Pro Leu Pro Lys Val Arg Ala Gln Gly	
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Thr Arg Lys Pro Pro Lys Tyr Glu Arg Phe Ile Arg Pro Met Gly Leu	
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Arg Phe Lys Lys Ala His Val Thr His Pro Glu Leu Lys Ala Thr Phe	
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Cys Leu Pro Ile Leu Gly Val Lys Lys Asn Pro Ser Ser Pro Leu Tyr	
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Gly Met Ile Tyr Thr Glu Met Thr Gly Lys Leu Ile Ser Ser Tyr Tyr		
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Gln Ser Val Leu Ser Tyr Ser Pro Ser Arg Ser Pro Ser Thr Ser Pro		
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Pro Val Ser Gly Tyr Asn Lys Leu Ala Ser Phe Ser Pro Ser Pro Pro		
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Ser	Arg	Tyr	Arg	Ser	Ser	Pro	Thr	Val	Tyr	Asn	Ser	Pro	Thr	Asp	Lys	
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Leu	Asp	His	Met	Asp	Ser	Trp	Thr	Ala	Lys	Phe	Arg	Asn	Trp	Ile	Asn	
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Ile	Thr	Ser	Leu	Lys	Gln	Ala	Ala	Leu	Val	Lys	Ala	Pro	Leu	Ile	Pro	
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Thr	Leu	Asn	Thr	Ile	Val	Gln	Tyr	Leu	Asp	Leu	Thr	Pro	Asn	Gln	Glu	
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Tyr	Leu	Phe	Glu	Arg	Ile	Lys	Glu	Leu	Ser	Gln	Gly	Gly	Cys	Met	Ser	
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Gln Thr Pro Lys Ala Gly Leu Arg Val Ser Ala Pro Glu Val Ser Val
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Gln Ile Gly Gly Ser Ile Thr Gly Pro Ser Val Glu Val Gln Ala Pro
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Lys	Gly	Thr	Lys	Val	Lys	Gly	Glu	Tyr	Asp	Val	Thr	Val	Pro	Lys	Leu	

400	405	410	
gaa gga gaa ctc aaa ggc cca aaa gtg gac att gat gcc cca gat gtg Glu Gly Glu Leu Lys Gly Pro Lys Val Asp Ile Asp Ala Pro Asp Val 415 420 425 430			1477
gat gtt cat ggc cca gac tgg cac ttg aag atg ccc aag atg aaa atg Asp Val His Gly Pro Asp Trp His Leu Lys Met Pro Lys Met Lys Met 435 440 445			1525
ccc aaa ttc agt gtg cca ggg ttc aaa gca gag ggc cca gaa gtg gat Pro Lys Phe Ser Val Pro Gly Phe Lys Ala Glu Gly Pro Glu Val Asp 450 455 460			1573
gtg aac ctg ccc aag gct gat gtg gac att tcc ggg ccc aag ata gat Val Asn Leu Pro Lys Ala Asp Val Asp Ile Ser Gly Pro Lys Ile Asp 465 470 475			1621
gtt act gct cct gat gtg agc att gag gaa cca gaa ggg aaa ttg aaa Val Thr Ala Pro Asp Val Ser Ile Glu Glu Pro Glu Gly Lys Leu Lys 480 485 490			1669
ggg ccc aag ttt aag atg cct gag atg aac atc aaa gtc ccc aag atc Gly Pro Lys Phe Lys Met Pro Glu Met Asn Ile Lys Val Pro Lys Ile 495 500 505 510			1717
tcc atg cct gat gtg gac tta cat ctg aaa ggc cct aac gta aag gga Ser Met Pro Asp Val Asp Leu His Leu Lys Gly Pro Asn Val Lys Gly 515 520 525			1765
gaa tat gat gtc aca atg cca aag gtt gaa agt gag att aaa gtt cct Glu Tyr Asp Val Thr Met Pro Lys Val Glu Ser Glu Ile Lys Val Pro 530 535 540			1813
gat gtt gaa ctt aaa agt gcc aaa atg gac att gat gtc cca gat gtg Asp Val Glu Leu Lys Ser Ala Lys Met Asp Ile Asp Val Pro Asp Val 545 550 555			1861
gag gtt caa ggc cca gac tgg cac ctg aag atg ccc aag atg aaa atg Glu Val Gln Gly Pro Asp Trp His Leu Lys Met Pro Lys Met Lys Met 560 565 570			1909
ccc aag ttc agc atg cct ggc ttc aaa gca gag ggc cca gaa gtg gat Pro Lys Phe Ser Met Pro Gly Phe Lys Ala Glu Gly Pro Glu Val Asp 575 580 585 590			1957
gtg aac ctg ccc aag gct gat gtg gac atc tca gga ccc aag gtg ggt Val Asn Leu Pro Lys Ala Asp Val Asp Ile Ser Gly Pro Lys Val Gly 595 600 605			2005
gtt gaa gtt cca gat gtg aat att gaa gga cct gaa gga aag ctg aag Val Glu Val Pro Asp Val Asn Ile Glu Gly Pro Glu Gly Lys Leu Lys 610 615 620			2053
ggc ccc aag ttc aag atg cca gag atg aat atc aag gcc ccc aag atc Gly Pro Lys Phe Lys Met Pro Glu Met Asn Ile Lys Ala Pro Lys Ile 625 630 635			2101

tcc atg cct gat gtg gac ttg cat atg aaa ggt cct aaa gta aag gga Ser Met Pro Asp Val Asp Leu His Met Lys Gly Pro Lys Val Lys Gly 640 645 650	2149
gaa tat gat atg aca gtg cca aag ctg gaa ggg gac ctg aaa ggc cca Glu Tyr Asp Met Thr Val Pro Lys Leu Glu Gly Asp Leu Lys Gly Pro 655 660 665 670	2197
aaa gta gat gtc agt gcc cca gat gtt gaa atg cag ggt cct gac tgg Lys Val Asp Val Ser Ala Pro Asp Val Glu Met Gln Gly Pro Asp Trp 675 680 685	2245
aac ttg aag atg cca aag att aaa atg ccc aaa ttt agc atg ccc agc Asn Leu Lys Met Pro Lys Ile Lys Met Pro Lys Phe Ser Met Pro Ser 690 695 700	2293
ctc aaa gga gag ggg cca gaa ttt gat gtg aac ctg tcc aaa gcg aat Leu Lys Gly Glu Gly Pro Glu Phe Asp Val Asn Leu Ser Lys Ala Asn 705 710 715	2341
gtg gac att tct gca cca aaa gta gat act aat gct cca gat ctg agc Val Asp Ile Ser Ala Pro Lys Val Asp Thr Asn Ala Pro Asp Leu Ser 720 725 730	2389
ctt gaa gga cct gaa ggg aag ttg aaa ggc ccg aag ttt aag atg cct Leu Glu Gly Pro Glu Gly Lys Leu Lys Gly Pro Lys Phe Lys Met Pro 735 740 745 750	2437
gag atg cac ttc aga gct cct aag atg cct ttg cca gat gtt gac ctg Glu Met His Phe Arg Ala Pro Lys Met Pro Leu Pro Asp Val Asp Leu 755 760 765	2485
gat ctt aaa gga ccc aaa atg aaa gga aat gta gat atc tct gca cca Asp Leu Lys Gly Pro Lys Met Lys Gly Asn Val Asp Ile Ser Ala Pro 770 775 780	2533
aag ata gag ggt gaa atg cag gtt cca gat gtg gac atc aga ggt ccc Lys Ile Glu Gly Glu Met Gln Val Pro Asp Val Asp Ile Arg Gly Pro 785 790 795	2581
aag gta gat att aaa gca cca gat gtg gaa ggc caa ggc ctg gac tgg Lys Val Asp Ile Lys Ala Pro Asp Val Glu Gly Gln Gly Leu Asp Trp 800 805 810	2629
agc ctg aaa ata ccc aag atg aaa atg ccc aag ttc agc atg ccc agc Ser Leu Lys Ile Pro Lys Met Lys Met Pro Lys Phe Ser Met Pro Ser 815 820 825 830	2677
ctc aaa ggc gag ggc cca gaa gtg gat gtg aac ttg cct aag gct gac Leu Lys Gly Glu Gly Pro Glu Val Asp Val Asn Leu Pro Lys Ala Asp 835 840 845	2725
gtt gat gtc tca gga ccc aag gtg gac atc gaa gcc cca gat gtg agc Val Asp Val Ser Gly Pro Lys Val Asp Ile Glu Ala Pro Asp Val Ser 850 855 860	2773

ctc gaa ggt cca gaa ggg aag ctg aag ggt ccc aag ttt aag atg cct Leu Glu Gly Pro Glu Gly Lys Leu Lys Gly Pro Lys Phe Lys Met Pro 865 870 875	2821
gag atg cat ttc aag acc ccc aag atc tcc atg cct gat gtg gac tta Glu Met His Phe Lys Thr Pro Lys Ile Ser Met Pro Asp Val Asp Leu 880 885 890	2869
cac ttg aaa ggc ccc aaa gtc aaa ggg gat gtg gat gtg tct gtg ccc His Leu Lys Gly Pro Lys Val Lys Gly Asp Val Asp Val Ser Val Pro 895 900 905 910	2917
aag gta gaa ggt gaa atg aaa gtg cca gat gtt gaa atc aaa gga ccc Lys Val Glu Gly Glu Met Lys Val Pro Asp Val Glu Ile Lys Gly Pro 915 920 925	2965
aaa atg gac att gat gcc cca gat gtg gag gtt caa ggc cca gac tgg Lys Met Asp Ile Asp Ala Pro Asp Val Glu Val Gln Gly Pro Asp Trp 930 935 940	3013
cac ctg aag atg ccc aag atg aaa atg ccc aag ttt agc atg cct ggc His Leu Lys Met Pro Lys Met Lys Met Pro Lys Phe Ser Met Pro Gly 945 950 955	3061
ttc aaa gga gag ggc cga gaa gtg gat gtg aac ctg ccc aag gct gac Phe Lys Gly Glu Gly Arg Glu Val Asp Val Asn Leu Pro Lys Ala Asp 960 965 970	3109
att gat gtc tca gga ccc aag gtg gat gtt gaa gtc cca gat gtg agc Ile Asp Val Ser Gly Pro Lys Val Asp Val Glu Val Pro Asp Val Ser 975 980 985 990	3157
ctt gag ggc ccg gaa gga aag ctg aag ggt ccc aag ttt aag atg cct Leu Glu Gly Pro Glu Gly Lys Leu Lys Gly Pro Lys Phe Lys Met Pro 995 1000 1005	3205
gag atg cac ttc aag gcc ccc aag atc tcc atg cct gat gtg gac ctg Glu Met His Phe Lys Ala Pro Lys Ile Ser Met Pro Asp Val Asp Leu 1010 1015 1020	3253
aat ctt aag ggg cca aaa ttg aag gga gat gtg gat gtg tcc ttg cct Asn Leu Lys Gly Pro Lys Leu Lys Gly Asp Val Asp Val Ser Leu Pro 1025 1030 1035	3301
gag gta gaa ggt gaa atg aaa gtg cca gat gtt gac att aaa ggg ccc Glu Val Glu Gly Glu Met Lys Val Pro Asp Val Asp Ile Lys Gly Pro 1040 1045 1050	3349
aaa gtt gac att agt gct cca gat gtg gat gtt cat ggc cca gat tgg Lys Val Asp Ile Ser Ala Pro Asp Val Asp Val His Gly Pro Asp Trp 1055 1060 1065 1070	3397
cac ctg aag atg ccc aag gtg aaa atg ccc aag ttc agc atg ccc ggc His Leu Lys Met Pro Lys Val Lys Met Pro Lys Phe Ser Met Pro Gly 1075 1080 1085	3445
ttc aaa gga gag ggc cct gaa gtg gat gtg aag ctg ccc aaa gct gac	3493

	1315	1320	1325	
aag ttg aag ggc ccc aag ttt aag atg cct gag atg cat ttc aag gcc				4213
Lys Leu Lys Gly Pro Lys Phe Lys Met Pro Glu Met His Phe Lys Ala				
	1330	1335	1340	
ccc aag atc tcc atg ccc gat gtg gac tta cac ttg aaa ggc ccc aaa				4261
Pro Lys Ile Ser Met Pro Asp Val Asp Leu His Leu Lys Gly Pro Lys				
	1345	1350	1355	
gtc aaa ggg gat atg gat gtg tct gtg ccc aag gta gaa ggt gaa atg				4309
Val Lys Gly Asp Met Asp Val Ser Val Pro Lys Val Glu Gly Glu Met				
	1360	1365	1370	
aaa gtg cca gat gtt gac att aaa ggg ccc aaa gtg gac att gat gcc				4357
Lys Val Pro Asp Val Asp Ile Lys Gly Pro Lys Val Asp Ile Asp Ala				
1375	1380	1385	1390	
cca gat gtg gag gtt cac gac cca gat tgg cac ctg aaa atg ccc aag				4405
Pro Asp Val Glu Val His Asp Pro Asp Trp His Leu Lys Met Pro Lys				
	1395	1400	1405	
atg aaa atg ccc aag ttc agt atg cct ggc ttc aaa gca gag ggc cct				4453
Met Lys Met Pro Lys Phe Ser Met Pro Gly Phe Lys Ala Glu Gly Pro				
	1410	1415	1420	
gaa gtg gat gtg aat ctc cga aag gct gac att gat gtg tct gga ccc				4501
Glu Val Asp Val Asn Leu Arg Lys Ala Asp Ile Asp Val Ser Gly Pro				
	1425	1430	1435	
agt gtg gac act gat gct cct gat ttg gat att gag gga cca gaa gga				4549
Ser Val Asp Thr Asp Ala Pro Asp Leu Asp Ile Glu Gly Pro Glu Gly				
	1440	1445	1450	
aag ttg aaa ggc tcc aaa ttt aag atg ccc aag ttg aat ata aaa gct				4597
Lys Leu Lys Gly Ser Lys Phe Lys Met Pro Lys Leu Asn Ile Lys Ala				
1455	1460	1465	1470	
ccc aag gtc tcc atg cca gat gtg gac ttg aat ttg aag gga ccc aaa				4645
Pro Lys Val Ser Met Pro Asp Val Asp Leu Asn Leu Lys Gly Pro Lys				
	1475	1480	1485	
ctg aag gga gag ata gat gct tct gtg cca gaa ctg gaa ggt gat ctc				4693
Leu Lys Gly Glu Ile Asp Ala Ser Val Pro Glu Leu Glu Gly Asp Leu				
	1490	1495	1500	
aga ggg ccg caa gtt gat gtc aaa ggt cct ctt gtg gaa gcg gag gtg				4741
Arg Gly Pro Gln Val Asp Val Lys Gly Pro Leu Val Glu Ala Glu Val				
	1505	1510	1515	
ccc gat gtt gat ctg gag tgt cct gat gca aag ctg aag ggc ccc aag				4789
Pro Asp Val Asp Leu Glu Cys Pro Asp Ala Lys Leu Lys Gly Pro Lys				
	1520	1525	1530	
ctt aag atg cct gag atg cac ttc aag gcc ccc aag atc tcc atg cct				4837
Leu Lys Met Pro Glu Met His Phe Lys Ala Pro Lys Ile Ser Met Pro				
1535	1540	1545	1550	

gat gtg gac tta cac ttg aaa ggc ccc aaa gtc aaa ggg gat gtg gat	4885
Asp Val Asp Leu His Leu Lys Gly Pro Lys Val Lys Gly Asp Val Asp	
1555 1560 1565	
gtg tct ttg cca aaa ttg gag gga gat tta aca ggc ccc agt gtg gat	4933
Val Ser Leu Pro Lys Leu Glu Gly Asp Leu Thr Gly Pro Ser Val Asp	
1570 1575 1580	
gtg gag gtg cct gat gtt gag ctg gag tgt cct gat gca aag ttg aaa	4981
Val Glu Val Pro Asp Val Glu Leu Glu Cys Pro Asp Ala Lys Leu Lys	
1585 1590 1595	
ggg ccc aag ttt aag atg cct gag atg cac ttc aag acc ccc aag atc	5029
Gly Pro Lys Phe Lys Met Pro Glu Met His Phe Lys Thr Pro Lys Ile	
1600 1605 1610	
tcc atg cct gat gtg aac tta aac ttg aaa ggc ccc aaa gtc aaa ggg	5077
Ser Met Pro Asp Val Asn Leu Asn Leu Lys Gly Pro Lys Val Lys Gly	
1615 1620 1625 1630	
gat atg gat gtg tct gtt ccc aaa att gga ggg aga ttt aac agg ccc	5125
Asp Met Asp Val Ser Val Pro Lys Ile Gly Gly Arg Phe Asn Arg Pro	
1635 1640 1645	
cag tgt gga tgt gga ggt gcc tga tggtgagctg gctgtcgttg ttctgagggc	5179
Gln Cys Gly Cys Gly Gly Ala *	
1650	
ggcatcactc tgggggtcagt ctctcccctg tcctttgagg acatacagac ctcacctatt	5239
gtttaagtgt ttgaaccagc cccgaacca agcaacacca gagtcctcct tacatttctt	5299
cagtgtgcaa accttacgca ccgtgaactt gggagtcaaa ccagctgtgc ccctcactag	5359
ccgggtaagc gcagggaggt atcgtgccac actgagcatc agttcccca tccgaatcag	5419
gatagaacaa ttccactgtt gcttggttta cccaactgct gctgttccta atctgac	5476

<210> 80
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (95)..(1411)

<400> 80	
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tgtgccagcc gggctctggc aggctcctgg cagc	
atg gca gtg aag ctt ggg	112
Met Ala Val Lys Leu Gly	
1 5	

acc ctc ctg ctg gcc ctt gcc ctg ggc ctg gcc cag cca gcc tct gcc	160
Thr Leu Leu Leu Ala Leu Ala Leu Gly Leu Ala Gln Pro Ala Ser Ala	
10 15 20	
cgc cgg aag ctg ctg gtg ttt ctg ctg gat ggt ttt cgc tca gac tac	208
Arg Arg Lys Leu Leu Val Phe Leu Leu Asp Gly Phe Arg Ser Asp Tyr	
25 30 35	
atc agt gat gag gcg ctg gag tca ttg cct ggt ttc aaa gag att gtg	256
Ile Ser Asp Glu Ala Leu Glu Ser Leu Pro Gly Phe Lys Glu Ile Val	
40 45 50	
agc agg gga gta aaa gtg gat tac ttg act cca gac ttc cct agt ctc	304
Ser Arg Gly Val Lys Val Asp Tyr Leu Thr Pro Asp Phe Pro Ser Leu	
55 60 65 70	
tcg tat ccc aat tat tat acc cta atg act ggc cgc cat tgt gaa gtc	352
Ser Tyr Pro Asn Tyr Tyr Thr Leu Met Thr Gly Arg His Cys Glu Val	
75 80 85	
cat cag atg atc ggg aac tac atg tgg gac ccc acc acc aac aag tcc	400
His Gln Met Ile Gly Asn Tyr Met Trp Asp Pro Thr Thr Asn Lys Ser	
90 95 100	
ttt gac att ggc gtc aac aaa gac agc cta atg cct ctc tgg tgg aat	448
Phe Asp Ile Gly Val Asn Lys Asp Ser Leu Met Pro Leu Trp Trp Asn	
105 110 115	
gga tca gaa cct ctg tgg gtc act ctg acc aag gcc aaa agg aag gtc	496
Gly Ser Glu Pro Leu Trp Val Thr Leu Thr Lys Ala Lys Arg Lys Val	
120 125 130	
tac atg tac tac tgg cca ggc tgt gag gtt gag att ctg ggt gtc aga	544
Tyr Met Tyr Tyr Trp Pro Gly Cys Glu Val Glu Ile Leu Gly Val Arg	
135 140 145 150	
ccc acc tac tgc cta gaa tat aaa aat gtc cca acg gat atc aat ttt	592
Pro Thr Tyr Cys Leu Glu Tyr Lys Asn Val Pro Thr Asp Ile Asn Phe	
155 160 165	
gcc aat gca gtc agc gat gct ctt gac tcc ttc aag agt ggc cgg gcc	640
Ala Asn Ala Val Ser Asp Ala Leu Asp Ser Phe Lys Ser Gly Arg Ala	
170 175 180	
gac ctg gca gcc ata tac cat gag cgc att gac gtg gaa ggc cac cac	688
Asp Leu Ala Ala Ile Tyr His Glu Arg Ile Asp Val Glu Gly His His	
185 190 195	
tac ggg cct gca tct ccg cag agg aaa gat gcc ctc aag gct gta gac	736
Tyr Gly Pro Ala Ser Pro Gln Arg Lys Asp Ala Leu Lys Ala Val Asp	
200 205 210	
act gtc ctg aag tac atg acc aag tgg atc cag gag cgg ggc ctg cag	784
Thr Val Leu Lys Tyr Met Thr Lys Trp Ile Gln Glu Arg Gly Leu Gln	
215 220 225 230	

gac cgc ctg aac gtc att att ttc tcg gat cac gga atg acc gac att	832
Asp Arg Leu Asn Val Ile Ile Phe Ser Asp His Gly Met Thr Asp Ile	
235 240 245	
ttc tgg atg gac aaa gtg att gag ctg aat aag tac atc agc ctg aat	880
Phe Trp Met Asp Lys Val Ile Glu Leu Asn Lys Tyr Ile Ser Leu Asn	
250 255 260	
gac ctg cag caa gtg aag gac cgc ggg cct gtt gtg agc ctt tgg ccg	928
Asp Leu Gln Gln Val Lys Asp Arg Gly Pro Val Val Ser Leu Trp Pro	
265 270 275	
gcc cct ggg aaa cac tct gag ata tat aac aaa ctg agc aca gtg gaa	976
Ala Pro Gly Lys His Ser Glu Ile Tyr Asn Lys Leu Ser Thr Val Glu	
280 285 290	
cac atg act gtc tac gag aaa gaa gcc atc cca agc agg ttc tat tac	1024
His Met Thr Val Tyr Glu Lys Glu Ala Ile Pro Ser Arg Phe Tyr Tyr	
295 300 305 310	
aag aaa gga aag ttt gtc tct cct ttg act tta gtg gct gat gaa ggc	1072
Lys Lys Gly Lys Phe Val Ser Pro Leu Thr Leu Val Ala Asp Glu Gly	
315 320 325	
tgg ttc ata act gag aat cga gag atg ctt ccg ttt tgg atg aac agc	1120
Trp Phe Ile Thr Glu Asn Arg Glu Met Leu Pro Phe Trp Met Asn Ser	
330 335 340	
acc ggc agg cgg gaa ggt tgg cag cgt gga tgg cac ggc tac gac aac	1168
Thr Gly Arg Arg Glu Gly Trp Gln Arg Gly Trp His Gly Tyr Asp Asn	
345 350 355	
gag ctg atg gac atg cgg ggc atc ttc ctg gcc ttc gga cct ggt agg	1216
Glu Leu Met Asp Met Arg Gly Ile Phe Leu Ala Phe Gly Pro Gly Arg	
360 365 370	
cga gga aat gac cag atg ctg tca gac ccc att ccc aag gaa gtg tct	1264
Arg Gly Asn Asp Gln Met Leu Ser Asp Pro Ile Pro Lys Glu Val Ser	
375 380 385 390	
gta agg ggg gct acg ggt gcc agg aga ggc tgc agg gat ttc ctt aca	1312
Val Arg Gly Ala Thr Gly Ala Arg Arg Gly Cys Arg Asp Phe Leu Thr	
395 400 405	
gac cct ctt tat gag cca agc aga gca aac cca gcc ggt ctg cat gaa	1360
Asp Pro Leu Tyr Glu Pro Ser Arg Ala Asn Pro Ala Gly Leu His Glu	
410 415 420	
aca tct ttt gct ggc ttc ctt tca aat gct tct tgg gtt tgg caa atg	1408
Thr Ser Phe Ala Gly Phe Leu Ser Asn Ala Ser Trp Val Trp Gln Met	
425 430 435	
tag ccaa atactttgcc ttgtaaaattt taaatcctga gtgcagtgaa gaaaatgtaa	1465
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aaaaaaaaaa aa	1477

<210> 81
 <211> 1395
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (256)..(1002)

<400> 81
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 ttggcacctc tgggccc aaa gggaaagaca ccagtggaaa gaggtgagca tctcctggac 120
 caccctcaag cttcaggtga gctgagcttc taacactacc atcaaagcaa ctggaacccc 180
 ttgaatttga tttctggaga cgcgagcata atccttttgc aaacatctca acgctggctc 240
 tccaggtgga gcacc atg gaa ggc gac tgt ctg agc tgc atg aag tat ctg 291
 Met Glu Gly Asp Cys Leu Ser Cys Met Lys Tyr Leu
 1 5 10
 atg ttt gta ttc aat ttc ttc ata ttt ctg ggc ggg gcc tgc ctg ctg 339
 Met Phe Val Phe Asn Phe Phe Ile Phe Leu Gly Gly Ala Cys Leu Leu
 15 20 25
 gcc atc ggc atc tgg gtc atg gtg gac ccc acc ggc ttc cgg gag atc 387
 Ala Ile Gly Ile Trp Val Met Val Asp Pro Thr Gly Phe Arg Glu Ile
 30 35 40
 gtg gct gcc aat cct ctg ctc ctc acg ggc gcc tac atc ctc ctg gcc 435
 Val Ala Ala Asn Pro Leu Leu Leu Thr Gly Ala Tyr Ile Leu Leu Ala
 45 50 55 60
 atg ggg ggc ctg ctc ttt ctg ctc ggc ttc ctg ggc tgc tgc ggg gcc 483
 Met Gly Gly Leu Leu Phe Leu Leu Gly Phe Leu Gly Cys Cys Gly Ala
 65 70 75
 gtc cgt gag aac aag tgt ctg ctg cta ttt ttc ttc ctg ttc atc ctg 531
 Val Arg Glu Asn Lys Cys Leu Leu Leu Phe Phe Phe Leu Phe Ile Leu
 80 85 90
 atc atc ttc ctg gca gag ctc tca gca gcc atc ctg gcc ttc atc ttc 579
 Ile Ile Phe Leu Ala Glu Leu Ser Ala Ala Ile Leu Ala Phe Ile Phe
 95 100 105
 agg gaa aat ctc acc cga gaa ttc ttc acc aag gag ctc acc aag cac 627
 Arg Glu Asn Leu Thr Arg Glu Phe Phe Thr Lys Glu Leu Thr Lys His
 110 115 120
 tac cag ggc aat aac gac aca gac gtc ttc tct gcc acc tgg aac tcg 675
 Tyr Gln Gly Asn Asn Asp Thr Asp Val Phe Ser Ala Thr Trp Asn Ser
 125 130 135 140

gtc atg atc aca ttt ggt tgc tgc ggg gtc aac ggg cct gaa gac ttt	723
Val Met Ile Thr Phe Gly Cys Cys Gly Val Asn Gly Pro Glu Asp Phe	
145 150 155	
aag ttt gca tct gtg ttt cga ctc ctg acc ctg gat agt gaa gag gtg	771
Lys Phe Ala Ser Val Phe Arg Leu Leu Thr Leu Asp Ser Glu Glu Val	
160 165 170	
ccg gag gcc tgc tgc cgg agg gaa ccc caa agt cgg gac ggg gtc ctg	819
Pro Glu Ala Cys Cys Arg Arg Glu Pro Gln Ser Arg Asp Gly Val Leu	
175 180 185	
ctg agc cgg gag gag tgc ctc ctg gga agg agc cta ttc cta aac aag	867
Leu Ser Arg Glu Glu Cys Leu Leu Gly Arg Ser Leu Phe Leu Asn Lys	
190 195 200	
cag ggc tgt tac acg gtg atc ctc aac acc ttc gag acc tac gtc tac	915
Gln Gly Cys Tyr Thr Val Ile Leu Asn Thr Phe Glu Thr Tyr Val Tyr	
205 210 215 220	
ttg gcc gga gcc ctt gcc atc ggg gta ctg gcc atc gag ctt ttc gcc	963
Leu Ala Gly Ala Leu Ala Ile Gly Val Leu Ala Ile Glu Leu Phe Ala	
225 230 235	
atg atc ttt gcc atg tgc ctc ttc cgg ggc atc cag tag agggatatggc	1012
Met Ile Phe Ala Met Cys Leu Phe Arg Gly Ile Gln *	
240 245	
ctgaagcctg aagactcgcc ccaccaccca ctgcccagca cccaatgtcc tcccgtgccc	1072
ctccccgctg tcctcttggc ccagggggag aagatgaggc catcagagat ggccaggaga	1132
agggccaggg gaatagagct attttttttaa caaaacaaaa tgaagacaaa aatatggact	1192
gatgtatcct cgcttgact cagggcaggt gccgtgggtt ctccagagac cccagcacct	1252
ggcccaggat agcaaggctg ctctagagac aaaggaacac aaggccaggc cactatgggc	1312
agcaagaccc gggccttatt ctcatggcgt gactgtgcc aagtggtt cggcaggggc	1372
agcattcgag agatcaggcc ggg	1395

<210> 82
 <211> 1840
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (264) .. (1508)

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gaactgtatc tcttccggct gaggacagag aagtatcttg gagacacggt tcagaggaag 1604
 tggaattact tttgccaga aaaatggcga atacatgaaa caaccagtga tcatgcttta 1664
 gaagcctaca gcaacattct gagactgctc caacatgctt gaagatctaa gcttttctct 1724
 tttaaaactg gcacatactc agagcagtct tcttagccta tggtcgtacg tgtcaagaca 1784
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<210> 83
 <211> 800
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (509) .. (685)

<400> 83
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 ttcattgttg agttgttgag actatgaaag actcattgtc tttgtattca gctcttaaat 120
 agtgtaacta tatccccacc tctgcttgct ttctttccct cccctccaat gataaagaaa 180
 atgataaatt ttctgttggt cattcaattc ttattttaaa taagactaag tataggcatt 240
 gtacctgaca ttgctacgtt tctaccagtg tttcaattta aagtgctagt gtttaaaaac 300
 attttcaagg gataaggcct tctgtacttt gcttatttga agaatacagt gtaggagcag 360
 tgaagtaaatt tctatggagt acatttctaa aataccacat ttctgaaatc ataaataagt 420
 ttattcaggt tctaaccctt tgctgtacac aagcagacag aaatgcatct gttacataaa 480
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 Met Leu Phe Lys Ser Phe Lys Asn
 1 5
 act cac cat ata aac ttg cat ttg agc ttg tgt gtt ctt ttg tta atg 580
 Thr His His Ile Asn Leu His Leu Ser Leu Cys Val Leu Leu Leu Met
 10 15 20
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 Cys Arg Val Leu Leu Ser Arg Asn Cys Gln Cys Val Leu Gly Leu Thr
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 caa gaa cag ttt ctt ctg gat tcc tta ttt gat tta ttt aac cta att 676
 Gln Glu Gln Phe Leu Leu Asp Ser Leu Phe Asp Leu Phe Asn Leu Ile
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 ata ttc taa tattgca aatattacca taagtgggta aaagtaaaat tcctcttctg 732

Ile Phe *

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ataaggaaat tttctccttg aaatcacgat accaaatagg aaaa atg atc tac aag 596
Met Ile Tyr Lys
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tgc ccc atg tgt agg gaa ttt ttc tct gag aga gca gat ctt ttt atg 644
Cys Pro Met Cys Arg Glu Phe Phe Ser Glu Arg Ala Asp Leu Phe Met
5 10 15 20

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His Gln Lys Ile His Thr Ala Glu Lys Pro His Lys Cys Asp Lys Cys
25 30 35

gat aag ggt ttc ttt cat ata tca gaa ctt cat att cat tgg aga gac 740
Asp Lys Gly Phe Phe His Ile Ser Glu Leu His Ile His Trp Arg Asp
40 45 50

cat aca gga gag aag gtc tat aaa tgt gat gat tgt ggt aag gat ttt 788
His Thr Gly Glu Lys Val Tyr Lys Cys Asp Asp Cys Gly Lys Asp Phe
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Ser Thr Thr Thr Lys Leu Asn Arg His Lys Lys Ile His Thr Val Glu	
70 75 80	
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Lys Pro Tyr Lys Cys Tyr Glu Cys Gly Lys Ala Phe Asn Trp Ser Ser	
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His Leu Gln Ile His Met Arg Val His Thr Gly Glu Lys Pro Tyr Val	
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Cys Ser Glu Cys Gly Arg Gly Phe Ser Asn Ser Ser Asn Leu Cys Met	
120 125 130	
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His Gln Arg Val His Thr Gly Glu Lys Pro Phe Lys Cys Glu Glu Cys	
135 140 145	
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Gly Lys Ala Phe Arg His Thr Ser Ser Leu Cys Met His Gln Arg Val	
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His Thr Gly Glu Lys Pro Tyr Lys Cys Tyr Glu Cys Gly Lys Ala Phe	
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Ser Gln Ser Ser Ser Leu Cys Ile His Gln Arg Val His Thr Gly Glu	
185 190 195	
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Lys Pro Tyr Arg Cys Cys Gly Cys Gly Lys Ala Phe Ser Gln Ser Ser	
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Ser Leu Cys Ile His Gln Arg Val His Thr Gly Glu Lys Pro Phe Lys	
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Cys Asp Glu Cys Gly Lys Ala Phe Ser Gln Ser Thr Ser Leu Cys Ile	
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His Gln Arg Val His Thr Lys Glu Arg Asn His Leu Lys Ile Ser Val	
245 250 255 260	
ata taa aacgttttgc taagagttta aaatcttaaa acccataagt gccactagga	1420
Ile *	
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            Met Gln Glu Asp Arg Asp Gly Ser Cys Ser Thr Val Gly Gly
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gta ggt tat ggg gac agt aag gat tgt atc ctg gag ccg ctt tcc ctg      155
Val Gly Tyr Gly Asp Ser Lys Asp Cys Ile Leu Glu Pro Leu Ser Leu
  15              20              25              30

cca gaa agt cca ggt ggc acc acc act tta gaa ggt tct cca tct gtg      203
Pro Glu Ser Pro Gly Gly Thr Thr Thr Leu Glu Gly Ser Pro Ser Val
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cct tgt att ttc tgt gaa gaa cat ttt cct gtg gct gaa caa gac aaa      251
Pro Cys Ile Phe Cys Glu Glu His Phe Pro Val Ala Glu Gln Asp Lys
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ctt ctg aag cac atg att att gag cat aag att gtc ata gct gat gtc      299
Leu Leu Lys His Met Ile Ile Glu His Lys Ile Val Ile Ala Asp Val
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aag ttg gtt gct gat ttc caa agg tac att tta tat tgg agg aaa agg      347
Lys Leu Val Ala Asp Phe Gln Arg Tyr Ile Leu Tyr Trp Arg Lys Arg
              80              85              90

ttc act gaa cag ccc atc aca gat ttt tgt agt gta ata aga att aat      395
Phe Thr Glu Gln Pro Ile Thr Asp Phe Cys Ser Val Ile Arg Ile Asn
  95              100              105              110

tcc act gct cca ttt gaa gaa caa gag aat tat ttt ttg tta tgt gac      443
Ser Thr Ala Pro Phe Glu Glu Gln Glu Asn Tyr Phe Leu Leu Cys Asp
              115              120              125

gtt tta cca gaa gat aga att ctt aga gaa gag ctt cag aaa cag aga      491
Val Leu Pro Glu Asp Arg Ile Leu Arg Glu Glu Leu Gln Lys Gln Arg
              130              135              140

ctg aga gaa att ctg gaa caa cag cag caa gaa cga aat gat acc aat      539
Leu Arg Glu Ile Leu Glu Gln Gln Gln Gln Glu Arg Asn Asp Thr Asn
              145              150              155

ttt cat ggc gtt tgt atg ttt tgc aat gaa gaa ttc ctt gga aac aga      587
Phe His Gly Val Cys Met Phe Cys Asn Glu Glu Phe Leu Gly Asn Arg
              160              165              170

tct gtt att ttg aac cac atg gcc aga gaa cat gct ttc aac att gga      635
Ser Val Ile Leu Asn His Met Ala Arg Glu His Ala Phe Asn Ile Gly
  175              180              185              190

ttg cca gac aac att gta aac tgc aat gaa ttt ttg tgt aca tta cag      683
Leu Pro Asp Asn Ile Val Asn Cys Asn Glu Phe Leu Cys Thr Leu Gln
              195              200              205

aaa aag ctt gac aat ttg cag tgc ttg tac tgt gag aag acc ttc agg      731

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Asp	Lys	Asn	Thr	Leu	Lys	Asp	His	Met	Arg	Lys	Lys	Gln	His	Arg	Lys	
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Ile	Asn	Pro	Lys	Asn	Arg	Glu	Tyr	Asp	Arg	Phe	Tyr	Val	Ile	Asn	Tyr	
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Leu	Glu	Leu	Gly	Lys	Ser	Trp	Glu	Glu	Val	Gln	Leu	Glu	Asp	Asp	Arg	
255					260					265					270	
gag	ttg	ctg	gac	cat	cag	gaa	gat	gac	tgg	tct	gat	tgg	gaa	gaa	cac	923
Glu	Leu	Leu	Asp	His	Gln	Glu	Asp	Asp	Trp	Ser	Asp	Trp	Glu	Glu	His	
			275					280						285		
cct	gcc	tct	gca	gtc	tgc	tta	ttt	tgt	gaa	aag	caa	gca	gaa	aca	att	971
Pro	Ala	Ser	Ala	Val	Cys	Leu	Phe	Cys	Glu	Lys	Gln	Ala	Glu	Thr	Ile	
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Glu	Lys	Leu	Tyr	Val	His	Met	Glu	Asp	Ala	His	Glu	Phe	Asp	Leu	Leu	
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Lys	Ile	Lys	Ser	Glu	Leu	Gly	Leu	Asn	Phe	Tyr	Gln	Gln	Val	Lys	Leu	
	320					325					330					
gtc	aat	ttt	att	cgg	agg	caa	gtt	cac	caa	tgc	aga	tgt	tat	ggc	tgc	1115
Val	Asn	Phe	Ile	Arg	Arg	Gln	Val	His	Gln	Cys	Arg	Cys	Tyr	Gly	Cys	
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cat	gtg	aag	ttc	aaa	tcc	aaa	gca	gac	tta	aga	act	cac	atg	gaa	gaa	1163
His	Val	Lys	Phe	Lys	Ser	Lys	Ala	Asp	Leu	Arg	Thr	His	Met	Glu	Glu	
			355					360						365		
act	aaa	cac	act	tcg	ctg	ctc	ccc	gat	aga	aag	acg	tgg	gat	caa	ctg	1211
Thr	Lys	His	Thr	Ser	Leu	Leu	Pro	Asp	Arg	Lys	Thr	Trp	Asp	Gln	Leu	
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Glu	Tyr	Tyr	Phe	Pro	Thr	Tyr	Glu	Asn	Asp	Thr	Leu	Leu	Cys	Thr	Leu	
	385						390					395				
tct	gac	agt	gaa	agt	gac	ctg	aca	gct	cag	gaa	caa	aat	gaa	aat	gtt	1307
Ser	Asp	Ser	Glu	Ser	Asp	Leu	Thr	Ala	Gln	Glu	Gln	Asn	Glu	Asn	Val	
	400					405					410					
ccc	atc	atc	agt	gaa	gat	aca	tct	aaa	ctg	tat	gct	ttg	aaa	caa	agc	1355
Pro	Ile	Ile	Ser	Glu	Asp	Thr	Ser	Lys	Leu	Tyr	Ala	Leu	Lys	Gln	Ser	
415					420				425						430	
agt	att	ttg	aac	cag	ttg	cta	cta	taa	gagta	cttgaaaacc	tagaagaaac					1407
Ser	Ile	Leu	Asn	Gln	Leu	Leu	Leu	*								

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Met Glu Ala Leu Asn Thr Ala Gln Gly Ala Arg Asp Phe Ile Tyr Ser
1 5 10 15
ctg cac tcc acg gag agg agc tgc ctg ctc aaa gag ctg cac cgc ttc 154
Leu His Ser Thr Glu Arg Ser Cys Leu Leu Lys Glu Leu His Arg Phe
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gag tct att gcc att gcc caa gaa aaa ttg gaa gct cca cca ccc acc 202
Glu Ser Ile Ala Ile Ala Gln Glu Lys Leu Glu Ala Pro Pro Pro Thr
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cca gga cag ctg aga tat gta ttc atc cac aat gcg ata cct ttc ata 250
Pro Gly Gln Leu Arg Tyr Val Phe Ile His Asn Ala Ile Pro Phe Ile
50 55 60
ggg ttt ggc ttt ttg gat aat gca att atg att gtt gct gga acc cat 298
Gly Phe Gly Phe Leu Asp Asn Ala Ile Met Ile Val Ala Gly Thr His
65 70 75 80
att gaa atg tct att gga att att ttg gga att tca act atg gca gct 346
Ile Glu Met Ser Ile Gly Ile Ile Leu Gly Ile Ser Thr Met Ala Ala
85 90 95
gct gct ttg gga aat ctt gtg tca gat cta gct gga ctt gga ctt gca 394
Ala Ala Leu Gly Asn Leu Val Ser Asp Leu Ala Gly Leu Gly Leu Ala
100 105 110
ggc tac gtt gaa gca ttg gct tcc agg tta ggc ctg tca att cct gat 442
Gly Tyr Val Glu Ala Leu Ala Ser Arg Leu Gly Leu Ser Ile Pro Asp
115 120 125

ctc aca cca aag caa gtt gac atg tgg caa aca cgt ctt agt aca cat 490
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 130 135 140

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 Leu Gly Lys Ala Val Gly Val Thr Ile Gly Cys Ile Leu Gly Met Phe
 145 150 155 160

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 Pro Leu Ile Phe Phe Gly Gly Gly Glu Glu Asp Glu Lys Leu Glu Thr
 165 170 175

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 Lys Ser *

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aataatttag catgtattat ggaaaacact aacttattgt ggcttgatct tcttaggaca 762

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catttttcgt tgttcctga tagttacatt tcaaccttgg gatttttcca aattacttaa 1002

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 Met Arg Phe Arg Val Ser Ser
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Gly Ser Glu Val Pro Asp Ser Ala His Leu Ala Pro Thr Pro Leu Phe	
25 30 35	
tcg gaa tcc ggg tgc tgc gga ttg agg tcc cgg ttc cta acg gac tgc	436
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40 45 50 55	
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Lys Met Glu Glu Gly Gly Asn Leu Gly Gly Leu Ile Lys Met Val His	
60 65 70	
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Leu Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp Val Thr Phe	
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Val Ser Gly Phe Leu Leu Phe Arg Ser Leu Pro Arg His Thr Phe Gly	
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Leu Val Gln Ser Lys Leu Phe Pro Phe Tyr Phe His Ile Ser Met Gly	
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tgt gcc ttc atc aac ctc tgc atc ttg gct tca cag cat gct tgg gct	676
Cys Ala Phe Ile Asn Leu Cys Ile Leu Ala Ser Gln His Ala Trp Ala	
120 125 130 135	
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Gln Leu Thr Phe Trp Glu Ala Ser Gln Leu Tyr Leu Leu Phe Leu Ser	
140 145 150	
ctt acg ctg gcc act gtc aac gcc cgc tgg ctg gaa ccc cgc acc aca	772
Leu Thr Leu Ala Thr Val Asn Ala Arg Trp Leu Glu Pro Arg Thr Thr	
155 160 165	
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Ala Ala Met Trp Ala Leu Gln Thr Val Glu Lys Glu Arg Gly Leu Gly	
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Gly Glu Val Pro Gly Ser His Gln Gly Pro Asp Pro Tyr Arg Gln Leu	
185 190 195	
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Arg Glu Lys Asp Pro Lys Tyr Ser Ala Leu Arg Thr Glu Phe Leu Pro	
200 205 210 215	
cta cat ggg ctg tcc tct ctt tgc aat ctg ggc tgc gtc ctg agc aat	964
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220 225 230	

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 15 20 25

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 Ser Asp Trp Met Leu Met Leu Tyr Phe Ala His Thr His Leu Thr Val
 30 35 40

aca gtc acc att ggg ttg ctt ttg att cca aag ttt tca cat tca agc 195
 Thr Val Thr Ile Gly Leu Leu Leu Ile Pro Lys Phe Ser His Ser Ser
 45 50 55

aat aac cca cga gat gat att gct aca gaa gca tat gag gat gag cta 243
 Asn Asn Pro Arg Asp Asp Ile Ala Thr Glu Ala Tyr Glu Asp Glu Leu
 60 65 70 75

gac atg ggc cga tct gga tcc tac ctg aac agc agt atc aat tca gcc 291
 Asp Met Gly Arg Ser Gly Ser Tyr Leu Asn Ser Ser Ile Asn Ser Ala
 80 85 90

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 Trp Ser Glu His Ser Leu Asp Pro Glu Asp Ile Arg Asp Glu Leu Lys
 95 100 105

aaa ctc tat gcc caa ctg gaa ata tat aaa aga aag aag atg atc aca 387
 Lys Leu Tyr Ala Gln Leu Glu Ile Tyr Lys Arg Lys Lys Met Ile Thr
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cag ata atc aat gga agt gtg gat gtt gat act gaa gac cgc cag aaa      557
Gln Ile Ile Asn Gly Ser Val Asp Val Asp Thr Glu Asp Arg Gln Lys
                               125                               130                               135

agg aaa cct gag tca gat gga aga act gct aaa gct ttg agg tca tta      605
Arg Lys Pro Glu Ser Asp Gly Arg Thr Ala Lys Ala Leu Arg Ser Leu
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caa ttt acg aat cca gga agg caa act gaa ttt gct cca gaa act ggt      653

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Gln Phe Thr Asn Pro Gly Arg Gln Thr Glu Phe Ala Pro Glu Thr Gly	
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Lys Arg Glu Lys Arg Arg Leu Thr Lys Asn Ala Thr Ala Gly Ser Asp	
170 175 180	
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Arg Gln Val Ile Pro Ala Lys Ser Lys Val Tyr Asp Ser Gln Gly Leu	
185 190 195 200	
ctg att ttt agt ggg atg gac ctc tgt gac tgc ctg gat gaa gac tgc	797
Leu Ile Phe Ser Gly Met Asp Leu Cys Asp Cys Leu Asp Glu Asp Cys	
205 210 215	
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Leu Gly Cys Phe Tyr Ala Cys Pro Ala Cys Gly Ser Thr Lys Cys Gly	
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gct gaa tgc cgc tgt gac cgc aag tgg ctg tat gag caa att gaa att	893
Ala Glu Cys Arg Cys Asp Arg Lys Trp Leu Tyr Glu Gln Ile Glu Ile	
235 240 245	
gaa gga gga gaa ata att cat aat aaa cat gct gga taa tctgcggtac	942
Glu Gly Gly Glu Ile Ile His Asn Lys His Ala Gly *	
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 Met Lys Asn Ser Ser Ser Val Ser Asn Thr Leu
 1 5 10
 aca aat gga tgt gtc atc aat gga cat ttg gac ttc ccc tcc acg acc 1058
 Thr Asn Gly Cys Val Ile Asn Gly His Leu Asp Phe Pro Ser Thr Thr
 15 20 25
 ccg ctc agt ggg atg gaa agc agg aat ggc cag tgc ttg aca gga act 1106
 Pro Leu Ser Gly Met Glu Ser Arg Asn Gly Gln Cys Leu Thr Gly Thr
 30 35 40

aac gga att agc agt gga tta gcc cca gga cag ccg ttt ccg agt agc Asn Gly Ile Ser Ser Gly Leu Ala Pro Gly Gln Pro Phe Pro Ser Ser 45 50 55	1154
cag ggt tct ctc tgc att agt ggg act gag gag cca gag aag acc ctg Gln Gly Ser Leu Cys Ile Ser Gly Thr Glu Glu Pro Glu Lys Thr Leu 60 65 70 75	1202
aga gct aac cct gag ttg tgc ggt tct ctg cac ctg aac ggg agt cca Arg Ala Asn Pro Glu Leu Cys Gly Ser Leu His Leu Asn Gly Ser Pro 80 85 90	1250
agt agc tgc ata gcc agt agg cct tcc tgg gtg gaa gac att ggg gat Ser Ser Cys Ile Ala Ser Arg Pro Ser Trp Val Glu Asp Ile Gly Asp 95 100 105	1298
aac ctg tac tat gga cac tac cac ggg ttt ggg gac act gct gaa agc Asn Leu Tyr Tyr Gly His Tyr His Gly Phe Gly Asp Thr Ala Glu Ser 110 115 120	1346
atc cca gaa ctg aac agt gtg gtc gag cat tcc aag tcc gtg aag gtg Ile Pro Glu Leu Asn Ser Val Val Glu His Ser Lys Ser Val Lys Val 125 130 135	1394
cag gag cgg tac gac agt gcc gtg ctg ggc acc atg cac ctg cac cac Gln Glu Arg Tyr Asp Ser Ala Val Leu Gly Thr Met His Leu His His 140 145 150 155	1442
ggc tcc tag agacgct gacctggctc tcggaaacgc aggagtcctt cctggtagcc Gly Ser *	1498
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ggaaggcaac gtggattctg tttttagac attaatgagc tttaa atg gga att 294
Met Gly Ile
1
ggg gat gat gta tgt cta caa aaa aaa aaa agt tgg agc ggc cgc caa 342
Gly Asp Asp Val Cys Leu Gln Lys Lys Lys Ser Trp Ser Gly Arg Gln
5 10 15
ctt agg ggc cac gtg agc cac ggc cac ggc cgc ata ggc aag cac cgg 390
Leu Arg Gly His Val Ser His Gly His Gly Arg Ile Gly Lys His Arg
20 25 30 35
aag cac ccc ggc ggc cgc ggt aat gct ggt ggt ctg cat cac cac cgg 438
Lys His Pro Gly Gly Arg Gly Asn Ala Gly Gly Leu His His His Arg
40 45 50
atc aac ttc gac aaa tac cac cca ggc tac ttt ggg aaa gtt ggt atg 486
Ile Asn Phe Asp Lys Tyr His Pro Gly Tyr Phe Gly Lys Val Gly Met
55 60 65
aag cat tac cac tta aag agg aac cag agc ttc tgc cca act gtc aac 534
Lys His Tyr His Leu Lys Arg Asn Gln Ser Phe Cys Pro Thr Val Asn
70 75 80
ctt gac aaa ttg tgg act ttg gtc agt gaa cag aca cgg gtg aat gct 582

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Ala Lys Asn Lys Thr Gly Ala Ala Pro Ile Ile Asp Val Val Arg Ser																	
100						105				110					115		
ggc tac tat aaa gtt ctg gga aag gga aag ctc cca aag cag cct gtc 678																	
Gly Tyr Tyr Lys Val Leu Gly Lys Gly Lys Leu Pro Lys Gln Pro Val																	
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Ile Val Lys Ala Lys Phe Phe Ser Arg Arg Ala Glu Glu Lys Ile Lys																	
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Thr Lys Asp Lys Glu Ser Leu Asn Phe Pro Phe Phe Trp Ala Pro Ile
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gga agc agc att tac aac gtg tct ggc ttg gtg gga gga aga ttg tca      865
Gly Ser Ser Ile Tyr Asn Val Ser Gly Leu Val Gly Gly Arg Leu Ser
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att gag gta tca tgt gtg ttc acc tgc ctc tct tgc cct att tct ttg      913
Ile Glu Val Ser Cys Val Phe Thr Cys Leu Ser Cys Pro Ile Ser Leu
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gtt gct ata aat ttc ctg ctt ctc aaa tat ctg gat ttt tgg cta cct      961
Val Ala Ile Asn Phe Leu Leu Leu Lys Tyr Leu Asp Phe Trp Leu Pro
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att tgg ctt ccg tct ttg gtg ttt ata tct gtc tgg ttt tag caggtct      1010
Ile Trp Leu Pro Ser Leu Val Phe Ile Ser Val Trp Phe *
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ctctgattcc tgaccacag ctctctcct tctctaatat tcaagtatgc tgcttcccta      1070

actcctcatt ccttctcctt gaatttcact ttacaattgc gctaggttct aacatcgttg      1130

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atctataccc tccatattct cagcaaagtt ggcataaatc tgacctgaat aaacaggggt      1490

ataacattat caggcttgta aaatacttta tcaaataaat gcatcagtta aagcaggggt      1550

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acgttttcagt tccttttcatt cattcctggg tttttctttt attttctaag aaggttgaag    300
aaggatgagt gatagagaag aaagcaacac cattgatttt tttttttaag aa      atg    355
                                   Met
                                   1

ata tat ata tgt ata tgt ttg tgt gtg tgt gtg tgt gtg tgt gta ttc      403
Ile Tyr Ile Cys Ile Cys Leu Cys Val Cys Val Cys Val Cys Val Phe
              5              10              15

tgt gca tta ttt tgt cat gat ctc aat tct ctt ctt tcc acc aaa gtt      451
Cys Ala Leu Phe Cys His Asp Leu Asn Ser Leu Leu Ser Thr Lys Val
              20              25              30

tgt cgt aat att ttc tcc tga ag gtgcattctg gtccttttaa attagtcagt      504
Cys Arg Asn Ile Phe Ser      *
              35              40

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atg ctt att ggt aaa acc tgg	711
Met Leu Ile Gly Lys Thr Trp	
1 5	
acg gac ttt gag cac atg gag acg atc gag aaa ggc tac tgt aac ccc	759
Thr Asp Phe Glu His Met Glu Thr Ile Glu Lys Gly Tyr Cys Asn Pro	
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Gly Ile His Leu Cys Ser Val Gly Ser Tyr Thr Ile Asn Phe Arg Val	
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Val Thr Lys Pro Ala Asn Ser Val Phe Thr Thr Lys Trp Ile Trp Tyr	
60 65 70	
tgg aag aat gaa tct ggc aca tgg att cag tat gga gaa gag aaa gac	951
Trp Lys Asn Glu Ser Gly Thr Trp Ile Gln Tyr Gly Glu Glu Lys Asp	
75 80 85	

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Lys Arg Lys Asn Ser Asn Val Asp Ser Ser Tyr Leu Glu Ser Leu Tyr
          90                      95                      100

caa tcc tgt ccg agg gga gtt gtg cca ttt cag gcg ggc tca cgg aac      1047
Gln Ser Cys Pro Arg Gly Val Val Pro Phe Gln Ala Gly Ser Arg Asn
          105                      110                      115

tat gag ctg agt ttc caa ggg atg att cag aca aac ata gct tcc aaa      1095
Tyr Glu Leu Ser Phe Gln Gly Met Ile Gln Thr Asn Ile Ala Ser Lys
          120                      125                      130                      135

act caa aag gat gtc atc aga aga cca aca ttt gtg cct cag tgg tat      1143
Thr Gln Lys Asp Val Ile Arg Arg Pro Thr Phe Val Pro Gln Trp Tyr
          140                      145                      150

gtg cag cag atg aag aga ggg cca gag taa g tgttctgaag cagctgtttg      1194
Val Gln Gln Met Lys Arg Gly Pro Glu *
          155                      160

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aattcgcggc cgcgctgcacg aaatatctct ttcaataatg aaagaataag aaaaagaaat      360

agaagagctg gaaacaatag gtaaagttta ggctaggcct tagacttctc ctgcattgta      420

atccttctgg tttgccacat atgcatgctg tcaggaagtt gatgaggt atg tac agg      477
                               Met Tyr Arg

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 5 10 15

cat ctg ctg aat gta tcc tct cag gca ata ctg ccc att gga gca cga 573
 His Leu Leu Asn Val Ser Ser Gln Ala Ile Leu Pro Ile Gly Ala Arg
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agc cgc caa ttt gtc aac gtg agt tga aatct ctttcccat tcacccacc 625
 Ser Arg Gln Phe Val Asn Val Ser *
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aaacttcgcg cttcacctag aaatgctttt ttttttctta tctcagtcta atgtatttta 805

aactagtctt tagctcattt aaccagcccc caatgtcctc ttctgttggg tgagcacctc 865

gcagtttgaa gagcattttg tttagtgaag tcaacaaata caaagtcagt gaaagaaacc 925

ccatatcctc tctgcaagct cttagtatca catcagatat tcaagccatg cagctctttc 985

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gtcccgggcc cggagcgcta ggagcgcgcg gaaggagcc atg gct ctg gac ggg 174
 Met Ala Leu Asp Gly
 1 5

ata agg atg cca gat ggc tgc tac gcg gac ggg acg tgg gaa ctg agt 222
 Ile Arg Met Pro Asp Gly Cys Tyr Ala Asp Gly Thr Trp Glu Leu Ser
 10 15 20

gtc cat gtg acg gac ctg aac cgc gat gtc acc ctg aga gtg acc ggc Val His Val Thr Asp Leu Asn Arg Asp Val Thr Leu Arg Val Thr Gly 25 30 35	270
gag gtg cac att gga ggc gtg atg ctt aag ctg gtg gag aaa ctc gat Glu Val His Ile Gly Gly Val Met Leu Lys Leu Val Glu Lys Leu Asp 40 45 50	318
gta aaa aaa gat tgg tct gac cat gct ctc tgg tgg gaa aag aag aga Val Lys Lys Asp Trp Ser Asp His Ala Leu Trp Trp Glu Lys Lys Arg 55 60 65	366
act tgg ctt ctg aag aca cat tgg acc tta gat aag tat ggt att cag Thr Trp Leu Leu Lys Thr His Trp Thr Leu Asp Lys Tyr Gly Ile Gln 70 75 80 85	414
gca gat gct aag ctt cag ttc acc cct cag cac aaa ctg ctc cgc ctg Ala Asp Ala Lys Leu Gln Phe Thr Pro Gln His Lys Leu Leu Arg Leu 90 95 100	462
cag ctt ccc aac atg aag tat gtg aag gtg aaa gtg aat ttc tct gat Gln Leu Pro Asn Met Lys Tyr Val Lys Val Lys Val Asn Phe Ser Asp 105 110 115	510
aga gtc ttc aaa gct gtt tct gac atc tgt aag act ttt aat atc aga Arg Val Phe Lys Ala Val Ser Asp Ile Cys Lys Thr Phe Asn Ile Arg 120 125 130	558
cac ccc gaa gaa ctt tct ctc tta aag aaa ccc aga gat cca aca aaa His Pro Glu Glu Leu Ser Leu Leu Lys Lys Pro Arg Asp Pro Thr Lys 135 140 145	606
aaa aaa aaa aaa aag cta gat gac cag tct gaa gat gag gca ctt gaa Lys Lys Lys Lys Lys Leu Asp Asp Gln Ser Glu Asp Glu Ala Leu Glu 150 155 160 165	654
tta gag ggg cct ctt atc act cct gga tca gga agt ata tat tca agc Leu Glu Gly Pro Leu Ile Thr Pro Gly Ser Gly Ser Ile Tyr Ser Ser 170 175 180	702
cca gga ctg tat agt aaa aca atg acc ccc act tat gat gct cat gat Pro Gly Leu Tyr Ser Lys Thr Met Thr Pro Thr Tyr Asp Ala His Asp 185 190 195	750
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cca gaa atc ttg gca aaa atg ttc aag cct caa gct ctt ctt gat aaa Pro Glu Ile Leu Ala Lys Met Phe Lys Pro Gln Ala Leu Leu Asp Lys 230 235 240 245	894
gca aaa atc aac caa gga tgg ctt gat tcc tca aga tct ctc atg gaa	942

470	475	480	485	
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Asn Leu Glu Val Gln Asn Ile Leu Ser Phe Leu Lys Met Gln His Leu				
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Asn Pro Asp Pro Gln Leu Ile Pro Glu Gln Ile Thr Thr Asp Ile Thr				
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cct gaa tgt ttg gtg tct ccc cgc tat cta aaa aag tat aag aac aag				1758
Pro Glu Cys Leu Val Ser Pro Arg Tyr Leu Lys Lys Tyr Lys Asn Lys				
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cag ata aca gcg aga atc ttg gag gcc cat cag aat gta gct cag atg				1806
Gln Ile Thr Ala Arg Ile Leu Glu Ala His Gln Asn Val Ala Gln Met				
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agt cta att gaa gcc aag atg aga ttt att caa gct tgg cag tca cta				1854
Ser Leu Ile Glu Ala Lys Met Arg Phe Ile Gln Ala Trp Gln Ser Leu				
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cct gaa ttt ggc atc act cac ttc att gca agg ttc caa ggg ggc aaa				1902
Pro Glu Phe Gly Ile Thr His Phe Ile Ala Arg Phe Gln Gly Gly Lys				
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aaa gaa gaa ctt att gga att gca tac aac aga ctg att cgg atg gat				1950
Lys Glu Glu Leu Ile Gly Ile Ala Tyr Asn Arg Leu Ile Arg Met Asp				
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gcc agc act gga gat gca att aaa aca tgg cgt ttc agc aac atg aaa				1998
Ala Ser Thr Gly Asp Ala Ile Lys Thr Trp Arg Phe Ser Asn Met Lys				
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cag tgg aat gtc aac tgg gaa atc aaa atg gtc acc gta gag ttt gca				2046
Gln Trp Asn Val Asn Trp Glu Ile Lys Met Val Thr Val Glu Phe Ala				
	615	620	625	
gat gaa gta cga ttg tcc ttc att tgt act gaa gta gat tgc aaa gtg				2094
Asp Glu Val Arg Leu Ser Phe Ile Cys Thr Glu Val Asp Cys Lys Val				
	630	635	640	645
gtt cat gaa ttc att ggt ggc tac ata ttt ctc tca aca cgt gca aaa				2142
Val His Glu Phe Ile Gly Gly Tyr Ile Phe Leu Ser Thr Arg Ala Lys				
	650	655	660	
gac caa aac gag agt tta gat gaa gag atg ttc tac aaa ctt acc agt				2190
Asp Gln Asn Glu Ser Leu Asp Glu Glu Met Phe Tyr Lys Leu Thr Ser				
	665	670	675	
ggg tgg gtg tga ata gaaatactgt ttaatgaaac tccacggcca taacaatatt				2245
Gly Trp Val *				
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													1				
att	ggg	ggt	tct	aac	cat	tta	gct	gtt	gtt	ctt	gat	gac	att	att	tta	103	
Ile	Gly	Gly	Ser	Asn	His	Leu	Ala	Val	Val	Leu	Asp	Asp	Ile	Ile	Leu		
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Ala	Val	Ile	Asp	Ser	Ile	Phe	Val	Trp	Phe	Ile	Phe	Ile	Ser	Leu	Ala		
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Gln	Thr	Met	Lys	Thr	Leu	Arg	Leu	Arg	Lys	Asn	Thr	Val	Lys	Phe	Ser		
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tta	tat	aga	cat	ttt	aaa	aat	act	ctg	atc	ttt	gct	gtg	ctg	gct	tct		247
Leu	Tyr	Arg	His	Phe	Lys	Asn	Thr	Leu	Ile	Phe	Ala	Val	Leu	Ala	Ser		
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Ile	Val	Phe	Met	Gly	Trp	Thr	Thr	Lys	Thr	Phe	Arg	Ile	Ala	Lys	Cys		
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caa	tca	gat	tgg	atg	gaa	cgc	tgg	gtt	gac	gat	gca	ttt	tgg	agc	ttc		343
Gln	Ser	Asp	Trp	Met	Glu	Arg	Trp	Val	Asp	Asp	Ala	Phe	Trp	Ser	Phe		
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ctt	ttt	tcg	ctt	atc	ctt	att	gta	atc	atg	ttt	ttg	tgg	aga	cca	tca		391
Leu	Phe	Ser	Leu	Ile	Leu	Ile	Val	Ile	Met	Phe	Leu	Trp	Arg	Pro	Ser		
100				105					110					115			
gca	aac	aat	cag	aga	tat	gcc	ttc	atg	ccc	tta	ata	gat	gat	tct	gat		439
Ala	Asn	Asn	Gln	Arg	Tyr	Ala	Phe	Met	Pro	Leu	Ile	Asp	Asp	Ser	Asp		
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gat	gaa	att	gag	gaa	ttc	atg	gta	act	tct	gaa	aat	tta	acc	gaa	gga		487
Asp	Glu	Ile	Glu	Glu	Phe	Met	Val	Thr	Ser	Glu	Asn	Leu	Thr	Glu	Gly		
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ata	aaa	tta	aga	gcc	tca	aaa	tca	gtt	tcc	aat	gga	aca	gct	aag	cct		535
Ile	Lys	Leu	Arg	Ala	Ser	Lys	Ser	Val	Ser	Asn	Gly	Thr	Ala	Lys	Pro		
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Ala	Thr	Ser	Glu	Asn	Phe	Asp	Glu	Asp	Leu	Lys	Trp	Val	Glu	Glu	Asn		
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att	ccc	tct	tca	ttc	aca	gat	gta	gct	ctt	cca	gtg	tta	gtg	gat	tca		631
Ile	Pro	Ser	Ser	Phe	Thr	Asp	Val	Ala	Leu	Pro	Val	Leu	Val	Asp	Ser		
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gat	gag	gaa	atc	atg	acc	aga	tct	gaa	atg	gct	gaa	aaa	atg	ttc	tct		679
Asp	Glu	Glu	Ile	Met	Thr	Arg	Ser	Glu	Met	Ala	Glu	Lys	Met	Phe	Ser		
			200					205					210				
tca	gaa	aag	ata	atg	tga	ttggaa	cccgtataag	aaatgtagtt	aagcctgaag								733
Ser	Glu	Lys	Ile	Met	*												
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Met Glu Val Val Asp Glu
1 5
acg gag gcg ctg cag cgc ttc ttc gaa ggc cac gac atc aac ggt gcc 163
Thr Glu Ala Leu Gln Arg Phe Phe Glu Gly His Asp Ile Asn Gly Ala
10 15 20
ctg gag ccc tcc aac ata gac acc agc atc ctg gag gag tac atc agc 211
Leu Glu Pro Ser Asn Ile Asp Thr Ser Ile Leu Glu Glu Tyr Ile Ser
25 30 35
aag gag gat gcc tcc gac ctc tgc ttc cct gac atc tct gct cca gcc 259
Lys Glu Asp Ala Ser Asp Leu Cys Phe Pro Asp Ile Ser Ala Pro Ala
40 45 50
agc tcg gcc tcc tac tcc cac ggg cag cct gcg atg cct ggc tcc agc 307
Ser Ser Ala Ser Tyr Ser His Gly Gln Pro Ala Met Pro Gly Ser Ser
55 60 65 70

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ggg gtc cac cac ctg agc ccc cct ggg ggt gga ccc tcc ccg ggg cgc	355
Gly Val His His Leu Ser Pro Pro Gly Gly Gly Pro Ser Pro Gly Arg	
758085	
cat ggt ccc ctc cca ccc ccg ggc tac ggc acc ccg ctg aac tgc aac	403
His Gly Pro Leu Pro Pro Pro Gly Tyr Gly Thr Pro Leu Asn Cys Asn	
9095100	
aac aac aac ggc atg ggc gct gcc ccc aag ccc ttc ccg ggg ggc acc	451
Asn Asn Asn Gly Met Gly Ala Ala Pro Lys Pro Phe Pro Gly Gly Thr	
105110115	
ggg ccc ccc atc aag gct gag ccc aag gct ccc tat gcc cca ggc aca	499
Gly Pro Pro Ile Lys Ala Glu Pro Lys Ala Pro Tyr Ala Pro Gly Thr	
120125130	
ctg ccg gac tct ccc cca gac tcg ggc tcc gag gcc tac tcc ccc cag	547
Leu Pro Asp Ser Pro Pro Asp Ser Gly Ser Glu Ala Tyr Ser Pro Gln	
135140145150	
cag gtg aat gag ccc cac ctc ctg cgc acg ata acc cct gag aca ctg	595
Gln Val Asn Glu Pro His Leu Leu Arg Thr Ile Thr Pro Glu Thr Leu	
155160165	
tgc cac gtg gga gtg ccc tcc cgc ctg gag cat ccg ccc cca cct cca	643
Cys His Val Gly Val Pro Ser Arg Leu Glu His Pro Pro Pro Pro Pro	
170175180	
gcc cac ttg cca ggc ccc ccg cca ccc cca cca ccc cca cct cac tac	691
Ala His Leu Pro Gly Pro Pro Pro Pro Pro Pro Pro Pro Pro His Tyr	
185190195	
cct gtc ctg cag cgg gat ctg tac atg aag gcc gag ccc ccg atc ccc	739
Pro Val Leu Gln Arg Asp Leu Tyr Met Lys Ala Glu Pro Pro Ile Pro	
200205210	
cac tac gct gcc atg ggg cag ggg ctg gtg ccc act gat ctt cac cac	787
His Tyr Ala Ala Met Gly Gln Gly Leu Val Pro Thr Asp Leu His His	
215220225230	
acc cag cag tcc cag atg ctg cac cag ctc ctg cag cag cac gga gct	835
Thr Gln Gln Ser Gln Met Leu His Gln Leu Leu Gln Gln His Gly Ala	
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Glu Leu Pro Thr His Pro Ser Lys Lys Arg Lys His Ser Glu Ser Pro	
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Pro Ser Thr Leu Asn Ala Gln Met Leu Asn Gly Met Ile Lys Gln Glu	
265270275	
cct ggg acc gtg aca gcc ctg cct ctg cac ccc act cga gcc cca tcg	979
Pro Gly Thr Val Thr Ala Leu Pro Leu His Pro Thr Arg Ala Pro Ser	
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cct Pro	ctc Leu	agc Ser	att Ile	gcc Ala	cgt Arg	gtc Val	cag Gln	aca Thr	ccg Pro	cct Pro	tgg Trp	cac His	ccg Pro	cca Pro	ggc Gly	1075
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				490			495				500					
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				505			510				515					
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cgc att gat gag ctg gag cgc tgg agc cac aag ctg gcc aag ctg cgg Arg Ile Asp Glu Leu Glu Arg Trp Ser His Lys Leu Ala Lys Leu Arg 695 700 705 710			2227
cgg ctc gac agc ctc aag tcc acc ggc agc tcg ggc gcc ttc agc cat Arg Leu Asp Ser Leu Lys Ser Thr Gly Ser Ser Gly Ala Phe Ser His 715 720 725			2275
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Cys	Ile	Ser	Gln	Arg	Phe	Leu	Gln	Gly	Thr	Ile	Ile	Ala	Leu	Val	Val	
760			765			770										
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Val	Met	Ala	Phe	Ser	Val	Val	Ser	Met	Ser	Thr	Leu	Tyr	Val	Leu	Ser	
775			780			785			790							
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Ser	Phe	Gly	Thr	Thr	Gln	Leu	Arg	Gln	Ser	Pro	Leu	Thr	Thr	Gly	Leu	
810			815			820										
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Pro	Gly	Ile	Gln	Pro	Ser	Leu	Leu	Leu	Val	Thr	Thr	Ser	Leu	Thr	Ser	
825			830			835										
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Ser	Ala	Pro	Gly	Ser	Ala	Val	Arg	Thr	Leu	Asp	Met	Cys	Ser	Ser	His	
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Pro	Cys	Pro	Val	Ile	Cys	Cys	Ser	Ser	Pro	Thr	Thr	Asn	Pro	Thr	Thr	
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Ser	Leu	Gly	Phe	His	Gly	Arg	Ala	Arg	Arg	Gly	Ala	Leu	Gln	Ser	Ser	
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970			975			980										

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agg tca aag gag gaa cca tgt gag gag ggg agc ctt cca cag agt ctc Arg Ser Lys Glu Glu Pro Cys Glu Glu Gly Ser Leu Pro Gln Ser Leu 1050 1055 1060	3283
cac acc cac cag gac acc cag ggc acc tct cac cgg tgg cca ata acc His Thr His Gln Asp Thr Gln Gly Thr Ser His Arg Trp Pro Ile Thr 1065 1070 1075	3331
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5847

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cgcgtaacacc tgttggttga aagctctcag cgggaca atg ctg acc cag ctg aaa	115
Met Leu Thr Gln Leu Lys	
1 5	
gca aaa tca gag ggg aag ctt gca aaa cag att tgc aaa gtt gtg ttg	163
Ala Lys Ser Glu Gly Lys Leu Ala Lys Gln Ile Cys Lys Val Val Leu	
10 15 20	
gat cat ttt gaa aaa cag tat tcc aaa gaa ctc gga gat gcc tgg aat	211
Asp His Phe Glu Lys Gln Tyr Ser Lys Glu Leu Gly Asp Ala Trp Asn	
25 30 35	
aca gta agg gag ata cta aca tct cca tca tgc tgg caa tat gct gtc	259
Thr Val Arg Glu Ile Leu Thr Ser Pro Ser Cys Trp Gln Tyr Ala Val	
40 45 50	
ctg ctt aac cga ttc aat tat cct ttt gaa ctg gaa aag gat tta cat	307
Leu Leu Asn Arg Phe Asn Tyr Pro Phe Glu Leu Glu Lys Asp Leu His	
55 60 65 70	
ttg aag ggc tat cac aca ctc tct cag gga tct tta ccc aac tat cct	355
Leu Lys Gly Tyr His Thr Leu Ser Gln Gly Ser Leu Pro Asn Tyr Pro	
75 80 85	
aaa tca gtg aag tgt tac ctt agc aga act ccg ggc cga atc cct tca	403
Lys Ser Val Lys Cys Tyr Leu Ser Arg Thr Pro Gly Arg Ile Pro Ser	
90 95 100	
gaa aga cac caa att gga aac ctg aaa aaa tat tat ctc cta aat gct	451
Glu Arg His Gln Ile Gly Asn Leu Lys Lys Tyr Tyr Leu Leu Asn Ala	
105 110 115	
gct tct ctt ctc cca gtg ttg gct ctg gaa tta agg gat ggg gag aag	499
Ala Ser Leu Leu Pro Val Leu Ala Leu Glu Leu Arg Asp Gly Glu Lys	
120 125 130	
gtt ctg gat ctc tgt gct gct cct gga ggg aaa tta ata gct ctg ctg	547
Val Leu Asp Leu Cys Ala Ala Pro Gly Gly Lys Leu Ile Ala Leu Leu	
135 140 145 150	

cag tgt gct tgt cca ggt tat ctt cat tgt aat gaa tat gat agt ctg Gln Cys Ala Cys Pro Gly Tyr Leu His Cys Asn Glu Tyr Asp Ser Leu 155 160 165	595
aga ttg agg tgg cta agg cag acg ttg gaa tct ttc atc cca cag cct Arg Leu Arg Trp Leu Arg Gln Thr Leu Glu Ser Phe Ile Pro Gln Pro 170 175 180	643
ttg ata aat gta att aaa gtg tct gaa ttg gat ggc aga aaa atg gga Leu Ile Asn Val Ile Lys Val Ser Glu Leu Asp Gly Arg Lys Met Gly 185 190 195	691
gat gcc cag cct gaa atg ttt gac aag gtg tta gtg gat gct ccg tgt Asp Ala Gln Pro Glu Met Phe Asp Lys Val Leu Val Asp Ala Pro Cys 200 205 210	739
tca aat gat cga agc tgg ttg ttt tct tct gac tct cag aag gca tcc Ser Asn Asp Arg Ser Trp Leu Phe Ser Ser Asp Ser Gln Lys Ala Ser 215 220 225 230	787
tgt agg ata agt caa agg agg aat ttg cct ctt cta cag ata gag ctg Cys Arg Ile Ser Gln Arg Arg Asn Leu Pro Leu Leu Gln Ile Glu Leu 235 240 245	835
tta agg tct gca att aag gcc tta cgt cct gga ggg ata ctt gta tac Leu Arg Ser Ala Ile Lys Ala Leu Arg Pro Gly Gly Ile Leu Val Tyr 250 255 260	883
tct aca tgc acg ctt tcc aag gca gaa aat caa gat gtg atc agt gaa Ser Thr Cys Thr Leu Ser Lys Ala Glu Asn Gln Asp Val Ile Ser Glu 265 270 275	931
att tta aac tcc cac ggt aac atc atg cct atg gac att aaa gga ata Ile Leu Asn Ser His Gly Asn Ile Met Pro Met Asp Ile Lys Gly Ile 280 285 290	979
gca agg act tgc tcc cac gac ttc aca ttt gct ccc act ggc cag gaa Ala Arg Thr Cys Ser His Asp Phe Thr Phe Ala Pro Thr Gly Gln Glu 295 300 305 310	1027
tgt ggg ctc tta gtg att cca gat aag ggc aaa gcc tgg ggc cca atg Cys Gly Leu Leu Val Ile Pro Asp Lys Gly Lys Ala Trp Gly Pro Met 315 320 325	1075
tat gta gcc aaa ttg aag aaa tca tgg agc aca gga aaa tgg tga cat Tyr Val Ala Lys Leu Lys Lys Ser Trp Ser Thr Gly Lys Trp * 330 335 340	1123
gaatttgtaa actgtgttta tgtgttatta tatatatatt tctgaactca gtacatgtta	1183
atattttaaataa aattatgcag taactttctc tgggtctgtt tggaatccta tttagttaat	1243
acttttagcat cttagaatct aggcttgagc gctacccaaa acttaatgaa tgatggctgc	1303
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ccctcatgac cgcgtgccag aagtcatcat cttcacattt gtagacgttg ttctagcgga	1423

agacaggctt tgcagatttc ggtgctttta gtgaactggg gttttccgta aactttttct 1483

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Met Val Val Ser Leu Arg Ala Leu Leu		
1	5	
ctg gct ctc agg cag aag ccc cac agc acc ggg acc att cat gag gtc		158
Leu Ala Leu Arg Gln Lys Pro His Ser Thr Gly Thr Ile His Glu Val		
10	15	20 25
act gcc cag ctc atg atg tcc gtg agg ctg tcc ttt tgg cca gta gcc		206
Thr Ala Gln Leu Met Met Ser Val Arg Leu Ser Phe Trp Pro Val Ala		
30	35	40
gtg tgc agc tgt gtg gca cag atg gct tcg ttc atc ctg atc aag gcc		254
Val Cys Ser Cys Val Ala Gln Met Ala Ser Phe Ile Leu Ile Lys Ala		
45	50	55
cca cct cag cca cag cag tcc ccc caa cct gtg ttg tcc acc cta tta		302
Pro Pro Gln Pro Gln Gln Ser Pro Gln Pro Val Leu Ser Thr Leu Leu		
60	65	70
ttc atg tac ctg cca ggc cct gct aga tag c accccgtggc attacataac		353
Phe Met Tyr Leu Pro Gly Pro Ala Arg *		
75	80	
acttcatgag tggctgtgtc ttgtaatttt ggggacagggt ttctctcttt ccctctcttt		413
tttttgtaa aagcccagag actgacaacc agctgcagtg tctaagtgtt cctcactgac		473
agggtggggc ctcaccaccc ctggaggggag cagcgttggc agggagacag cctggcccag		533
tgaccttggg cccaagccag cccctccagg gcttttcaggg aagcgccatc cattttcaaa		593
gatgtcaaac gtcacttctt cctgtagggc ccgagtcctg cctcctatca ggGCCagatc		653
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                                     Met
                                     1
cag ctc ttc aat gga gga tgc cca ccc cct cct cct gtc ctg aat ggt      163
Gln Leu Phe Asn Gly Gly Cys Pro Pro Pro Pro Pro Val Leu Asn Gly
                    5                      10                      15
gag gac gtg ctt cct gac ctg aac ctc ctc cca ccc ctt caa ccg ccc      211
Glu Asp Val Leu Pro Asp Leu Asn Leu Leu Pro Pro Leu Gln Pro Pro
                20                      25                      30
ctt cca ggg ctt ctg cct tct gaa aag gag gct cct gct cca atg ggg      259
Leu Pro Gly Leu Leu Pro Ser Glu Lys Glu Ala Pro Ala Pro Met Gly
                35                      40                      45
gcc tca ctc att gca aac tta aag cag ctg cac ctg tcc ccg ccc ccg      307
Ala Ser Leu Ile Ala Asn Leu Lys Gln Leu His Leu Ser Pro Pro Pro
                50                      55                      60                      65
ccc cca cca cag gcc cca gcg gag gga cct tca gtc cag ccc ggt ccc      355
Pro Pro Pro Gln Ala Pro Ala Glu Gly Pro Ser Val Gln Pro Gly Pro
                    70                      75                      80
ctc agg ccc atg gag gaa gag ctg cca cct ccc ccg gca gaa cct gtt      403
Leu Arg Pro Met Glu Glu Glu Leu Pro Pro Pro Pro Ala Glu Pro Val
                    85                      90                      95
gag aaa ggg gca tcc aca gac atc tgt gcc ttc tgc cac aag acc gtg      451
Glu Lys Gly Ala Ser Thr Asp Ile Cys Ala Phe Cys His Lys Thr Val
                100                      105                      110
ttc ccc cga gag ctg gct gtg gag gcc atg aag agg cag tac cat gcc      499
Phe Pro Arg Glu Leu Ala Val Glu Ala Met Lys Arg Gln Tyr His Ala
                115                      120                      125
cag tgc ttc acg tgc cgc acc tgc cgc cgc cag ctg gct ggg cag agc      547
Gln Cys Phe Thr Cys Arg Thr Cys Arg Arg Gln Leu Ala Gly Gln Ser
                130                      135                      140                      145
ttc tac cag aag gat ggg cga ccc ctc tgc gaa ccc tgc tac cag gac      595

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Phe Tyr Gln Lys Asp Gly Arg Pro Leu Cys Glu Pro Cys Tyr Gln Asp	
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Thr Leu Glu Arg Cys Gly Lys Cys Gly Glu Val Val Arg Asp His Ile	
165 170 175	
atc agg gcc ctg ggc cag gcc ttc cac ccc tcc tgc ttc acg tgt gtg	691
Ile Arg Ala Leu Gly Gln Ala Phe His Pro Ser Cys Phe Thr Cys Val	
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acc tgc gcc cgg tgc att ggg gat gag agc ttt gcc ctg ggc agc cag	739
Thr Cys Ala Arg Cys Ile Gly Asp Glu Ser Phe Ala Leu Gly Ser Gln	
195 200 205	
aac gag gtg tac tgc ctg gac gac ttc tac agg aaa ttc gcc ccc gtc	787
Asn Glu Val Tyr Cys Leu Asp Asp Phe Tyr Arg Lys Phe Ala Pro Val	
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Cys Ser Ile Cys Glu Asn Pro Ile Ile Pro Arg Asp Gly Lys Asp Ala	
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ttc aaa atc gaa tgc atg gga aga aac ttc cat gaa aat tgc tac agg	883
Phe Lys Ile Glu Cys Met Gly Arg Asn Phe His Glu Asn Cys Tyr Arg	
245 250 255	
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Cys Glu Asp Cys Arg Ile Leu Leu Ser Val Glu Pro Thr Asp Gln Gly	
260 265 270	
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Cys Tyr Pro Leu Asn Asn His Leu Phe Cys Lys Pro Cys His Val Lys	
275 280 285	
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Arg Ser Ala Ala Gly Cys Cys *	
290 295	
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 Met Tyr Ile Ser Pro Glu Glu Phe Lys Pro Ile Ala
 1 5 10
 gag aag cta aca ggg tca act ccc gcg gcc agc tac gag gag gag gag 336
 Glu Lys Leu Thr Gly Ser Thr Pro Ala Ala Ser Tyr Glu Glu Glu Glu
 15 20 25
 ttg ccc cct gac cct agc gag gag acg ctc acc ata gaa gcc cga ttc 384
 Leu Pro Pro Asp Pro Ser Glu Glu Thr Leu Thr Ile Glu Ala Arg Phe
 30 35 40
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 Gln Pro Leu Leu Pro Glu Thr Met Thr Lys Ser Lys Asp Gly Phe Leu
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 Ala Ser Pro Ser Ala Val Phe Ala Thr Arg His Phe Gln Pro Phe Leu
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 Pro Pro Pro Gly Gln Glu Leu Gly Glu Pro Trp Trp Ile Ile Pro Ser
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 110 115 120
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 Pro Pro Pro Lys Gly Lys Glu Val Ile Ile His Arg Leu Leu Ser Met
 125 130 135 140
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 Phe His Pro Arg Pro Phe Val Lys Thr Arg Phe Ala Pro Gln Gly Ala
 145 150 155
 gtg gcc tgc ctg act gcc atc agc gac ttc tac tac act gtg atg ttc 768
 Val Ala Cys Leu Thr Ala Ile Ser Asp Phe Tyr Tyr Thr Val Met Phe
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 Arg Ile His Ala Glu Phe Gln Leu Ser Glu Pro Pro Asp Phe Pro Phe
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 tgg ttc tcc cct gct cag ttc acc ggc cac atc atc ctc tcc aaa gac 864
 Trp Phe Ser Pro Ala Gln Phe Thr Gly His Ile Ile Leu Ser Lys Asp

190	195	200	
gcc acc cac gtc cgc gac ttc cgg ctc ttc gtg ccc aac cac agg tct			912
Ala Thr His Val Arg Asp Phe Arg Leu Phe Val Pro Asn His Arg Ser			
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ctg aat gtg gac atg gag tgg ctt tac ggg gcc agt gaa agc agc aac			960
Leu Asn Val Asp Met Glu Trp Leu Tyr Gly Ala Ser Glu Ser Ser Asn			
	225	230	235
atg gag gtg gac atc ggc tac ata ccc cag atg gag ctg gag gcc acg			1008
Met Glu Val Asp Ile Gly Tyr Ile Pro Gln Met Glu Leu Glu Ala Thr			
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ggc ccc tct gtg ccc tcc gtg atc ctg gat gag gat ggc agc atg atc			1056
Gly Pro Ser Val Pro Ser Val Ile Leu Asp Glu Asp Gly Ser Met Ile			
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Asp Ser His Leu Pro Ser Gly Glu Pro Leu Gln Phe Val Phe Glu Glu			
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Ile Lys Trp Gln Gln Glu Leu Ser Trp Glu Glu Ala Ala Arg Arg Leu			
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Glu Val Ala Met Tyr Pro Phe Lys Lys Val Ser Tyr Leu Pro Phe Thr			
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Glu Ala Phe Asp Arg Ala Lys Ala Glu Asn Lys Leu Val His Ser Ile			
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Leu Leu Trp Gly Ala Leu Asp Asp Gln Ser Cys *			
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<212> DNA
<213> Homo sapiens
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Gln Cys Leu Ala Ser Gln Ala Ala Ala Ser Arg Asp Cys Phe Arg Arg
5 10 15

gaa ccc acg ctt ctg acc tgt gct ctg tct ttg cag ttc tgc acg gag 154
Glu Pro Thr Leu Leu Thr Cys Ala Leu Ser Leu Gln Phe Cys Thr Glu
20 25 30

cta aac cag ccg acc ctg cc² aac atc cgc aag tgg aag ggg ccc cgg 202
Leu Asn Gln Pro Thr Leu Pro Asn Ile Arg Lys Trp Lys Gly Pro Arg
35 40 45

gga tgc tgg aag gct gtt gtt gct gag aag ccc tcg aat cag ctc cag 250
Gly Cys Trp Lys Ala Val Val Ala Glu Lys Pro Ser Asn Gln Leu Gln
50 55 60 65

aag gta ccc tcg tct gca aag cct ggc ctt tcc ctt cat tta att tat 298
Lys Val Pro Ser Ser Ala Lys Pro Gly Leu Ser Leu His Leu Ile Tyr

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aca tac ttt tcc cct aat caa ggg cat tta aaa att tcc ttt gcc aat				346
Thr Tyr Phe Ser Pro Asn Gln Gly His Leu Lys Ile Ser Phe Ala Asn				
	85	90	95	
atc ccc ggt tca att ttg tat ttc tgc cca att ttt aaa tcc ttg cca				394
Ile Pro Gly Ser Ile Leu Tyr Phe Cys Pro Ile Phe Lys Ser Leu Pro				
	100	105	110	
ttc att tcc aaa tgc cct ggt ttt cgg ttc acg ttt aga ttg gta atg				442
Phe Ile Ser Lys Cys Pro Gly Phe Arg Phe Thr Phe Arg Leu Val Met				
	115	120	125	
gac tcc tgc caa gaa gga aat gag agc ctt agg gtg ttg gga gag agg				490
Asp Ser Cys Gln Glu Gly Asn Glu Ser Leu Arg Val Leu Gly Glu Arg				
	130	135	140	145
agg gga gaa agg caa caa atg ggt att tct gtc ctt tgt cct tct aat				538
Arg Gly Glu Arg Gln Gln Met Gly Ile Ser Val Leu Cys Pro Ser Asn				
	150	155	160	
ccc ttc gcc aca gtt ctg tct tct gcc aag ttt gtg cag agc tca tta				586
Pro Phe Ala Thr Val Leu Ser Ser Ala Lys Phe Val Gln Ser Ser Leu				
	165	170	175	
ctc gtt gac tga aaa tttcagattc accttagttc acacatgaag tatttgcttc				641
Leu Val Asp *				
	180			
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gatttttggtt ttgaattttc tttcatcagt atcacccata tgagcaggta agggtaaactc				761
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1509

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<211> 1889
<212> DNA
<213> Homo sapiens

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<222> (781)..(942)

<400> 106

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Met Ser Asp Cys Val Leu Gly Cys Thr Pro Gln His Cys Arg Leu Gln
1 5 10 15
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Ser Pro Val Phe Ala Arg Asp Thr Val Leu Glu Val Glu Val Leu Leu
20 25 30
tac tca tca ctg cga ttt gca cat tgc tcc gtg gac act cgg agg cct 924
Tyr Ser Ser Leu Arg Phe Ala His Cys Ser Val Asp Thr Arg Arg Pro
35 40 45
gcg ttc tgt tcc cta taa atggaa gcgtgctctg agcctgtctg cctccctcgg 978
Ala Phe Cys Ser Leu *
50

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ctgctgctgg tcctcagtac cagcgcccg ggggtgtccac aaccacttgg gacagaagaa 1038
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<222> (246) .. (632)

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gctca      atg aca gtc gag ctt tgg cta agg ctc cgg gga aag ggt cta 287
            Met Thr Val Glu Leu Trp Leu Arg Leu Arg Gly Lys Gly Leu
            1             5             10

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Ala Met Leu His Val Thr Arg Gly Val Trp Gly Ser Arg Val Arg Val	
15 20 25 30	
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Trp Pro Leu Leu Pro Ala Leu Leu Gly Pro Pro Arg Ala Leu Ser Ser	
35 40 45	
ctg gca gcc aaa atg ggg gag tat cgc aag atg tgg aac ccc agg gag	431
Leu Ala Ala Lys Met Gly Glu Tyr Arg Lys Met Trp Asn Pro Arg Glu	
50 55 60	
ccc cgc gac tgg gcc cag cag tac cgc gag cgc ttc att ccc ttc tcc	479
Pro Arg Asp Trp Ala Gln Gln Tyr Arg Glu Arg Phe Ile Pro Phe Ser	
65 70 75	
aag gag cag ctg ctc cgc ctc cta ata cag gta aca gga att cca ctc	527
Lys Glu Gln Leu Leu Arg Leu Leu Ile Gln Val Thr Gly Ile Pro Leu	
80 85 90	
gag tcc ggc aga gaa ggc ggc ttt gga ggc gtt ctc agc cca cgt gga	575
Glu Ser Gly Arg Glu Gly Gly Phe Gly Gly Val Leu Ser Pro Arg Gly	
95 100 105 110	
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Leu Leu His Pro Val Pro Leu Pro Pro Asn Pro Gly Pro Ala Ala Gly	
115 120 125	
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aagtgcttg atg aac ttt aag cta ggg aat ttc agc tat caa aaa aac 708
Met Asn Phe Lys Leu Gly Asn Phe Ser Tyr Gln Lys Asn
1 5 10
cca ctg aaa ttg gga gag ctt caa gga aac cac ttc act gtt gtt ctc 756
Pro Leu Lys Leu Gly Glu Leu Gln Gly Asn His Phe Thr Val Val Leu
15 20 25
aga aat ata aca gga act gat gac caa gta cag caa gct atg aac tct 804
Arg Asn Ile Thr Gly Thr Asp Asp Gln Val Gln Gln Ala Met Asn Ser
30 35 40 45
ctc aag gag att gga ttt att aac tac tat gga atg caa aga ttt gga 852
Leu Lys Glu Ile Gly Phe Ile Asn Tyr Tyr Gly Met Gln Arg Phe Gly
50 55 60

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Leu Glu Gly Lys Thr Pro Pro Val Phe Ala Ser Glu Gly Lys Tyr Arg	
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Ala Leu Lys Met Asp Phe Ser Leu Pro Pro Ser Thr Tyr Ala Thr Met	
305 310 315	
gcc att cga gaa gtg cta aaa atg gat acc agt atc aag aac cag acg	1668
Ala Ile Arg Glu Val Leu Lys Met Asp Thr Ser Ile Lys Asn Gln Thr	
320 325 330	
cag ctg aat aca acc tgg ctt cgc tga gcagt accttgtcca cagattagaa	1720
Gln Leu Asn Thr Thr Trp Leu Arg *	
335 340	
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gag cta gat gaa gaa gga gca ggc ggg ttc acg gct aaa gca atc gtt 579
 Glu Leu Asp Glu Glu Gly Ala Gly Gly Phe Thr Ala Lys Ala Ile Val
 170 175 180 185

cag aga gac aga gtg gat gaa gag gcc ttg aat ttc ccc tac gag gta 627
 Gln Arg Asp Arg Val Asp Glu Glu Ala Leu Asn Phe Pro Tyr Glu Val
 190 195 200

tgt tgg cag ccc ctc ctc tag ag ggctcttagc aaaacccaaa gagagatttg 680
 Cys Trp Gln Pro Leu Leu *
 205

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 <213> Homo sapiens

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Met Val Arg Leu Gly Leu Phe Ser
1 5
tgt tta ttg gcc att tat agt tta ctg tgg att gtt tgt atc cct tac 2140
Cys Leu Leu Ala Ile Tyr Ser Leu Leu Trp Ile Val Cys Ile Pro Tyr
10 15 20
ctg ctt tct att ggg tta tgt gtg gat ata ttg ttt tta ttt gtt cag 2188
Leu Leu Ser Ile Gly Leu Cys Val Asp Ile Leu Phe Leu Phe Val Gln
25 30 35 40
cat ctc ctt ccc cat ctt ctg gta aca caa cct tta ttt att tgt ggg 2236
His Leu Leu Pro His Leu Leu Val Thr Gln Pro Leu Phe Ile Cys Gly
45 50 55
gaa cct att ccc tgt ggc tta ggt gag cat gtg acc agg cct ggc ctc 2284
Glu Pro Ile Pro Cys Gly Leu Gly Glu His Val Thr Arg Pro Gly Leu

75

80

85

gaa cca act cca gcc gat gga aga atc ata tat cga aaa cca gtc aag 343
Glu Pro Thr Pro Ala Asp Gly Arg Ile Ile Tyr Arg Lys Pro Val Lys
90 95 100

cat ccc tca gat gaa aaa tat tca ggt tta aca gca agc tca aaa aag 391
His Pro Ser Asp Glu Lys Tyr Ser Gly Leu Thr Ala Ser Ser Lys Lys
105 110 115

aag aag cca aat gaa gat gaa gta aat cag gac tcg gtc aaa aag aac 439
Lys Lys Pro Asn Glu Asp Glu Val Asn Gln Asp Ser Val Lys Lys Asn
120 125 130

tca caa aaa caa att aaa aat agt agc ctc ctt tct ttt gac aac gaa 487
Ser Gln Lys Gln Ile Lys Asn Ser Ser Leu Leu Ser Phe Asp Asn Glu
135 140 145 150

gat gaa aat gag taa gtgtaaatat tttgaattta gtctactttg aaagtatatg 542
Asp Glu Asn Glu *
155

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agtttaggaa atagagaaaa aaatttaata aactacatct attcatcaat acccctctga 662

cttaaaatgc caactctata gaaattagct agtattaaca ttttggtatt tcccttggtg 722

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<211> 573

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cgctgggaag ggacggccct cgcccgcggt g atg gtg gtt agc aag atg aac 172
Met Val Val Ser Lys Met Asn
1 5

aaa gat gcg cag atg aga gca gcg att aac caa aag ttg ata gaa act 220
Lys Asp Ala Gln Met Arg Ala Ala Ile Asn Gln Lys Leu Ile Glu Thr
10 15 20

gga gaa aga gaa cgc ctc aaa gag ttg ctg aga gct aaa tta att gaa	268
Gly Glu Arg Glu Arg Leu Lys Glu Leu Leu Arg Ala Lys Leu Ile Glu	
25 30 35	
tgt ggc tgg aag gat cag ttg aag gca cac tgt aaa gag gta att aaa	316
Cys Gly Trp Lys Asp Gln Leu Lys Ala His Cys Lys Glu Val Ile Lys	
40 45 50 55	
gaa aaa gga cta gaa cac gtt act gtt gat gac ttg gtg gct gaa atc	364
Glu Lys Gly Leu Glu His Val Thr Val Asp Asp Leu Val Ala Glu Ile	
60 65 70	
act cca aaa ggc aga gcc ctg gta cct gac agt gta aag aag gag ctc	412
Thr Pro Lys Gly Arg Ala Leu Val Pro Asp Ser Val Lys Lys Glu Leu	
75 80 85	
cta caa aga ata aga aca ttc ctt gct cag cat gcc agc ctt taa gat	460
Leu Gln Arg Ile Arg Thr Phe Leu Ala Gln His Ala Ser Leu *	
90 95 100	

tgaattagat tgtgttggtg tgggttttatt tctgaaagta aaacttgcca taaattagaa	520
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aattagaatc ttttcacatg agactacaga gaaagatttg tatttgtaac aaaaaattag	300
ctgggcatgg tggcaggtgc ctgtaatccc agctacttgg gaggctgagg caggagaatc	360
gcttgaaccc gggaggcgga ggttgagcaa ctacactgcg ctgcatcgga ctcgacgccc	420
gctggtgacg cacacgctgc gccggaagtg tgaactgtct gcctccgggc tttgtc	476
atg gcg gct gct gct gca cgc tgg aac cat gtg tgg gtc ggc acc gag	524
Met Ala Ala Ala Ala Ala Arg Trp Asn His Val Trp Val Gly Thr Glu	
1 5 10 15	
act ggg atc ttg aaa ggg gta aat ctt cag cga aaa cag gcg gcg aac	572

Thr	Gly	Ile	Leu	Lys	Gly	Val	Asn	Leu	Gln	Arg	Lys	Gln	Ala	Ala	Asn	
20								25				30				
ttc	acg	gcc	gga	gga	cag	ccg	cgg	cgc	gag	gag	gca	gtg	agc	gcc	ctg	620
Phe	Thr	Ala	Gly	Gly	Gln	Pro	Arg	Arg	Glu	Glu	Ala	Val	Ser	Ala	Leu	
35				40				45								
tgt	tgg	ggc	acc	ggc	ggc	gag	acc	cag	atg	ctg	gtg	ggc	tgc	gcg	gac	668
Cys	Trp	Gly	Thr	Gly	Gly	Glu	Thr	Gln	Met	Leu	Val	Gly	Cys	Ala	Asp	
50				55				60								
agg	acg	gtg	aag	cac	ttc	agc	acc	gag	gat	ggc	ata	ttc	cag	ggt	cag	716
Arg	Thr	Val	Lys	His	Phe	Ser	Thr	Glu	Asp	Gly	Ile	Phe	Gln	Gly	Gln	
65				70				75				80				
aga	cac	tgc	ccg	ggc	ggg	gag	ggc	atg	ttc	cgt	ggc	ctc	gcc	cag	gcc	764
Arg	His	Cys	Pro	Gly	Gly	Glu	Gly	Met	Phe	Arg	Gly	Leu	Ala	Gln	Ala	
85				90				95								
gac	ggc	acc	ctc	atc	aca	tgt	gtg	gat	tct	ggg	att	ctc	aga	gtc	tgg	812
Asp	Gly	Thr	Leu	Ile	Thr	Cys	Val	Asp	Ser	Gly	Ile	Leu	Arg	Val	Trp	
100				105				110								
cat	gac	aag	gac	aag	gac	aca	tcc	tct	gac	cca	ctc	ctg	gaa	ctg	aga	860
His	Asp	Lys	Asp	Lys	Asp	Thr	Ser	Ser	Asp	Pro	Leu	Leu	Glu	Leu	Arg	
115				120				125								
gtg	ggc	cct	ggg	gtg	tgt	agg	atg	cgc	caa	gac	cca	gca	cac	ccc	cat	908
Val	Gly	Pro	Gly	Val	Cys	Arg	Met	Arg	Gln	Asp	Pro	Ala	His	Pro	His	
130				135				140								
gtg	gtt	gcc	aca	ggt	ggg	aaa	gag	aat	gct	ttg	aag	ata	tgg	gac	ctg	956
Val	Val	Ala	Thr	Gly	Gly	Lys	Glu	Asn	Ala	Leu	Lys	Ile	Trp	Asp	Leu	
145				150				155				160				
cag	ggc	tct	gag	gaa	cct	gtg	ttc	agg	gcc	aag	aac	gtg	cgg	aat	gac	1004
Gln	Gly	Ser	Glu	Glu	Pro	Val	Phe	Arg	Ala	Lys	Asn	Val	Arg	Asn	Asp	
165				170				175								
tgg	ctg	gac	ttg	cgg	gtt	ccc	atc	tgg	gac	cag	gac	ata	cag	ttt	ctc	1052
Trp	Leu	Asp	Leu	Arg	Val	Pro	Ile	Trp	Asp	Gln	Asp	Ile	Gln	Phe	Leu	
180				185				190								
cca	gga	tca	cag	aag	ctt	gtc	acc	tgc	aca	ggg	tac	cac	cag	gtc	cgt	1100
Pro	Gly	Ser	Gln	Lys	Leu	Val	Thr	Cys	Thr	Gly	Tyr	His	Gln	Val	Arg	
195				200				205								
gtt	tat	gat	cca	gca	tcc	ccc	cag	cgc	cgg	cca	gtc	cta	gag	acc	acc	1148
Val	Tyr	Asp	Pro	Ala	Ser	Pro	Gln	Arg	Arg	Pro	Val	Leu	Glu	Thr	Thr	
210				215				220								
tat	gga	gag	tac	cca	cta	aca	gcc	atg	acc	ctc	act	ccg	gga	ggc	aac	1196
Tyr	Gly	Glu	Tyr	Pro	Leu	Thr	Ala	Met	Thr	Leu	Thr	Pro	Gly	Gly	Asn	
225				230				235				240				
tca	gtg	att	gtg	gga	aac	act	cat	ggg	cag	ctg	gca	gaa	att	gac	ctt	1244
Ser	Val	Ile	Val	Gly	Asn	Thr	His	Gly	Gln	Leu	Ala	Glu	Ile	Asp	Leu	

245	250	255	
cgg caa ggg cgt cta ctg ggc tgt ctg	aag ggg ctg gca ggc agt gtg	1292	
Arg Gln Gly Arg Leu Leu Gly Cys Leu	Lys Gly Leu Ala Gly Ser Val		
260	265	270	
cgt ggg ttg cag tgc cac cct tca aag cct	cta cta gcc tcc tgt ggc	1340	
Arg Gly Leu Gln Cys His Pro Ser Lys Pro	Leu Leu Ala Ser Cys Gly		
275	280	285	
ttg gac aga gtc ttg agg ata cac agg atc	cag aat cca cgg ggt ctg	1388	
Leu Asp Arg Val Leu Arg Ile His Arg Ile	Gln Asn Pro Arg Gly Leu		
290	295	300	
gag cat aag gtt tat ctc aag tct caa ttg	aac tgc ctc ctc ttg tca	1436	
Glu His Lys Val Tyr Leu Lys Ser Gln Leu	Asn Cys Leu Leu Leu Ser		
305	310	315	
ggc agg gac aac tgg gag gat gag ccc caa	gag cct caa gaa ccc aac	1484	
Gly Arg Asp Asn Trp Glu Asp Glu Pro Gln	Glu Pro Gln Glu Pro Asn		
325	330	335	
aag gtg ccc cta gaa gac aca gag aca gat	gaa ctt tgg gca tcc ttg	1532	
Lys Val Pro Leu Glu Asp Thr Glu Thr Asp	Glu Leu Trp Ala Ser Leu		
340	345	350	
gag gca gct gcc aag cgg aag ctc tgc ggt	ttg gag cag ccc caa gga	1580	
Glu Ala Ala Ala Lys Arg Lys Leu Ser Gly	Leu Glu Gln Pro Gln Gly		
355	360	365	
gct ctc caa acg aga cgg aga aag aag aag	cgg cct ggg tcc acc agc	1628	
Ala Leu Gln Thr Arg Arg Arg Lys Lys Lys	Arg Pro Gly Ser Thr Ser		
370	375	380	
ccc tga cgcccctgtg ccctctttgt aaataaactg	ctgaacaccc aaaaaaaaaa	1684	
Pro *			
385			
aaa		1687	

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 <213> Homo sapiens

<220>
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 Met Leu Leu

caa gtt gta cga gaa ggg aag ttc tcg ggg ttt ctg acc tcc tgc agc 165
 Gln Val Val Arg Glu Gly Lys Phe Ser Gly Phe Leu Thr Ser Cys Ser
 5 10 15

ctc ctc ttg cct cgg gct gcc cag atc ttg gcg gct gag gct ggc tta 213
 Leu Leu Leu Pro Arg Ala Ala Gln Ile Leu Ala Ala Glu Ala Gly Leu
 20 25 30 35

cct tcg agc cgt tcc ttc atg gga ttt gct gct ccc ttc acc aac aag 261
 Pro Ser Ser Arg Ser Phe Met Gly Phe Ala Ala Pro Phe Thr Asn Lys
 40 45 50

cga aag gct tac tcg gag cgt aga atc atg ggg tac tca atg cag gag 309
 Arg Lys Ala Tyr Ser Glu Arg Arg Ile Met Gly Tyr Ser Met Gln Glu
 55 60 65

atg tat gag gtg gtg tcc aac gtc cag gag tat cgt gag ttt gtg ccc 357
 Met Tyr Glu Val Val Ser Asn Val Gln Glu Tyr Arg Glu Phe Val Pro
 70 75 80

tgg tgt aag aag tct ctg gtg gta tcc agc cgt aag ggt cat ttg aaa 405
 Trp Cys Lys Lys Ser Leu Val Val Ser Ser Arg Lys Gly His Leu Lys
 85 90 95

gcc cag ctg gag gtt ggc ttt cca cct gtc atg gaa cgt tac acc tct 453
 Ala Gln Leu Glu Val Gly Phe Pro Pro Val Met Glu Arg Tyr Thr Ser
 100 105 110 115

gca gtt tcc atg gtc aaa cct cac atg gtc aag gct gtt tgt act gat 501
 Ala Val Ser Met Val Lys Pro His Met Val Lys Ala Val Cys Thr Asp
 120 125 130

ggc aag ctc ttc aac cac tta gag act att tgg cga ttc agc cct ggt 549
 Gly Lys Leu Phe Asn His Leu Glu Thr Ile Trp Arg Phe Ser Pro Gly
 135 140 145

att cct gcc tat cct cga acc tgc act gtg gac ttt tcg att tcc ttt 597
 Ile Pro Ala Tyr Pro Arg Thr Cys Thr Val Asp Phe Ser Ile Ser Phe
 150 155 160

gaa ttt cgt tct ctg ctg cac tcc cag ctg gcc acc atg ttt ttt gat 645
 Glu Phe Arg Ser Leu Leu His Ser Gln Leu Ala Thr Met Phe Phe Asp
 165 170 175

gag gtt gtc aaa cag aat gtt gct gcc ttt gag cgt cgg gca gcc acc 693
 Glu Val Val Lys Gln Asn Val Ala Ala Phe Glu Arg Arg Ala Ala Thr
 180 185 190 195

aag ttt ggt cca gaa aca gcc atc ccc cgt gaa ctg atg ttc cat gag 741
 Lys Phe Gly Pro Glu Thr Ala Ile Pro Arg Glu Leu Met Phe His Glu
 200 205 210

gtg cac cag act tga ggcaagggat tgctccctga cctcccttct accccacttc 796
 Val His Gln Thr *
 215

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cctacacaat tctcttattt atttggtttg gctcctgttc caatttgaaa ggagtctgtg      856
ttcataatac tgtttctcct ctcaatttcc cagaaattgg gttctatgct ggctggaaat      916
gttgggggaa agagaaggca aaggatgtgg aaatgagatg tgcttaggaa agggtcaggc      976
ccatcgtagg agcaccatat gcctgcagcc ttttcactac gaattagaat aaggactatg     1036
tggttggtctc tggaccttat caagacacct tagtgtctga ccaggggacg atagtaactt     1096
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<212> DNA
<213> Homo sapiens

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cctgaccaac atggagaaac cccatctcta cttaaaaaaa aaaaaatacg aatttaccca     180
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caacaagagc aaaactccat ctcaaaaaga aaaaagaaag aaagaaatgc taggggaaaa     360
tgttttaact agtcattctt cccagtagct a    atg aag ctg act ttt aaa aag      412
                               Met Lys Leu Thr Phe Lys Lys
                               1          5

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Lys Ala Val Ser Phe Ala Asp Ala Ala Ala Ala Gln Gly Pro Leu Leu
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cca gcc atg gtc aac ccc acc atg ttt ttc cac att gct gtc gat ggc      508

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25 30 35	
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Ala His Ser Ser Pro Trp Pro Ala Phe Thr Glu Thr Ile His Ala Asp	
40 45 50	
agc gtg gcc aag cgt ccg gag cac aat aga tct gaa gcc ttg aag gtg	366
Ser Val Ala Lys Arg Pro Glu His Asn Arg Ser Glu Ala Leu Lys Val	
55 60 65	
tcc tgt ggc aag tgt ggc aat ggg ttg ggc cac gag ttc ctg aac gac	414
Ser Cys Gly Lys Cys Gly Asn Gly Leu Gly His Glu Phe Leu Asn Asp	
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Gly Pro Lys Pro Gly Gln Ser Arg Phe *	
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 Met Glu Met Arg Leu Pro Ile Arg Ser Pro Ile Lys Arg
 1 5 10

 gac ttt tta tca gga att cag att gaa ttt aag cag tct tct cac cag 156
 Asp Phe Leu Ser Gly Ile Gln Ile Glu Phe Lys Gln Ser Ser His Gln
 15 20 25

 aga agt tta agg gcc agg ttg tac tgg ctt cag gtt gat aat cag tta 204
 Arg Ser Leu Arg Ala Arg Leu Tyr Trp Leu Gln Val Asp Asn Gln Leu
 30 35 40 45

 cca ggt gca atg ttc cct gtt gta ttt cat cct gtt gcc cct cca aaa 252
 Pro Gly Ala Met Phe Pro Val Val Phe His Pro Val Ala Pro Pro Lys
 50 55 60

 tct att gct tta gat tca gag ccc aag cct ttc att gat gtg agt gtc 300
 Ser Ile Ala Leu Asp Ser Glu Pro Lys Pro Phe Ile Asp Val Ser Val
 65 70 75

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 Ile Thr Arg Phe Asn Glu Tyr Ser Lys Val Leu Gln Phe Lys Tyr Phe
 80 85 90

 atg gtc ctc att cag gaa atg gcc tta aaa att gat caa ggg ttt cta 396
 Met Val Leu Ile Gln Glu Met Ala Leu Lys Ile Asp Gln Gly Phe Leu
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 gga gct att att gca ctg ttt acc cca aca aca gac cct gaa gct gaa 444
 Gly Ala Ile Ile Ala Leu Phe Thr Pro Thr Thr Asp Pro Glu Ala Glu
 110 115 120 125

 aga aga cgg aca aag tta atc caa caa gat att gat gct cta aat gca 492
 Arg Arg Arg Thr Lys Leu Ile Gln Gln Asp Ile Asp Ala Leu Asn Ala
 130 135 140

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 Glu Leu Met Glu Thr Ser Met Thr Asp Met Ser Ile Leu Ser Phe Phe
 145 150 155

 gaa cat ttc cat att tct cct gtg aag ttg cat ttg agt ttg tct ttg 588
 Glu His Phe His Ile Ser Pro Val Lys Leu His Leu Ser Leu Ser Leu
 160 165 170

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 Gly Ser Gly Gly Glu Glu Ser Asp Lys Glu Lys Gln Glu Met Phe Ala

175	180	185	
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Val His Ser Val Asn Leu Leu Leu Lys Ser Ile Gly Ala Thr Leu Thr			
190	195	200	205
gat gtg gat gac ctt ata ttc aaa ctt gct tat tat gaa att cga tat			732
Asp Val Asp Asp Leu Ile Phe Lys Leu Ala Tyr Tyr Glu Ile Arg Tyr			
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Gln Phe Tyr Lys Arg Asp Gln Leu Ile Trp Ser Val Val Arg His Tyr			
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Ser Glu Gln Phe Leu Lys Gln Met Tyr Val Leu Val Leu Gly Leu Asp			
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Val Leu Gly Asn Pro Phe Gly Leu Ile Arg Gly Leu Ser Glu Gly Val			
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gaa gct tta ttc tat gaa ccc ttc cag ggt gct gtt caa ggc cct gaa			924
Glu Ala Leu Phe Tyr Glu Pro Phe Gln Gly Ala Val Gln Gly Pro Glu			
	270	275	280
gaa ttt gca gag ggg tta gtg att gga gtg aga agc ctc ttt gga cac			972
Glu Phe Ala Glu Gly Leu Val Ile Gly Val Arg Ser Leu Phe Gly His			
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aca gta ggt ggt gca gca gga gtt gta tct cga atc acc ggt tct gtt			1020
Thr Val Gly Gly Ala Ala Gly Val Val Ser Arg Ile Thr Gly Ser Val			
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ggg aaa ggt ttg gca gca att aca atg gac aag gaa tat cag caa aaa			1068
Gly Lys Gly Leu Ala Ala Ile Thr Met Asp Lys Glu Tyr Gln Gln Lys			
	320	325	330
aga aga gaa gag ttg agt cga cag ccc aga gat ttt gga gac agc ctg			1116
Arg Arg Glu Glu Leu Ser Arg Gln Pro Arg Asp Phe Gly Asp Ser Leu			
	335	340	345
gcc aga gga gga aag ggc ttt ctg cga gga gtt gtt ggt gga gtg act			1164
Ala Arg Gly Gly Lys Gly Phe Leu Arg Gly Val Val Gly Gly Val Thr			
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gga ata ata aca aaa cct gtg gaa ggt gcc aaa aag gaa gga gct gct			1212
Gly Ile Ile Thr Lys Pro Val Glu Gly Ala Lys Lys Glu Gly Ala Ala			
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gga ttc ttt aaa gga att gga aaa ggg ctt gtg ggt gct gtg gcc cgt			1260
Gly Phe Phe Lys Gly Ile Gly Lys Gly Leu Val Gly Ala Val Ala Arg			
	385	390	395
cca act ggt gga atc gta gat atg gcc agt agt acc ttc caa ggc att			1308
Pro Thr Gly Gly Ile Val Asp Met Ala Ser Ser Thr Phe Gln Gly Ile			
	400	405	410

cag agg gca gca gaa tca act gag gaa gta tct agc ctc cgt ccc cct Gln Arg Ala Ala Glu Ser Thr Glu Glu Val Ser Ser Leu Arg Pro Pro 415 420 425	1356
cgc ctg atc cat gaa gat ggc atc att cgt cct tat gac aga cag gaa Arg Leu Ile His Glu Asp Gly Ile Ile Arg Pro Tyr Asp Arg Gln Glu 430 435 440 445	1404
tct gag ggc tct gac tta ctt gag aat cat atc aaa aag ttg gaa gga Ser Glu Gly Ser Asp Leu Leu Glu Asn His Ile Lys Lys Leu Glu Gly 450 455 460	1452
gag act tac cga tac cac tgt gct att cct gga agc aag aag aca atc Glu Thr Tyr Arg Tyr His Cys Ala Ile Pro Gly Ser Lys Lys Thr Ile 465 470 475	1500
ctt atg gtt aca aat agg cga gtg ttg tgt ata aag gaa gtt gaa atc Leu Met Val Thr Asn Arg Arg Val Leu Cys Ile Lys Glu Val Glu Ile 480 485 490	1548
ctg ggc ctt atg tgt gta gac tgg caa tgt cca ttt gaa gat ttt gta Leu Gly Leu Met Cys Val Asp Trp Gln Cys Pro Phe Glu Asp Phe Val 495 500 505	1596
ttt cct cct agt gtc agt gaa aat gtg cta aaa att tca gtt aag gaa Phe Pro Pro Ser Val Ser Glu Asn Val Leu Lys Ile Ser Val Lys Glu 510 515 520 525	1644
cag ggt ctg ttc cac aaa aaa gac agt gcc aat caa ggc tgt gtt cga Gln Gly Leu Phe His Lys Lys Asp Ser Ala Asn Gln Gly Cys Val Arg 530 535 540	1692
aaa gtt tac ctg aag gac acc gcc aca gca gag aga gca tgt aat gcc Lys Val Tyr Leu Lys Asp Thr Ala Thr Ala Glu Arg Ala Cys Asn Ala 545 550 555	1740
att gag gat gca cag tca acg aga cag cag caa aaa ttg atg aag cag Ile Glu Asp Ala Gln Ser Thr Arg Gln Gln Gln Lys Leu Met Lys Gln 560 565 570	1788
tca tca gtg aga ctt ctc aga ccc caa ttg cca tct taa tcacagacct Ser Ser Val Arg Leu Leu Arg Pro Gln Leu Pro Ser *	1837
575 580 585	
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	140		145		150	
ttc att cca aat cag aca gaa gca atg gaa ttt gat atc ttc cag aga						833
Phe Ile Pro Asn Gln Thr Glu Ala Met Glu Phe Asp Ile Phe Gln Arg						
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tgg aaa gag tgc agg gga aag agc cct gcc cag gcg gaa ctc tcc tat						881
Trp Lys Glu Cys Arg Gly Lys Ser Pro Ala Gln Ala Glu Leu Ser Tyr						
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ctg aat aaa gcg aag tgg ctg gaa atg tat ggg gta gac atg cac gtt						929
Leu Asn Lys Ala Lys Trp Leu Glu Met Tyr Gly Val Asp Met His Val						
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gtc agg gga aga gat gcc tgt gaa tat tct ctt gga ctg acc ccg aca						977
Val Arg Gly Arg Asp Gly Cys Glu Tyr Ser Leu Gly Leu Thr Pro Thr						
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ggc ata tta atc ttt gaa gga gct aac aaa ata ggc tta ttc ttt tgg						1025
Gly Ile Leu Ile Phe Glu Gly Ala Asn Lys Ile Gly Leu Phe Phe Trp						
	220		225		230	
cct aaa att acc aaa atg gat ttt aaa aag agc aaa ttg aca ctc gtg						1073
Pro Lys Ile Thr Lys Met Asp Phe Lys Lys Ser Lys Leu Thr Leu Val						
	235		240		245	
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Val Val Glu Asp Asp Asp Gln Gly Arg Glu Gln Glu His Thr Phe Val						
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Phe Arg Leu Asp Ser Ala Arg Thr Cys Lys His Leu Trp Lys Cys Ala						
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Val Glu His His Ala Phe Phe Arg Leu Arg Thr Pro Gly Asn Ser Lys						
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Ser Asn Arg Ser Asp Phe Ile Arg Leu Gly Ser Arg Phe Arg Phe Ser						
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Gly Arg Thr Glu Tyr Gln Ala Thr His Gly Ser Arg Leu Arg Arg Thr						
	315		320		325	
agc acc ttt gag agg aag cct agt aaa cgt tat cca tcc cgg aga cat						1361
Ser Thr Phe Glu Arg Lys Pro Ser Lys Arg Tyr Pro Ser Arg Arg His						
	330		335		340	
tca acg ttc aaa gca agc aac cca gtg ata gca gcc cag ctc tgc tct						1409
Ser Thr Phe Lys Ala Ser Asn Pro Val Ile Ala Ala Gln Leu Cys Ser						
	345		350		355	360

aaa aca aat cca gaa gtc cat aat tac cag cct caa tat cat cct aat	1457
Lys Thr Asn Pro Glu Val His Asn Tyr Gln Pro Gln Tyr His Pro Asn	
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Ile His Pro Ser Gln Pro Arg Trp His Pro His Ser Pro Asn Val Arg	
380 385 390	
cca tcc ttt cag gat gac agg tgc cat tgg aaa gca tgc gcc agt gga	1553
Pro Ser Phe Gln Asp Asp Arg Ser His Trp Lys Ala Ser Ala Ser Gly	
395 400 405	
gat gac agc cat ttt gat tat gtc cac gac cag aac cag aag aac tta	1601
Asp Asp Ser His Phe Asp Tyr Val His Asp Gln Asn Gln Lys Asn Leu	
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gga ggg atg caa agt atg atg tat cga gat aaa ctc atg act gca ctt	1649
Gly Gly Met Gln Ser Met Met Tyr Arg Asp Lys Leu Met Thr Ala Leu	
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ttccaaatta tattggtggt catcagaagt aggtgatagg aagaaatact tctcaagggt 240
gcaaaa atg cag agt aat aaa act ttt aac ttg gag aag caa aac cat 288
Met Gln Ser Asn Lys Thr Phe Asn Leu Glu Lys Gln Asn His
1 5 10
act cca aga aag cat cat caa cat cac cac cag cag cag cac cac cag 336
Thr Pro Arg Lys His His Gln His His His Gln Gln Gln His His Gln
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cag caa cag cag cag ccg cca cca ccg cca ata cct gca aat ggg caa 384
Gln Gln Gln Gln Gln Pro Pro Pro Pro Pro Ile Pro Ala Asn Gly Gln
35 40 45
cag gcc agc agc caa agt gtg tat atg cta gat gaa ggc ttg act att 432
Gln Ala Ser Ser Gln Ser Val Tyr Met Leu Asp Glu Gly Leu Thr Ile
50 55 60
gac ctg aag aat ttt aga aaa cca gga gag aag acc ttc acc caa cga 480
Asp Leu Lys Asn Phe Arg Lys Pro Gly Glu Lys Thr Phe Thr Gln Arg

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atg agg aaa cta ttt gag aaa tat gga aag gca ggc gaa gtc ttc att			576
Met Arg Lys Leu Phe Glu Lys Tyr Gly Lys Ala Gly Glu Val Phe Ile			
95	100	105	110
cat aag gat aaa gga ttt ggc ttt atc cgc ttg gaa acc cga acc cta			624
His Lys Asp Lys Gly Phe Gly Phe Ile Arg Leu Glu Thr Arg Thr Leu			
115	120	125	
gcg gag att gcc aaa gtg gag ctg gac aat atg cca ctc cgt gga aag			672
Ala Glu Ile Ala Lys Val Glu Leu Asp Asn Met Pro Leu Arg Gly Lys			
130	135	140	
cag ctg cgt gtg cgc ttt gcc tgc cat agt gca tcc ctt aca gtt cga			720
Gln Leu Arg Val Arg Phe Ala Cys His Ser Ala Ser Leu Thr Val Arg			
145	150	155	
aac ctt cct cag tat gtg tcc aac gaa ctg ctg gaa gaa gcc ttt tct			768
Asn Leu Pro Gln Tyr Val Ser Asn Glu Leu Leu Glu Glu Ala Phe Ser			
160	165	170	
gtg ttt ggc cag gta gag agg gct gta gtc att gtg gat gat cga gga			816
Val Phe Gly Gln Val Glu Arg Ala Val Val Ile Val Asp Asp Arg Gly			
175	180	185	190
agg ccc tca gga aaa ggc att gtt gag ttc tca ggg aag cca gct gct			864
Arg Pro Ser Gly Lys Gly Ile Val Glu Phe Ser Gly Lys Pro Ala Ala			
195	200	205	
cgg aaa gct ctg gac aga tgc agt gaa ggc tcc ttc ctg cta acc aca			912
Arg Lys Ala Leu Asp Arg Cys Ser Glu Gly Ser Phe Leu Leu Thr Thr			
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Phe Pro Arg Pro Val Thr Val Glu Pro Met Asp Gln Leu Asp Asp Glu			
225	230	235	
gag gga ctt cca gag aag ctg gtt ata aaa aac cag caa ttt cac aag			1008
Glu Gly Leu Pro Glu Lys Leu Val Ile Lys Asn Gln Gln Phe His Lys			
240	245	250	
gaa cga gag cag cca ccc aga ttt gca cag cct ggc tcc ttt gag tat			1056
Glu Arg Glu Gln Pro Pro Arg Phe Ala Gln Pro Gly Ser Phe Glu Tyr			
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gaa tat gcc atg cgc tgg aag gca ctc att gag atg gag aag cag cag			1104
Glu Tyr Ala Met Arg Trp Lys Ala Leu Ile Glu Met Glu Lys Gln Gln			
275	280	285	
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 <222> (54)..(686)

<400> 120

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Ser Ser Val Gln Gly Gln Gly Pro Val Thr Met Glu Ala Glu Arg Ser		
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aag gcc aca gcc gtg gcc ctg ggc agt ttc ccg gca ggt ggc ccg gcc		200
Lys Ala Thr Ala Val Ala Leu Gly Ser Phe Pro Ala Gly Gly Pro Ala		
35 40 45		
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Glu Leu Ser Leu Arg Leu Gly Glu Pro Leu Thr Ile Val Ser Glu Asp		
50 55 60 65		
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Gly Asp Trp Trp Thr Val Leu Ser Glu Val Ser Gly Arg Glu Tyr Asn		
70 75 80		
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Ile Pro Ser Val His Val Ala Lys Val Ser His Gly Trp Leu Tyr Glu		
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Gly Leu Ser Arg Glu Lys Ala Glu Glu Leu Leu Leu Pro Gly Asn		
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Pro Gly Gly Ala Phe Leu Ile Arg Glu Ser Gln Thr Arg Arg Gly Ser		
115 120 125		
tac tct ctg tca gtc cgc ctc agc cgc cct gca tcc tgg gac cgg atc		488
Tyr Ser Leu Ser Val Arg Leu Ser Arg Pro Ala Ser Trp Asp Arg Ile		
130 135 140 145		
aga cac tac agg atc cac tgc ctt gac aat ggc tgg ctg tac atc tca		536
Arg His Tyr Arg Ile His Cys Leu Asp Asn Gly Trp Leu Tyr Ile Ser		
150 155 160		
ccg cgc ctc acc ttc ccc tca ctc cag gcc ctg ggg gac cat tac tct		584
Pro Arg Leu Thr Phe Pro Ser Leu Gln Ala Leu Gly Asp His Tyr Ser		
165 170 175		

Gln Cys Gly Lys Pro Gln Glu Ser Thr Gly Arg Gly Ser Ala Phe Leu	
230 235 240	
aaa gct gtc cag ggt agc ggg gac aca tct agg cac tgt cta cct acc	943
Lys Ala Val Gln Gly Ser Gly Asp Thr Ser Arg His Cys Leu Pro Thr	
245 250 255 260	
cta gca gat gcc aaa ggt ctc cag gac act ggg ggc act gtg aac tat	991
Leu Ala Asp Ala Lys Gly Leu Gln Asp Thr Gly Gly Thr Val Asn Tyr	
265 270 275	
ttc tgg ggt att cca ttc tgc cct gat gga gta gac cct aac cag tat	1039
Phe Trp Gly Ile Pro Phe Cys Pro Asp Gly Val Asp Pro Asn Gln Tyr	
280 285 290	
acc aag gtc att ctc tgc cag ttg gag gtt tat caa aag agc ctg aaa	1087
Thr Lys Val Ile Leu Cys Gln Leu Glu Val Tyr Gln Lys Ser Leu Lys	
295 300 305	
atg gct cag agg cag ctc ctt aat aaa aaa ggt ttt ggg gaa cca gtg	1135
Met Ala Gln Arg Gln Leu Leu Asn Lys Lys Gly Phe Gly Glu Pro Val	
310 315 320	
tta cct aga cct ccc tct ctg atc cag aat gaa tgt ggc caa gga gag	1183
Leu Pro Arg Pro Pro Ser Leu Ile Gln Asn Glu Cys Gly Gln Gly Glu	
325 330 335 340	
cag gct agt gag aaa aat gaa tgc atc tca gaa gat atg gga gat gaa	1231
Gln Ala Ser Glu Lys Asn Glu Cys Ile Ser Glu Asp Met Gly Asp Glu	
345 350 355	
gac aaa gag gag agg cag gag tct agg gca tct gac tgg cac tca aaa	1279
Asp Lys Glu Glu Arg Gln Glu Ser Arg Ala Ser Asp Trp His Ser Lys	
360 365 370	
acc aag gat ttc cag gaa agc tca att aaa agc ttg aaa gag aaa ctt	1327
Thr Lys Asp Phe Gln Glu Ser Ser Ile Lys Ser Leu Lys Glu Lys Leu	
375 380 385	
ttg ttg gag gaa gaa cca aca acc agt cat ggt cag tct tcc caa ggg	1375
Leu Leu Glu Glu Glu Pro Thr Thr Ser His Gly Gln Ser Ser Gln Gly	
390 395 400	
att gtt gaa gaa act tct gaa gag gga aac tct gta cct gct tca caa	1423
Ile Val Glu Glu Thr Ser Glu Glu Gly Asn Ser Val Pro Ala Ser Gln	
405 410 415 420	
agt gtt gct gct ttg acc agt aag aga agc tta gtc ctt atg cca gag	1471
Ser Val Ala Ala Leu Thr Ser Lys Arg Ser Leu Val Leu Met Pro Glu	
425 430 435	
agt tct gca gaa gaa atc act gtt tgt cct gag aca cag cta agt tcc	1519
Ser Ser Ala Glu Glu Ile Thr Val Cys Pro Glu Thr Gln Leu Ser Ser	
440 445 450	
tct gaa act ttt gac ctt gaa aga gaa gtc tct cca ggt agc aga gat	1567
Ser Glu Thr Phe Asp Leu Glu Arg Glu Val Ser Pro Gly Ser Arg Asp	

455	460	465	
atc ttg gat gga gtc aga ata ata atg gca gat aag gag gtt ggt aac Ile Leu Asp Gly Val Arg Ile Ile Met Ala Asp Lys Glu Val Gly Asn 470 475 480			1615
aag gaa gat gct gag aag gaa gta gct att tct acc ttc tca tcc agt Lys Glu Asp Ala Glu Lys Glu Val Ala Ile Ser Thr Phe Ser Ser Ser 485 490 495 500			1663
aac cag gta tcc tgc ccg cta tgt gac caa tgc ttt cca ccc aca aag Asn Gln Val Ser Cys Pro Leu Cys Asp Gln Cys Phe Pro Pro Thr Lys 505 510 515			1711
att gaa cga cat gcc atg tac tgc aat ggt ctg atg gag gaa gat aca Ile Glu Arg His Ala Met Tyr Cys Asn Gly Leu Met Glu Glu Asp Thr 520 525 530			1759
gta ttg act cgg aga caa aaa gag gcc aag acc aag agt gac agt ggg Val Leu Thr Arg Arg Gln Lys Glu Ala Lys Thr Lys Ser Asp Ser Gly 535 540 545			1807
aca gct gcc cag act tct cta gac att gac aag aat gag aag tgt tac Thr Ala Ala Gln Thr Ser Leu Asp Ile Asp Lys Asn Glu Lys Cys Tyr 550 555 560			1855
ctc tgt aaa tcc ctg gtc cca ttt aga gag tat cag tgt cat gtg gac Leu Cys Lys Ser Leu Val Pro Phe Arg Glu Tyr Gln Cys His Val Asp 565 570 575 580			1903
tcc tgt ctc cag ctt gca aag gct gac caa gga gat gga cct gaa ggg Ser Cys Leu Gln Leu Ala Lys Ala Asp Gln Gly Asp Gly Pro Glu Gly 585 590 595			1951
agt gga aga gca tgt tca act gtg gag ggg aag tgg cag cag agg ctg Ser Gly Arg Ala Cys Ser Thr Val Glu Gly Lys Trp Gln Gln Arg Leu 600 605 610			1999
aag aac cca aag gaa aaa ggc cac agt gaa ggc cga ctc ctt agt ttc Lys Asn Pro Lys Glu Lys Gly His Ser Glu Gly Arg Leu Leu Ser Phe 615 620 625			2047
ttg gaa cag tct gag cac aag act tca gat gca gac atc aag tct tca Leu Glu Gln Ser Glu His Lys Thr Ser Asp Ala Asp Ile Lys Ser Ser 630 635 640			2095
gaa aca gga gcc ttc agg gtg cct tca cca ggg atg gaa gag gca ggc Glu Thr Gly Ala Phe Arg Val Pro Ser Pro Gly Met Glu Glu Ala Gly 645 650 655 660			2143
tgc agc aga gag atg cag agt tct ttc aca cgt cgt gac tta aat gaa Cys Ser Arg Glu Met Gln Ser Ser Phe Thr Arg Arg Asp Leu Asn Glu 665 670 675			2191
tct ccc gtc aag tct ttt gtt tcc att tca gaa gcc aca gat tgc tta Ser Pro Val Lys Ser Phe Val Ser Ile Ser Glu Ala Thr Asp Cys Leu 680 685 690			2239

gtg gac ttt aaa aag caa gtt act gtc cag cca ggt agt cgg aca cgg	2287
Val Asp Phe Lys Lys Gln Val Thr Val Gln Pro Gly Ser Arg Thr Arg	
695 700 705	
acc aaa gct ggc aga gga aga agg aga aaa ttc tga attt ctagggtcca	2337
Thr Lys Ala Gly Arg Gly Arg Arg Arg Lys Phe *	
710 715 720	
aaagttgaca aaaccattag taggaggggt gggccatggt cattaagcca tagtgggtccc	2397
tagttcattg ttgagcaagt tttagccctg cagttttcac caccagcacc taccagcat	2457
tctgggttttt atgttttttta tgatctatgc agacaactgt gtattctgtt ttataacagt	2517
ttgtttgaat ttacttacag ttaaaaaatt taaatat	2554

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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (599)..(1648)

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cccccgga cccggagaag gtctacagag cggcctgcgc cagcgagtga gtaccgcgcg	120
cctgcgcaca gtcgcgcca cccctccctg cctccttttc ttctcagcg ggtccgcggc	180
ccgctactct ccgggagggg cgcttcccga cgccaagaca aaaggatgcc acggagaaaag	240
aaaaaagtta aagaagtctc cgaatctcgg aacctggaga agaaggatgt ggaaactacc	300
agttctgtca gtgtgaagag gaagcgtaga cttgaggatg cattcattgt gatatccgat	360
agtgatggag aggaaccaa ggaggaaaat gggttgcaga aaacgaagac aaaacagtcg	420
aatagagcaa agtgtttggc caaaagaaaa atcgcacaga tgacagaaga agaacagttt	480
gctctggctc tcaaaatgag tgagcaggaa gctagggagg tgaacagcca ggaggaggaa	540
gaagaggagc tcttgaggaa agccattgct gaaagcctga atagttgccg gccttctg	598
atg ctt ccg cta cca gat ctc gac ctc tgg cca ctg gac cgt ctt ccc	646
Met Leu Pro Leu Pro Asp Leu Asp Leu Trp Pro Leu Asp Arg Leu Pro	
1 5 10 15	
agt ccc atc aag aga aaa cca cag act ctg ggc tca ctg aag tct tcc	694
Ser Pro Ile Lys Arg Lys Pro Gln Thr Leu Gly Ser Leu Lys Ser Ser	
20 25 30	

caa ggg att gtt gaa gaa act tct gaa gag gga aac tct gta cct gct Gln Gly Ile Val Glu Glu Thr Ser Glu Glu Gly Asn Ser Val Pro Ala 35 40 45	742
tca caa agt gtt gct gct ttg acc agt aag aga agc tta gtc ctt atg Ser Gln Ser Val Ala Ala Leu Thr Ser Lys Arg Ser Leu Val Leu Met 50 55 60	790
cca gag agt tct gca gaa gaa atc act gtt tgt cct gag acc cag cta Pro Glu Ser Ser Ala Glu Glu Ile Thr Val Cys Pro Glu Thr Gln Leu 65 70 75 80	838
agt tcc tct gaa act ttt gac ctt gaa aga gaa gtc tct cca ggt agc Ser Ser Ser Glu Thr Phe Asp Leu Glu Arg Glu Val Ser Pro Gly Ser 85 90 95	886
aga gat atc ttg gat gga gtc aga ata ata atg gca gat aag gag gtt Arg Asp Ile Leu Asp Gly Val Arg Ile Ile Met Ala Asp Lys Glu Val 100 105 110	934
ggt aac aag gaa gat gct gag aag gaa gta gct att tct acc ttc tca Gly Asn Lys Glu Asp Ala Glu Lys Glu Val Ala Ile Ser Thr Phe Ser 115 120 125	982
tcc agt aac cag gta tcc tgc ccg cta tgt gac caa tgc ttt cca ccc Ser Ser Asn Gln Val Ser Cys Pro Leu Cys Asp Gln Cys Phe Pro Pro 130 135 140	1030
aca aag att gaa cga cat gcc atg tac tgc aat ggt ctg atg gag gaa Thr Lys Ile Glu Arg His Ala Met Tyr Cys Asn Gly Leu Met Glu Glu 145 150 155 160	1078
gat aca gta ttg act cgg aga caa aaa gag gcc aag acc aag agt gac Asp Thr Val Leu Thr Arg Arg Gln Lys Glu Ala Lys Thr Lys Ser Asp 165 170 175	1126
agt ggg aca gct gcc cag act tct cta gac att gac aag aat gag aag Ser Gly Thr Ala Ala Gln Thr Ser Leu Asp Ile Asp Lys Asn Glu Lys 180 185 190	1174
tgt tac ctc tgt aaa tcc ctg gtc cca ttt aga gag tat cag tgt cat Cys Tyr Leu Cys Lys Ser Leu Val Pro Phe Arg Glu Tyr Gln Cys His 195 200 205	1222
gtg gac tcc tgt ctc cag ctt gca aag gct gac caa gga gat gga cct Val Asp Ser Cys Leu Gln Leu Ala Lys Ala Asp Gln Gly Asp Gly Pro 210 215 220	1270
gaa ggg agt gga aga gca tgt tca act gtg gag ggg aag tgg cag cag Glu Gly Ser Gly Arg Ala Cys Ser Thr Val Glu Gly Lys Trp Gln Gln 225 230 235 240	1318
agg ctg aag aac cca aag gaa aaa ggc cac agt gaa ggc cga ctc ctt Arg Leu Lys Asn Pro Lys Glu Lys Gly His Ser Glu Gly Arg Leu Leu 245 250 255	1366
agt ttc ttg gaa cag tct gag cac aag act tca gat gca gac atc aag	1414

Ser Phe Leu Glu Gln Ser Glu His Lys Thr Ser Asp Ala Asp Ile Lys	
260 265 270	
tct tca gaa aca gga gcc ttc agg gtg cct tca cca ggg atg gaa gag	1462
Ser Ser Glu Thr Gly Ala Phe Arg Val Pro Ser Pro Gly Met Glu Glu	
275 280 285	
gca ggc tgc agc aga gag atg cag agt tct ttc aca cgt cgt gac tta	1510
Ala Gly Cys Ser Arg Glu Met Gln Ser Ser Phe Thr Arg Arg Asp Leu	
290 295 300	
aat gaa tct ccc gtc aag tct ttt gtt tcc att tca gaa gcc aca gat	1558
Asn Glu Ser Pro Val Lys Ser Phe Val Ser Ile Ser Glu Ala Thr Asp	
305 310 315 320	
tgc tta gtg gac ttt aaa aag caa gtt act gtc cag cca ggt agt cgg	1606
Cys Leu Val Asp Phe Lys Lys Gln Val Thr Val Gln Pro Gly Ser Arg	
325 330 335	
aca cgg acc aaa gct ggc aga gga aga agg aga aaa ttc tga atttcta	1655
Thr Arg Thr Lys Ala Gly Arg Gly Arg Arg Arg Lys Phe *	
340 345 350	
gggtccaaaa gttgacaaaa ccattagtag gaggggtggg ccatgttcat taagccatag	1715
tggtccctag ttcattgttg agcaagtttt agccctgcag ttttcaccac cagcacctac	1775
ccagcattct gggttttatg ttttttatga tctatgcaga caactgtgta ttctgtttta	1835
taacagtttg tttgaattta cttacagtta aaaaatttaa atat	1879

<210> 123
 <211> 2288
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (208)..(663)

<220>
 <221> misc_feature
 <222> (1)...(2288)
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tgttttgcta ggcaaagtta caagtgcact aatgggagct caaatgtgtg tgtgtctctc	120
tgtgtgtttg tgtgtgtgtg tgcactcaag acctctaaca gcctcgaagc ctgggggtggc	180
atcccggcct tgccattagc atgcctc atg cat cat cag atg aca agg aca	231
Met His His Gln Met Thr Arg Thr	

	1	5	
acc ctc atg acg aag caa cat gaa tta ggg ggc ctc ttg gcc ttg gtc			279
Thr Leu Met Thr Lys Gln His Glu Leu Gly Gly Leu Leu Ala Leu Val			
10 15 20			
caa aat tgt caa tca gaa atg aac ata aag gac tcc aga gca gtg gga			327
Gln Asn Cys Gln Ser Glu Met Asn Ile Lys Asp Ser Arg Ala Val Gly			
25 30 35 40			
ctg tct gtc aaa aga ctc tgt ata tct ttt gtg gat gag ttt tgt gag			375
Leu Ser Val Lys Arg Leu Cys Ile Ser Phe Val Asp Glu Phe Cys Glu			
45 50 55			
aga aca gag aga cca ttg tac ctg gca caa ggg ctc ttc atg aaa agg			423
Arg Thr Glu Arg Pro Leu Tyr Leu Ala Gln Gly Leu Phe Met Lys Arg			
60 65 70			
gag act tac tgg gag gtg caa gac agt ggc att tct cct ctc ctc ttg			471
Glu Thr Tyr Trp Glu Val Gln Asp Ser Gly Ile Ser Pro Leu Leu Leu			
75 80 85			
ctg ctc agc aca gcc ctg gat tgc agc ccc gag gct gag acc aga caa			519
Leu Leu Ser Thr Ala Leu Asp Cys Ser Pro Glu Ala Glu Thr Arg Gln			
90 95 100			
agc ccg gga ggc aga aag atg ctc caa gaa cca aca cta tca atg tct			567
Ser Pro Gly Gly Arg Lys Met Leu Gln Glu Pro Thr Leu Ser Met Ser			
105 110 115 120			
ttg caa atc ctc aca gga ttc ctg tgg gtc cag ctt tgg aac tgg gaa			615
Leu Gln Ile Leu Thr Gly Phe Leu Trp Val Gln Leu Trp Asn Trp Glu			
125 130 135			
acc ttt ctt cgg atc cgc act cat tcc act gat gcc agc tgc ccc tga			663
Thr Phe Leu Arg Ile Arg Thr His Ser Thr Asp Ala Ser Cys Pro *			
140 145 150			
aggatgccag tactgtggtg tgtgagtctc agcagccgcc cacacgctcc taactctgct			723
gcatggcaga tgcctaggtg gaaatagcaa aaacaaggcc caggctgggg ccagggccag			783
aggggaaggc cctggattct cactcatgtg agatcttgaa tctctttctt tgttctgttt			843
gtttagttag tatcatctgg taaaatagtt aaaaaacaac aaaaaactct gtatctgttt			903
ctagcatgtg ctgcattgac tctattaatc acatttcaaa ttcaccctac attcctctcc			963
tcttcactag cctctctgaa ggtgtcctgg ccagccctgg agaagcactg gtgtctgcag			1023
caccctcag ttcctgtgcc tcagcccaca ggccactgtg ataatggtct gtttagcact			1083
tctgtattta ttgtaagaat gattataatg aagatacaca ctgtaactac aagaaattat			1143
aaatgttttt cacatcaggc tgttcttttt ttttttttgg aggcgagggt aaagcattac			1203
tatttgcaaa gcactctgta gctccctgtt atggggatag gtaactaatc agaataataa			1263

tgtcactcgc atccacttct tagaacctgg ctccaaagga aaataagctg atagactcaa 1323
 tcactttcct gaggatggag gcctatggca tgtgtggctg caggtcgcga agctgcttaa 1383
 tgggtgctggg aagcctagag gaattaaata aagaccctgg aggaggtggg atcggagctg 1443
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 gatggtctgt actctgctag aacacaggat gcttctgctc tccctgctct ggcactcctgc 1923
 cagggtgtct ggccacgcac aggcattgaag acagccggga agccagagtt cccacgaagc 1983
 actcactcct tggacttgct cccacccac tggggagagc actcctggag caggaaatga 2043
 gcatctctca tctccctgaa ttccacatcc actggctgaa tgatcaggga ggcatagcag 2103
 tgagagccat aggtcggcag agggaaactca ggccctcctt taggatggcc atcacctcat 2163
 ctcaatccag ccaaatcaac catctagagc acacaggccg agagaaatgt aataaaatat 2223
 aacatgagac acgtatgaaa tttaactttt ccggtagcca cactagaaaa aggtaaaaaa 2283
 aaaaa 2288

<210> 124
 <211> 1047
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (95) .. (934)

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 Met Glu Asn Ser Glu Lys
 1 5
 act gaa gtg gtt ctc ctt gct tgt ggt tca ttc aat ccc atc acc aac 160

Thr	Glu	Val	Val	Leu	Leu	Ala	Cys	Gly	Ser	Phe	Asn	Pro	Ile	Thr	Asn		
			10					15					20				
atg	cac	ctc	agg	ttg	ttt	gag	ctg	gcc	aag	gac	tac	atg	aat	gga	aca		208
Met	His	Leu	Arg	Leu	Phe	Glu	Leu	Ala	Lys	Asp	Tyr	Met	Asn	Gly	Thr		
		25					30					35					
gga	agg	tac	aca	gtt	gtc	aaa	ggc	atc	atc	tct	cct	gtt	ggg	gat	gcc		256
Gly	Arg	Tyr	Thr	Val	Val	Lys	Gly	Ile	Ile	Ser	Pro	Val	Gly	Asp	Ala		
		40				45					50						
tac	aag	aag	aaa	gga	ctc	att	cct	gcc	tat	cac	cgg	gtc	atc	atg	gca		304
Tyr	Lys	Lys	Lys	Gly	Leu	Ile	Pro	Ala	Tyr	His	Arg	Val	Ile	Met	Ala		
	55				60					65					70		
gaa	ctt	gct	acc	aag	aat	tct	aaa	tgg	gtg	gaa	gtt	gat	aca	tgg	gaa		352
Glu	Leu	Ala	Thr	Lys	Asn	Ser	Lys	Trp	Val	Glu	Val	Asp	Thr	Trp	Glu		
				75				80						85			
agt	ctt	cag	aag	gag	tgg	aaa	gag	act	ctg	aag	gtg	cta	aga	cac	cat		400
Ser	Leu	Gln	Lys	Glu	Trp	Lys	Glu	Thr	Leu	Lys	Val	Leu	Arg	His	His		
			90					95					100				
caa	gag	aaa	ttg	gag	gct	agt	gac	tgt	gat	cac	cag	cag	aac	tca	cct		448
Gln	Glu	Lys	Leu	Glu	Ala	Ser	Asp	Cys	Asp	His	Gln	Gln	Asn	Ser	Pro		
		105					110					115					
act	cta	gaa	agg	cct	gga	agg	aag	agg	aag	tgg	act	gaa	aca	caa	gat		496
Thr	Leu	Glu	Arg	Pro	Gly	Arg	Lys	Arg	Lys	Trp	Thr	Glu	Thr	Gln	Asp		
	120					125					130						
tct	agt	caa	aag	aaa	tcc	cta	gag	cca	aaa	aca	aaa	gct	gtg	cca	aag		544
Ser	Ser	Gln	Lys	Lys	Ser	Leu	Glu	Pro	Lys	Thr	Lys	Ala	Val	Pro	Lys		
	135				140					145					150		
gtc	aag	ctg	ctg	tgt	ggg	gca	gat	tta	ttg	gag	tcc	ttt	gct	gtt	ccc		592
Val	Lys	Leu	Leu	Cys	Gly	Ala	Asp	Leu	Leu	Glu	Ser	Phe	Ala	Val	Pro		
				155				160						165			
aat	ttg	tgg	aag	agt	gaa	gac	atc	acc	caa	atc	gtg	gcc	aac	tat	ggg		640
Asn	Leu	Trp	Lys	Ser	Glu	Asp	Ile	Thr	Gln	Ile	Val	Ala	Asn	Tyr	Gly		
			170				175						180				
ctc	ata	tgt	gtt	act	cgg	gct	gga	aat	gat	gct	cag	aag	ttt	atc	tat		688
Leu	Ile	Cys	Val	Thr	Arg	Ala	Gly	Asn	Asp	Ala	Gln	Lys	Phe	Ile	Tyr		
		185					190					195					
gaa	tcg	gat	gtg	ctg	tgg	aaa	cac	cgg	agc	aac	att	cac	gtg	gtg	aat		736
Glu	Ser	Asp	Val	Leu	Trp	Lys	His	Arg	Ser	Asn	Ile	His	Val	Val	Asn		
	200					205					210						
gaa	tgg	atc	gct	aat	gac	atc	tca	tcc	aca	aaa	atc	cgg	aga	gcc	ctc		784
Glu	Trp	Ile	Ala	Asn	Asp	Ile	Ser	Ser	Thr	Lys	Ile	Arg	Arg	Ala	Leu		
	215				220					225					230		
aga	agg	ggc	cag	agc	att	cgc	tac	ttg	gta	cca	gat	ctt	gtc	caa	gaa		832
Arg	Arg	Gly	Gln	Ser	Ile	Arg	Tyr	Leu	Val	Pro	Asp	Leu	Val	Gln	Glu		

235	240	245	
tac att gaa aag cat aat ttg tac agc tct gag agt gaa gac agg aat			880
Tyr Ile Glu Lys His Asn Leu Tyr Ser Ser Glu Ser Glu Asp Arg Asn			
250	255	260	
gct ggg gtc atc ctg gcc cct ttg cag aga aac act gca gaa gct aag			928
Ala Gly Val Ile Leu Ala Pro Leu Gln Arg Asn Thr Ala Glu Ala Lys			
265	270	275	
aca tag gaattctaca gcatgatatt tcagacttcc catttgggga tctgaaacaa			984
Thr *			
280			
tctgggagtt aataactggg gaaagaagtt gtgatctgtt gcctaaacta aagcttaaaa			1044
ggt			1047

<210> 125
 <211> 474
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (28) .. (399)

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ctt cgc ggg aag aag aag gag gag ctg ctg aaa cag ctg gac gac ctg		99
Leu Arg Gly Lys Lys Lys Glu Glu Leu Leu Lys Gln Leu Asp Asp Leu		
10 15 20		
aag gtg gag ctg tcc cag ctg cgc gtc gcc aaa gtg aca ggc ggt gcg		147
Lys Val Glu Leu Ser Gln Leu Arg Val Ala Lys Val Thr Gly Gly Ala		
25 30 35 40		
gcc tcc aag ctc tct aag atc cga gtc gtc cgg aaa tcc att gcc cgt		195
Ala Ser Lys Leu Ser Lys Ile Arg Val Val Arg Lys Ser Ile Ala Arg		
45 50 55		
gtt ctc aca gtt att aac cag act cag aaa gaa aac ctc agg aaa ttc		243
Val Leu Thr Val Ile Asn Gln Thr Gln Lys Glu Asn Leu Arg Lys Phe		
60 65 70		
tac aag ggc aag aag tac aag ccc ctg gac ctg cgg cct aag aag aca		291
Tyr Lys Gly Lys Lys Tyr Lys Pro Leu Asp Leu Arg Pro Lys Lys Thr		
75 80 85		
cgt gcc atg cgc cgc cgg ctc aac aag cac gag gag aac ctg aag acc		339
Arg Ala Met Arg Arg Arg Leu Asn Lys His Glu Glu Asn Leu Lys Thr		

90	95	100	
aag aag cag cag cgg aag gag cgg ctg tac ccg ctg cag aag tac aca			387
Lys Lys Gln Gln Arg Lys Glu Arg Leu Tyr Pro Leu Gln Lys Tyr Thr			
105	110	115	120
gtg aac gcc tga acg tcacatgggt tcataaaaga gagctggccg aagagaacaa			442
Val Asn Ala *			
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ccagaacaca ctgctacaag gtcccg	171
atg gcc acg tct ctg gat ttt aaa	
Met Ala Thr Ser Leu Asp Phe Lys	
1 5	
act tat gta gat cag gca tgt aga gct gct gag gag ttt gtc aat att	219
Thr Tyr Val Asp Gln Ala Cys Arg Ala Ala Glu Glu Phe Val Asn Ile	
10 15 20	
tac tat gag aca atg gat aaa aga aga cgg gca cta acc agg ctg tat	267
Tyr Tyr Glu Thr Met Asp Lys Arg Arg Arg Ala Leu Thr Arg Leu Tyr	
25 30 35 40	
ctg gac aag gcc acc tta ata tgg aat gga aat gct gtt tca ggg ctg	315
Leu Asp Lys Ala Thr Leu Ile Trp Asn Gly Asn Ala Val Ser Gly Leu	
45 50 55	
gat gcc cta aat aat ttt ttt gac aca ttg cct tct agt gag ttc cag	363
Asp Ala Leu Asn Asn Phe Phe Asp Thr Leu Pro Ser Ser Glu Phe Gln	
60 65 70	
gtc aat atg tta gat tgc caa cca gtt cat gag caa gca act cag tcc	411
Val Asn Met Leu Asp Cys Gln Pro Val His Glu Gln Ala Thr Gln Ser	
75 80 85	
caa act aca gtt ctt gtt gtg acc agt gga act gtg aag ttt gat gga	459
Gln Thr Thr Val Leu Val Val Thr Ser Gly Thr Val Lys Phe Asp Gly	
90 95 100	

aac aaa caa cat ttc ttc aac cag aac ttc ctg ctg act gct cag tcc	507
Asn Lys Gln His Phe Phe Asn Gln Asn Phe Leu Leu Thr Ala Gln Ser	
105 110 115 120	
act ccc aac aat act gtg tgg aag att gca agt gat tgc ttc cgt ttt	555
Thr Pro Asn Asn Thr Val Trp Lys Ile Ala Ser Asp Cys Phe Arg Phe	
125 130 135	
caa gat tgg tct agt agt taa ag gggcaaaagt ccattctcat ttggtccatt	608
Gln Asp Trp Ser Ser Ser *	
140	
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cactaatgac attcttataa taatattaaa cacatgatct tggtactaac atactcactg	848
tgaaccagc ctattgcaaa aataaaatct ttttataata ttatctatgg gatgtcagca	908
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acacattgcc tgttttcagt taacactggg aatgccattt taatatatgg ctttttcaaa	1028
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tctgtataac ttttaaattg ctggaactac tcgtataagg actagactgt atttttgaca 2528
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aaaaaa 2594

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ttggggcaaag gagaaattca gttttcagta gcatcattgg aagtattatg acttgtgctt 180
aaacttttac cagtgcattc ttttgataaa tagaaatagt aacaaaat atg aat ttt 237
Met Asn Phe
1
aaa tat gtg ggg aga tac ata aag aac att gct tat ttg ttc ttg aaa 285
Lys Tyr Val Gly Arg Tyr Ile Lys Asn Ile Ala Tyr Leu Phe Leu Lys
5 10 15
ata aca gtg att caa ata ttt cat tca gat tta cct atg cct aat gaa 333
Ile Thr Val Ile Gln Ile Phe His Ser Asp Leu Pro Met Pro Asn Glu
20 25 30 35
aaa aat gat gca gaa ctt gat tct cca cct tca aag aaa aaa aga tta 381
Lys Asn Asp Ala Glu Leu Asp Ser Pro Pro Ser Lys Lys Lys Arg Leu
40 45 50

ggt ttt ttc cag act tat gat aca gaa tat tta aaa gtt ggt ttt att Gly Phe Phe Gln Thr Tyr Asp Thr Glu Tyr Leu Lys Val Gly Phe Ile 55 60 65	429
atc tgt cct gga tca aaa gaa agt tca cca agg cca cag tgt gtc att Ile Cys Pro Gly Ser Lys Glu Ser Ser Pro Arg Pro Gln Cys Val Ile 70 75 80	477
tgt gga gag atc tta tcc agt gaa aac atg aag cca gca aat ctt tct Cys Gly Glu Ile Leu Ser Ser Glu Asn Met Lys Pro Ala Asn Leu Ser 85 90 95	525
cat cat ttg aag aca aaa cat tca gaa tta gaa aac aaa cca gta gat His His Leu Lys Thr Lys His Ser Glu Leu Glu Asn Lys Pro Val Asp 100 105 110 115	573
ttt ttt gaa caa aaa tct tta gaa atg gaa tgt caa aat agt tct tta Phe Phe Glu Gln Lys Ser Leu Glu Met Glu Cys Gln Asn Ser Ser Leu 120 125 130	621
aaa aag tgt tta cta gtt gaa aag tca ctt gtg aaa gct tct tat tta Lys Lys Cys Leu Leu Val Glu Lys Ser Leu Val Lys Ala Ser Tyr Leu 135 140 145	669
att gct ttc caa act gct gca agc aag aag cca ttc tcc att gct gaa Ile Ala Phe Gln Thr Ala Ala Ser Lys Lys Pro Phe Ser Ile Ala Glu 150 155 160	717
gaa tta att aaa cca tat tta gta gaa atg tgt tca gaa gtt ttg ggt Glu Leu Ile Lys Pro Tyr Leu Val Glu Met Cys Ser Glu Val Leu Gly 165 170 175	765
tca agt gct gga gac aaa atg aaa act att cca ctt tct aat gtt aca Ser Ser Ala Gly Asp Lys Met Lys Thr Ile Pro Leu Ser Asn Val Thr 180 185 190 195	813
att caa cac agg att gat gaa cta tct gca gac att gaa gac cag ctg Ile Gln His Arg Ile Asp Glu Leu Ser Ala Asp Ile Glu Asp Gln Leu 200 205 210	861
att caa aag gtc aga gag tca aag tgg ttt gcc ctt cag ata gat gag Ile Gln Lys Val Arg Glu Ser Lys Trp Phe Ala Leu Gln Ile Asp Glu 215 220 225	909
tca tca gaa atc tca aat atc aca ctt ctt ttg tgc tat att cgt ttc Ser Ser Glu Ile Ser Asn Ile Thr Leu Leu Leu Cys Tyr Ile Arg Phe 230 235 240	957
att gat tat gat tgt cgt gat gta aaa gaa gaa tta tta ttt tgc att Ile Asp Tyr Asp Cys Arg Asp Val Lys Glu Glu Leu Leu Phe Cys Ile 245 250 255	1005
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aaa tat att gat agt aaa tct ctg aat tgg aaa cat tgt gtt ggt ctc Lys Tyr Ile Asp Ser Lys Ser Leu Asn Trp Lys His Cys Val Gly Leu 280 285 290	1101
tgt acc gat ggg gct gca agc atg act ggc agg tat tct ggt tta aaa Cys Thr Asp Gly Ala Ala Ser Met Thr Gly Arg Tyr Ser Gly Leu Lys 295 300 305	1149
gca aaa att caa gaa gtt gcc atg aat aca gcg gca ttt aca cat tgt Ala Lys Ile Gln Glu Val Ala Met Asn Thr Ala Ala Phe Thr His Cys 310 315 320	1197
ttt att cac cgt gaa cgt tta gtg gca gaa aag ttg tct cca tgt tta Phe Ile His Arg Glu Arg Leu Val Ala Glu Lys Leu Ser Pro Cys Leu 325 330 335	1245
cat aaa att ctt ttg cag tca gca caa att tta agt ttt ata aag agc His Lys Ile Leu Leu Gln Ser Ala Gln Ile Leu Ser Phe Ile Lys Ser 340 345 350 355	1293
aat gca tta aat tca cgt atg tta aca att ttg tgt gaa gag atg gga Asn Ala Leu Asn Ser Arg Met Leu Thr Ile Leu Cys Glu Glu Met Gly 360 365 370	1341
tct gag cat gtg agt tta ccg ctt cat gct gaa gta cgt tgg ata tca Ser Glu His Val Ser Leu Pro Leu His Ala Glu Val Arg Trp Ile Ser 375 380 385	1389
aga ggg aga atg tta aaa aga tta ttt gaa tta cga cat gag att gaa Arg Gly Arg Met Leu Lys Arg Leu Phe Glu Leu Arg His Glu Ile Glu 390 395 400	1437
ata ttt tta agt caa aag cat tca gat ttg gcc aag tat ttt cat gat Ile Phe Leu Ser Gln Lys His Ser Asp Leu Ala Lys Tyr Phe His Asp 405 410 415	1485
gag gaa tgg gtt gga aag ctg gcc tac tta tca gat ata ttt tca ctt Glu Glu Trp Val Gly Lys Leu Ala Tyr Leu Ser Asp Ile Phe Ser Leu 420 425 430 435	1533
ata aat gaa tta aat tta agt ctc caa gga act ttg act act ttc ttc Ile Asn Glu Leu Asn Leu Ser Leu Gln Gly Thr Leu Thr Thr Phe Phe 440 445 450	1581
aat ttg tgt aat aaa att gat gta ttt aag aga aag tta aaa atg tgg Asn Leu Cys Asn Lys Ile Asp Val Phe Lys Arg Lys Leu Lys Met Trp 455 460 465	1629
ttg aag cgc aca caa gag aat gat tat gac atg ttc cct tca ttt tct Leu Lys Arg Thr Gln Glu Asn Asp Tyr Asp Met Phe Pro Ser Phe Ser 470 475 480	1677
gaa ttc tca aat tca tca ggc tta aat atg aca gac atc aca agg att Glu Phe Ser Asn Ser Ser Gly Leu Asn Met Thr Asp Ile Thr Arg Ile 485 490 495	1725
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<222> (97) .. (798)

<400> 128

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Met Pro Cys Arg Arg Glu	
1 5	
gag gaa gag gaa gcc ggc gag gag gcg gag ggg gag gaa gag gag gac	162
Glu Glu Glu Glu Ala Gly Glu Glu Ala Glu Gly Glu Glu Glu Glu Asp	
10 15 20	
gac agc ttc ctc ctg ctg cag cag tcg gtg acg ctg ggc agc tcg ggc	210
Asp Ser Phe Leu Leu Leu Gln Gln Ser Val Thr Leu Gly Ser Ser Gly	
25 30 35	
gag gtg gac cgg ctg gtg gcc cag atc ggc gag acg ctg cag ctg gac	258
Glu Val Asp Arg Leu Val Ala Gln Ile Gly Glu Thr Leu Gln Leu Asp	
40 45 50	
gcg gcg cag gac agc ccg gcc tcg ccg tgc gcg ccc ccg ggg gtg ccg	306
Ala Ala Gln Asp Ser Pro Ala Ser Pro Cys Ala Pro Pro Gly Val Pro	
55 60 65 70	
ctg cgg gcc ccg ggg ccc ctg gct gcg gcg gtg ccg acg gac aag gcc	354
Leu Arg Ala Pro Gly Pro Leu Ala Ala Ala Val Pro Thr Asp Lys Ala	
75 80 85	
cgg ccc ccg gcg gtg ccg ctg ctg ctg ccg ccc gct tcg gct gag acg	402
Arg Pro Pro Ala Val Pro Leu Leu Leu Pro Pro Ala Ser Ala Glu Thr	
90 95 100	
gtg ggc ccg gcg ccc tct ggg gcc ctg cgc tgc gcc cta ggg gac cgc	450
Val Gly Pro Ala Pro Ser Gly Ala Leu Arg Cys Ala Leu Gly Asp Arg	
105 110 115	
ggc cgc gtg cgc gga cgc gct gcg ccc tac tgc gtg gcg gag gtc gcc	498
Gly Arg Val Arg Gly Arg Ala Ala Pro Tyr Cys Val Ala Glu Val Ala	
120 125 130	
gca ggc ccc agc gcg ctg ccg ggg ccg tgc cgg cga gga tgg ctc agg	546
Ala Gly Pro Ser Ala Leu Pro Gly Pro Cys Arg Arg Gly Trp Leu Arg	
135 140 145 150	
gac gcg gtc acc tcc cgc cgc ttg cag cag cgc cga tgg acc caa gcc	594
Asp Ala Val Thr Ser Arg Arg Leu Gln Gln Arg Arg Trp Thr Gln Ala	
155 160 165	
ggg gca cgc gcc ggc gac gac gac ccg cat cgg ctc ctc cag cag ctc	642
Gly Ala Arg Ala Gly Asp Asp Asp Pro His Arg Leu Leu Gln Gln Leu	
170 175 180	
gtg ctc tcg gga aac ctc atc aag gaa gcc gtg cgg aga ctc caa cga	690
Val Leu Ser Gly Asn Leu Ile Lys Glu Ala Val Arg Arg Leu Gln Arg	
185 190 195	

gcc gtc gcc gcg gtt gca gcc acg ggc ccc gca agc gcc cct ggg ccc Ala Val Ala Ala Val Ala Ala Thr Gly Pro Ala Ser Ala Pro Gly Pro 200 205 210	738
ggg gga ggc cgc agc gga cct gac cgc att gcc ctg cag ccc tca ggc Gly Gly Gly Arg Ser Gly Pro Asp Arg Ile Ala Leu Gln Pro Ser Gly 215 220 225 230	786
tcc ttg ctc tga cgc aggcctcctg gaggaggaag tggaggccgc tgcgtagacc Ser Leu Leu *	841
caacagcgtc cagttcctac taactctgag ctgaagccga cgtcgccagc ctgggagcga	901
ccacttttggc tgcggggagg cgcgtgggga gagatctcaa ccagagaagt taccagccgc	961
ggcgaggccg tcggagaaaa cttaagcgtg gagaaatgta tgcgccaggg tgcttcctg	1021
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<400> 129

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Met Ala Gly Ser Gly Cys Ala Trp Gly Ala Glu	
1 5 10	
ccg ccg cgt ttt ctg gag gcc ttc ggg cgg ctg tgg cag gta cag agc	159
Pro Pro Arg Phe Leu Glu Ala Phe Gly Arg Leu Trp Gln Val Gln Ser	
15 20 25	
cgt ctg ggt agc ggc tcc tcc gcc tcg gtg tat cgg gtt cgc tgc tgc	207
Arg Leu Gly Ser Gly Ser Ser Ala Ser Val Tyr Arg Val Arg Cys Cys	
30 35 40	
ggc aac cct ggc tcg ccc ccc ggc gcc ctc aag cag ttc ttg ccg cca	255
Gly Asn Pro Gly Ser Pro Pro Gly Ala Leu Lys Gln Phe Leu Pro Pro	
45 50 55	
gga acc acc ggg gct gcg gcc tct gcc gcc gag tat ggt ttc cgc aaa	303
Gly Thr Thr Gly Ala Ala Ala Ser Ala Ala Glu Tyr Gly Phe Arg Lys	
60 65 70 75	
gag agg gcg gcg ctg gaa cag ttg cag ggt cac aga aac atc gtg act	351
Glu Arg Ala Ala Leu Glu Gln Leu Gln Gly His Arg Asn Ile Val Thr	
80 85 90	
ttg tat gga gtg ttt aca atc cac ttt tct cca aat gtg cca tca cgc	399
Leu Tyr Gly Val Phe Thr Ile His Phe Ser Pro Asn Val Pro Ser Arg	
95 100 105	
tgt ctg ttg ctt gaa ctc ctg gat gtc agt gtt tcg gaa ttg ctc tta	447
Cys Leu Leu Leu Glu Leu Leu Asp Val Ser Val Ser Glu Leu Leu Leu	
110 115 120	
tat tcc agt cac cag ggt tgt tcc atg tgg atg ata cag cat tgc gcc	495
Tyr Ser Ser His Gln Gly Cys Ser Met Trp Met Ile Gln His Cys Ala	
125 130 135	
cga gat gtt ttg gag gcc ctt gct ttt ctt cat cat gag ggc tat gtc	543
Arg Asp Val Leu Glu Ala Leu Ala Phe Leu His His Glu Gly Tyr Val	
140 145 150 155	
cat gcg gac ctc aaa cca cgt aac ata ttg tgg agt gca gag aat gaa	591

380	385	390	395	
ggg aag ttt gtt gtg gct aca ttc tac ccg ctg agt gcc tac aag agg				1311
Gly Lys Phe Val Val Ala Thr Phe Tyr Pro Leu Ser Ala Tyr Lys Arg				
	400	405	410	
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Gly Tyr Leu Tyr Gln Thr Leu Leu *				
	415	420		
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ttcaagacca gcctgggcaa cacagcaaga ccccatatc tctacaaaa aaacaaaaca	180
aaacaaaaca aacaaacaaa aaaaacagcc ggttgcggtg gcacatgctt gcagtcctcg	240
ttactcaaga agcagaagca agaggattgc ttgagcccaa cagtgcttgc aaaagacaaa	300
gaacgcctgc aagcc atg atg acc cac ctg cat gtg aag tct aca gaa ccc	351
Met Met Thr His Leu His Val Lys Ser Thr Glu Pro	

	1	5	10	
aaa gcc gcc cct cag ccc ttg aat ctg gta tca agt gtc act ctc tcc				399
Lys Ala Ala Pro Gln Pro Leu Asn Leu Val Ser Ser Val Thr Leu Ser				
	15	20	25	
aag tcc gca tcg gag gct tct cca cag agc tta cct cat act cca acg				447
Lys Ser Ala Ser Glu Ala Ser Pro Gln Ser Leu Pro His Thr Pro Thr				
	30	35	40	
acc cca acc gcc ccc ctg act ccc gtc acc caa ggc ccc tct gtc atc				495
Thr Pro Thr Ala Pro Leu Thr Pro Val Thr Gln Gly Pro Ser Val Ile				
	45	50	55	60
aca acc acc agc atg cac acg gtg gga ccc atc cgc agg cgg tac tca				543
Thr Thr Thr Ser Met His Thr Val Gly Pro Ile Arg Arg Arg Tyr Ser				
	65	70	75	
gac aaa tac aac gtg ccc att tcg tca gca gat att gcg cag aac caa				591
Asp Lys Tyr Asn Val Pro Ile Ser Ser Ala Asp Ile Ala Gln Asn Gln				
	80	85	90	
gaa ttt tat aag aac gca gaa gtt aga cca cca ttt aca tat gca tct				639
Glu Phe Tyr Lys Asn Ala Glu Val Arg Pro Pro Phe Thr Tyr Ala Ser				
	95	100	105	
tta att agg cag gcc att ctc gaa tct cca gaa aag cag cta aca cta				687
Leu Ile Arg Gln Ala Ile Leu Glu Ser Pro Glu Lys Gln Leu Thr Leu				
	110	115	120	
aat gag atc tat aac tgg ttc aca cga atg ttt gct tac ttc cga cgc				735
Asn Glu Ile Tyr Asn Trp Phe Thr Arg Met Phe Ala Tyr Phe Arg Arg				
	125	130	135	140
aac gcg gcc acg tgg aag aat gca gtg cgt cat aat ctt agt ctt cac				783
Asn Ala Ala Thr Trp Lys Asn Ala Val Arg His Asn Leu Ser Leu His				
	145	150	155	
aag tgt ttt gtg cga gta gaa aac gtt aaa ggg gca gta tgg aca gtg				831
Lys Cys Phe Val Arg Val Glu Asn Val Lys Gly Ala Val Trp Thr Val				
	160	165	170	
gat gaa gta gaa ttc caa aaa cga agg cca caa aag atc agt ggt aac				879
Asp Glu Val Glu Phe Gln Lys Arg Arg Pro Gln Lys Ile Ser Gly Asn				
	175	180	185	
cct tcc ctt att aaa aac atg cag agc agc cac gcc tac tgc aca cct				927
Pro Ser Leu Ile Lys Asn Met Gln Ser Ser His Ala Tyr Cys Thr Pro				
	190	195	200	
ctc aat gca gct tta cag gct tca atg gct gag aat agt ata cct cta				975
Leu Asn Ala Ala Leu Gln Ala Ser Met Ala Glu Asn Ser Ile Pro Leu				
	205	210	215	220
tac act acc gct tcc atg gga aat ccc act ctg ggc aac tta gcc agc				1023
Tyr Thr Thr Ala Ser Met Gly Asn Pro Thr Leu Gly Asn Leu Ala Ser				
	225	230	235	

gca ata cgg gaa gag ctg aac ggg gca atg gag cat acc aac agc aac 1071
Ala Ile Arg Glu Glu Leu Asn Gly Ala Met Glu His Thr Asn Ser Asn
240 245 250

gag agt gac agc agt cca ggc aga tct cct atg caa gcc gtg cat cct 1119
Glu Ser Asp Ser Ser Pro Gly Arg Ser Pro Met Gln Ala Val His Pro
255 260 265

gta cac gtc aaa gaa gag ccc ctc gat cca gag gaa gct gaa ggg ccc 1167
Val His Val Lys Glu Glu Pro Leu Asp Pro Glu Glu Ala Glu Gly Pro
270 275 280

ctg tcc tta gtg aca aca gcc aac cac agt cca gat ttt gac cat gac 1215
Leu Ser Leu Val Thr Thr Ala Asn His Ser Pro Asp Phe Asp His Asp
285 290 295 300

aga gat tac gaa gat gaa cca gta aac gag gac atg gag tga ctatcgg 1264
Arg Asp Tyr Glu Asp Glu Pro Val Asn Glu Asp Met Glu *
305 310

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<210> 131
<211> 847
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (91)..(657)

<400> 131
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aggccttggc tccttgaact tttggccgcc atg tgc ttc ccg aag gtc ctc 111
Met Cys Phe Pro Lys Val Leu
1 5

tct gat gac atg aag aag ctg aag gcc cga atg cac cag gcc ata gaa 159
Ser Asp Asp Met Lys Lys Leu Lys Ala Arg Met His Gln Ala Ile Glu
10 15 20

aga ttt tat gat aaa atg caa aat gca gaa tca gga cgt gga cag gtg 207
Arg Phe Tyr Asp Lys Met Gln Asn Ala Glu Ser Gly Arg Gly Gln Val
25 30 35

atg tcg agc ctg gca gag ctg gag gac gac ttc aaa gag ggc tac ctg 255
Met Ser Ser Leu Ala Glu Leu Glu Asp Asp Phe Lys Glu Gly Tyr Leu
40 45 50 55

gag aca gtg gcg gct tat tat gag gag cag cac cca gag ctc act cct 303
Glu Thr Val Ala Ala Tyr Tyr Glu Glu Gln His Pro Glu Leu Thr Pro
60 65 70

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cta ctt gaa aaa gaa aga gat gga tta cgg tgc cga ggc aac aga tcc      351
Leu Leu Glu Lys Glu Arg Asp Gly Leu Arg Cys Arg Gly Asn Arg Ser
              75                      80                      85

cct gtc ccg gat gtt gag gat ccc gca acc gag gag cct ggg gag agc      399
Pro Val Pro Asp Val Glu Asp Pro Ala Thr Glu Glu Pro Gly Glu Ser
              90                      95                      100

ttt tgt gac aag gtc atg aga tgg ttc cag gcc atg ctg cag cgg ctg      447
Phe Cys Asp Lys Val Met Arg Trp Phe Gln Ala Met Leu Gln Arg Leu
              105                      110                      115

cag acc tgg tgg cac ggg gtt ctg gcc tgg gtg aag gag aag gtg gtg      495
Gln Thr Trp Trp His Gly Val Leu Ala Trp Val Lys Glu Lys Val Val
              120                      125                      130                      135

gcc ctg gtc cat gca gtg cag gcc ctc tgg aaa cag ttc cag agt ttc      543
Ala Leu Val His Ala Val Gln Ala Leu Trp Lys Gln Phe Gln Ser Phe
              140                      145                      150

tgc tgc tct ctg tca gag ctc ttc atg tcc tct ttc cag tcc tac gga      591
Cys Cys Ser Leu Ser Glu Leu Phe Met Ser Ser Phe Gln Ser Tyr Gly
              155                      160                      165

gcc cca cgg ggg gac aag gag gag ctg aca ccc cag aag tgc tct gaa      639
Ala Pro Arg Gly Asp Lys Glu Glu Leu Thr Pro Gln Lys Cys Ser Glu
              170                      175                      180

ccc caa tcc tca aaa tga agatac tgacaccacc ttgcccctcc ccgtcaccgc      693
Pro Gln Ser Ser Lys *
              185

gcacccaccc tgacccctcc ctcagctgtc ctgtgccccg ccctctcccg cacactcagt      753

ccccctgcct ggcgttctct cgcagctct gacctggctg tgtcgccctg gcactttaat      813

aaaacctgct tatacttccc tgaaaaaaaa aaaa                                847

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<210> 132
<211> 526
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (33)..(419)

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<400> 132
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                               Met Pro Lys Ser Lys Glu Leu
                               1                      5

gtt tct tca agc tct tct ggc agt gat tct gac agt gag gtt gac aaa      101

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Val	Ser	Ser	Ser	Ser	Ser	Gly	Ser	Asp	Ser	Asp	Ser	Glu	Val	Asp	Lys		
	10						15					20					
aag	tta	aag	agg	aaa	aag	caa	gtt	gct	cca	gaa	aaa	cct	gta	aag	aaa		149
Lys	Leu	Lys	Arg	Lys	Lys	Gln	Val	Ala	Pro	Glu	Lys	Pro	Val	Lys	Lys		
	25					30					35						
caa	aag	aca	ggt	gag	act	tcg	aga	gcc	ctg	tca	tct	tct	aaa	cag	agc		197
Gln	Lys	Thr	Gly	Glu	Thr	Ser	Arg	Ala	Leu	Ser	Ser	Ser	Lys	Gln	Ser		
	40				45					50					55		
agc	agc	agc	aga	gat	gat	aac	atg	ttt	cag	att	ggg	aaa	atg	agg	tac		245
Ser	Ser	Ser	Arg	Asp	Asp	Asn	Met	Phe	Gln	Ile	Gly	Lys	Met	Arg	Tyr		
				60					65					70			
gtt	agt	gtt	cgc	gat	ttt	aaa	ggc	aaa	gtg	cta	att	gat	att	aga	gaa		293
Val	Ser	Val	Arg	Asp	Phe	Lys	Gly	Lys	Val	Leu	Ile	Asp	Ile	Arg	Glu		
			75				80						85				
tat	tgg	atg	gat	cct	gaa	ggt	gaa	atg	aaa	cca	gga	aga	aaa	ggt	att		341
Tyr	Trp	Met	Asp	Pro	Glu	Gly	Glu	Met	Lys	Pro	Gly	Arg	Lys	Gly	Ile		
		90					95					100					
tct	tta	aat	cca	gaa	caa	tgg	atc	cag	tcc	agc	aga	aaa	gat	atg	atg		389
Ser	Leu	Asn	Pro	Glu	Gln	Trp	Ile	Gln	Ser	Ser	Arg	Lys	Asp	Met	Met		
	105					110						115					
aca	ttg	atg	aag	cac	gtg	agc	ggt	ctg	taa	t	aatg	cgagcc	agatta	aattt			440
Thr	Leu	Met	Lys	His	Val	Ser	Gly	Leu	*								
	120				125												
atcctgtact	gtagatttg	gggtaatctg	tcttatcaca	aaggatgttg	acttctagat												500
gttctccaga	ttatgtatat	tgtgat															526

<210> 133
 <211> 1884
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (157)..(864)

<400> 133																	
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actttttatt	ctactatgta	tatgtatgga	atagtattaa	taaatgaact	agggaaggat												120
gtaataaatt	agacatctct	tcattttaga	gagaag	atg	gaa	aca	aca	ttg	ctt								174
				Met	Glu	Thr	Thr	Leu	Leu								
				1				5									
ttc	ttt	tct	caa	ata	aat	atg	tgt	gaa	tca	aaa	gaa	aaa	act	ttt	ttc		222

tacatctgct tctaacatat cgcattgttta tggtaagatt tgggtcccatc ctttaaactg 960
 aaatatgtca tgtgaaatta ttttaaaaat gtaaaaacaa aactttctgc taacaaaata 1020
 catacagtat ctgccagtat attctgtaaa accttctatt tgatgtcatt ccatttataa 1080
 tcagaaaaaa aacttatttc ttaatcaaaa ggcagtacaa aaaaagtaat aatgttttat 1140
 aagattgtag agttaagtaa aagttaagct tttgcaaagt tgtcaaaagt tcaaacaaaa 1200
 gtctagttgg gattttttac caaagcagca taatatgtgt tatataaaca taataatact 1260
 cagatatcca aatgttcaga tagcattttt cataatgaat gttctctttt ttttggaat 1320
 agtgtagaag tgatctgggt cttacaatgg gagatgaaga acatttatta ttgggttact 1380
 actaaccttg tccaagaat agtaatatca cctctagtta taagccagca acaggaactt 1440
 ttgtgaagac acattcatct ctacagaact tcagattaaa tataatctag attaatact 1500
 gagaataaga tccacatttg aactcattcc taagtgaaca tggacgtacc cagttatata 1560
 aagtacttct gttggtcaca gaaacatgac cagattttgc atatctccag gtaggggaact 1620
 aagtagacta ccttatcacc ggctaagaaa acttgctact aaactattag gccatcaatg 1680
 gcttgaataa aaaccagaga aggtttttcc caggacgtct catgtttggc cctttagaat 1740
 tggggtagaa atcagaaatg agatgagggg aagaagcaag gagtctaagg ccctagcgat 1800
 ttgggcatct gccacattgg ttcatttca gaaagtgtta tctcattgat tatattcttg 1860
 ttaagcaatc tccttaagta atta 1884

<210> 134
 <211> 1601
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (868)..(1098)

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 ctttacacat gtttgcatat aatctccaaa ttccaaagtt aaggccaagg gatggattgt 120
 agctatggaa acagatgata tggaagacat ccaacaagga ggaaaagcac acgcacgcct 180
 caccctgcc tcattctctgc ccagggtgt cctgacagca cagacgttc agggagacag 240

gcctggggac agtcatgtca tcacccttgc aacaaccacc caaaggaaaa gagagcgctg	300
aacagtttag gaaagggctc gcgtctaaga catcaagcga catacagaga tgtgcaaaac	360
ttggtgagaa ttaaaattga cctttgggag agggtagggg caggatgttt tatgacactg	420
tagaaaagac aggaggaacc cgctgcatg gagattgggg ggagctggaa gcaagcagcc	480
aacaggacag agttccagaa ctcatgcaga tggggaagag gtgacagccc ttccccactg	540
gcctcccccg tggaggtgga gtagacagat cccgggaaag gcaggaaaag ggccttgctt	600
tctttccctg tttcctaagc cgtggtcacc ctagcctatg aagctggaag ctatatctct	660
tccaatccca atttaccatt cctgtaaaca ggcccattca gggctgcctg agcaaattggg	720
gacttgccga ggcagctgca actagacttg ggctaagccg tctgggtcta ctcaagaatt	780
cgagtctgaa gatgaccaag cttgagttat tcaactgaga gtgaggtgtc aaggcggaag	840
cgactgtccc cagggaaggg ctgtgag	891
atg gat ggg cgt gag tca gct ttt	
Met Asp Gly Arg Glu Ser Ala Phe	
1 5	
cca aaa ctc aag tac ctg gga cag gac aac tcg cta gca gct cag tca	939
Pro Lys Leu Lys Tyr Leu Gly Gln Asp Asn Ser Leu Ala Ala Gln Ser	
10 15 20	
cct ccg tgg cgg aca cag ata agg atg tta aga cca gaa aac cag aga	987
Pro Pro Trp Arg Thr Gln Ile Arg Met Leu Arg Pro Glu Asn Gln Arg	
25 30 35 40	
cta ggg ccc cgt cct cag ccc tca cag cat gac aca gat gcc tcc ctc	1035
Leu Gly Pro Arg Pro Gln Pro Ser Gln His Asp Thr Asp Ala Ser Leu	
45 50 55	
gga gag cag ggt ctc tcg gca tcc agc ggc gtg gtc tgc att ctg ctc	1083
Gly Glu Gln Gly Leu Ser Ala Ser Ser Gly Val Val Cys Ile Leu Leu	
60 65 70	
tac ctc atg ctc tag gccccatgcc atcgtctcgg ccctagaccg tgaaaactgc	1138
Tyr Leu Met Leu *	
75	
cagtcacccg ggacctgctc ctaggggctg gcctgcacag ccggatggcc tgtgggcggg	1198
gtggaagtgc ccactccac tccagatggg cctgctggcc actgaccac ctgtgctgag	1258
ggagagcgcc agcctccagc ttaggtacac ggcgcccacc ccagctcca cgggaaaccc	1318
ataaccacca gaaacatctc aatcaagaga cgggtgtgtg ggggtggcact aactgcacag	1378
agaccactcc acgccggctg aggtagaaaag aaggcaactg aacacacagc agctagggca	1438
ggggcagggg ggggctgcag gtggtgtgaa gaagagccca gctgtcatct aaggcaaact	1498
gccccactg aggaccagcg ccaggcccta cctcccccaa cctgtgcgca tctcaatcac	1558

agcagacact gtgacggcca caggcggacg cgtgggtcgt ccc

1601

<210> 135
<211> 941
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (194)..(820)

<400> 135

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gaaggagaca	tcgaagcagg	gcgagggcgca	gagggcggtg	cggactcatg	ccccagtcgg	120
cagtgcgggg	tcccaagccc	tgcagtgcta	cagctttgag	cacacctact	ttggcccctt	180
tgacctcagg	gcc	atg aag ctg ccc agc atc tcc tgt cct cat gag tgc				229
		Met Lys Leu Pro Ser Ile Ser Cys Pro His Glu Cys				
		1 5 10				
ttt gag gct atc ctg tct ctg gac acc ggg tat cgc gcg ccg gtg acc						277
Phe Glu Ala Ile Leu Ser Leu Asp Thr Gly Tyr Arg Ala Pro Val Thr						
15 20 25						
ctg gtg cgg aag ggc tgc tgg acc ggg cct cct gcg ggc cag acg caa						325
Leu Val Arg Lys Gly Cys Trp Thr Gly Pro Pro Ala Gly Gln Thr Gln						
30 35 40						
tcg aac ccg gac gcg ctg ccg cca gac tac tcg gtg gtg cgc ggc tgc						373
Ser Asn Pro Asp Ala Leu Pro Pro Asp Tyr Ser Val Val Arg Gly Cys						
45 50 55 60						
aca act gac aaa tgc aac gcc cac ctc atg act cat gac gcc ctc ccc						421
Thr Thr Asp Lys Cys Asn Ala His Leu Met Thr His Asp Ala Leu Pro						
65 70 75						
aac ctg agc caa gca ccc gac ccg ccg acg ctc agc ggc gcc gag tgc						469
Asn Leu Ser Gln Ala Pro Asp Pro Pro Thr Leu Ser Gly Ala Glu Cys						
80 85 90						
tac gcc tgt atc ggg gtc cac cag gat gac tgc gct atc ggc agg tcc						517
Tyr Ala Cys Ile Gly Val His Gln Asp Asp Cys Ala Ile Gly Arg Ser						
95 100 105						
cga cga gtc cag tgt cac cag gac cag acc gcc tgc ttc cag ggc aat						565
Arg Arg Val Gln Cys His Gln Asp Gln Thr Ala Cys Phe Gln Gly Asn						
110 115 120						
ggc aga atg aca gtt ggc aat ttc tca gtc cct gtg tac atc aga acc						613
Gly Arg Met Thr Val Gly Asn Phe Ser Val Pro Val Tyr Ile Arg Thr						
125 130 135 140						

tgc cac cgg ccc tcc tgc acc acc gag ggc acc acc agc ccc tgg aca	661
Cys His Arg Pro Ser Cys Thr Thr Glu Gly Thr Thr Ser Pro Trp Thr	
145 150 155	
gcc atc gac ctc cag ggc tcc tgc tgt gag ggg tac ctc tgc aac agg	709
Ala Ile Asp Leu Gln Gly Ser Cys Cys Glu Gly Tyr Leu Cys Asn Arg	
160 165 170	
aaa tcc atg acc cag ccc ttc acc agt gct tca gcc acc acc cct ccc	757
Lys Ser Met Thr Gln Pro Phe Thr Ser Ala Ser Ala Thr Thr Pro Pro	
175 180 185	
cga gca cta cag gtc ctg gcc ctg ctc ctc cca gtc ctc ctg ctg gtg	805
Arg Ala Leu Gln Val Leu Ala Leu Leu Leu Pro Val Leu Leu Leu Val	
190 195 200	
ggg ctc tca gca tag accgcccctc caggatgctg gggacagggc tcacacacct	860
Gly Leu Ser Ala *	
205	
cattcttgct gcttcagccc ctatcacata gctcactgga aaatgatgtt aaagtaagaa	920
ttgcaataaa aaaaaaaaaa a	941

<210> 136
 <211> 534
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (120)..(335)

<400> 136	
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ggcgcttctg catctgtggg ccgagcattc ttcaggtcat ctgaaccttc tgagaaaac	119
atg gtc aac gtc ttg aaa gga gtg ctt ata gaa tgt gat cct gcc atg	167
Met Val Asn Val Leu Lys Gly Val Leu Ile Glu Cys Asp Pro Ala Met	
1 5 10 15	
aag cag ttt ctg ctg tac ttg gat gag tcc aat gcc ctg ggg aag aag	215
Lys Gln Phe Leu Leu Tyr Leu Asp Glu Ser Asn Ala Leu Gly Lys Lys	
20 25 30	
ttc atc att caa gac att gat gac act cac gtc ttt gta ata gca gaa	263
Phe Ile Ile Gln Asp Ile Asp Asp Thr His Val Phe Val Ile Ala Glu	
35 40 45	
ttg gtt aat gtc ctc cag gag cga gtg ggt gaa tta atg gac caa aat	311
Leu Val Asn Val Leu Gln Glu Arg Val Gly Glu Leu Met Asp Gln Asn	
50 55 60	

<210> 138
<211> 691
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (197)..(691)

<400> 138

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gcatgggtga ctaagggctt cctgtggact ggcaaatgag agcaaacacc tgtggcttga      120
gcactgcccc ctaaagcagg ccttacagat ctcttacact cgtgggtggga agagtctagt      180
gtgaaactgg ggtgga      atg ggg tgt cca cgt atg ttc cct ttt gcc tta      229
                        Met Gly Cys Pro Arg Met Phe Pro Phe Ala Leu
                        1          5          10

cta tat gtt ctg tca gtt tct ttc agg aaa atc ttc atc tta caa ctt      277
Leu Tyr Val Leu Ser Val Ser Phe Arg Lys Ile Phe Ile Leu Gln Leu
                        15          20          25

gta ggg ctg gtg tta act tac gac ttc act aac tgt gac ttt gag aag      325
Val Gly Leu Val Leu Thr Tyr Asp Phe Thr Asn Cys Asp Phe Glu Lys
                        30          35          40

att aaa gca gcc tat ctc agt act att tct aaa gac ctg att aca tat      373
Ile Lys Ala Ala Tyr Leu Ser Thr Ile Ser Lys Asp Leu Ile Thr Tyr
                        45          50          55

atg agt ggg acc aaa agt acc gag ttc aac aac acc gtc tct tgt agc      421
Met Ser Gly Thr Lys Ser Thr Glu Phe Asn Asn Thr Val Ser Cys Ser
                        60          65          70          75

aat cgg cca cat tgc ctt act gaa atc cag agc cta acc ttc aat ccc      469
Asn Arg Pro His Cys Leu Thr Glu Ile Gln Ser Leu Thr Phe Asn Pro
                        80          85          90

acc gcc ggc tgc gcg tcg ctc gcc aaa gaa atg ttc gcc atg aaa act      517
Thr Ala Gly Cys Ala Ser Leu Ala Lys Glu Met Phe Ala Met Lys Thr
                        95          100          105

aag gct gcc tta gct atc tgg tgc cca ggc tat tcg gaa act cag ata      565
Lys Ala Ala Leu Ala Ile Trp Cys Pro Gly Tyr Ser Glu Thr Gln Ile
                        110          115          120

aat gct act cag gca atg aag aag agg aga aaa agg aaa gtc aca acc      613
Asn Ala Thr Gln Ala Met Lys Lys Arg Arg Lys Arg Lys Val Thr Thr
                        125          130          135

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aat aaa tgt ctg gaa caa gtg tca caa tta caa gga ttg tgg cgt cgc 661
 Asn Lys Cys Leu Glu Gln Val Ser Gln Leu Gln Gly Leu Trp Arg Arg
 140 145 150 155

ttc aat cga cct tta ctg aaa caa cag taa 691
 Phe Asn Arg Pro Leu Leu Lys Gln Gln *
 160 165

<210> 139
 <211> 924
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (172)..(696)

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 gctgttttcgg ttttctgggc tcctcgcccc ttttctcccc tgttgcagct gggagcggac 120
 gaagcgcgaa gctgggattt tttactgtct cctgaagaat ttaacacaaa c atg gat 177
 Met Asp
 1
 atc aga cca aat cat aca att tat atc aac aat atg aat gac aaa att 225
 Ile Arg Pro Asn His Thr Ile Tyr Ile Asn Asn Met Asn Asp Lys Ile
 5 10 15
 aaa aag gaa gaa ttg aag aga tcc cta tat gcc ctg ttt tct cag ttt 273
 Lys Lys Glu Glu Leu Lys Arg Ser Leu Tyr Ala Leu Phe Ser Gln Phe
 20 25 30
 ggt cat gtg gtg gac att gtg gct tta aag acc atg aag atg agg ggg 321
 Gly His Val Val Asp Ile Val Ala Leu Lys Thr Met Lys Met Arg Gly
 35 40 45 50
 cag gcc ttt gtc ata ttt aag gaa ctg ggc tca tcc aca aat gcc ttg 369
 Gln Ala Phe Val Ile Phe Lys Glu Leu Gly Ser Ser Thr Asn Ala Leu
 55 60 65
 aga cag cta caa gga ttt cca ttt tat ggt aaa cca atg cga ata cag 417
 Arg Gln Leu Gln Gly Phe Pro Phe Tyr Gly Lys Pro Met Arg Ile Gln
 70 75 80
 tat gca aaa aca gat tcg gat ata ata tca aaa atg cgt gga act ttt 465
 Tyr Ala Lys Thr Asp Ser Asp Ile Ile Ser Lys Met Arg Gly Thr Phe
 85 90 95
 gct gac aaa gaa aag aaa aaa gaa aag aaa aaa gcc aaa act gtg gaa 513
 Ala Asp Lys Glu Lys Lys Lys Glu Lys Lys Lys Ala Lys Thr Val Glu
 100 105 110

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cag act gca aca acc aca aac aaa aag cct ggc ttc aag gaa gta cgt      561
Gln Thr Ala Thr Thr Thr Asn Lys Lys Pro Gly Phe Lys Glu Val Arg
115                      120                      125                      130

ctg gta cca ggg agg cat gac att gct ttt gtt gaa ttt gaa aat gat      609
Leu Val Pro Gly Arg His Asp Ile Ala Phe Val Glu Phe Glu Asn Asp
                      135                      140                      145

ggg cag gct gga gct gcc agg gat gct tta cag gga ttt aag atc aca      657
Gly Gln Ala Gly Ala Ala Arg Asp Ala Leu Gln Gly Phe Lys Ile Thr
                      150                      155                      160

ccg tcc cat gct atg aag atc acc tat gcc aag aaa taa catttgggat      706
Pro Ser His Ala Met Lys Ile Thr Tyr Ala Lys Lys *
                      165                      170                      175

agtcgtcttt aaaagacttg gtgttattta cagtgtttgt tttgataaca tttggctggg      766

tcattttaat agttagagat gaggaggagt aaaagtgaat tttttgtgaa ggacttaa      826

tatccagtgt ttcttttagcc ttggtgaact atgaaatagc aaggccttaa ttttgtacaa      886

taaactttta tttgtattct gtgtaaaaaa aaaaaaaa      924

<210> 140
<211> 1773
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (141)..(1667)

<400> 140
tccggatcct gttagacacc ggcgggcgcg agccgttgca gttctctttg ggtgatcgct      60

ccttccctct tcaacggatc cctccccgcc tccatcctcg ttctgtggga gagaccagcc      120

ttctggtgct gcagtcagga      atg gag ctt gac agc gct ctg gaa gcc cca      170
                        Met Glu Leu Asp Ser Ala Leu Glu Ala Pro
                        1                      5                      10

tcg cag gaa gac tct aat ttg tcc gag gag ttg tct cac tcc gcc ttt      218
Ser Gln Glu Asp Ser Asn Leu Ser Glu Glu Leu Ser His Ser Ala Phe
                        15                      20                      25

gga cag gcc ttc tcc aag att tta cac tgt ctt gcc cgc ccg gag gca      266
Gly Gln Ala Phe Ser Lys Ile Leu His Cys Leu Ala Arg Pro Glu Ala
                        30                      35                      40

cga cga ggc aat gta aaa gat gca gtt ctt aaa gac ctc ggt gat cta      314
Arg Arg Gly Asn Val Lys Asp Ala Val Leu Lys Asp Leu Gly Asp Leu
                        45                      50                      55

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ata gaa gcc aca gaa ttt gat agg tta ttt gag ggg act ggt gca cgg Ile Glu Ala Thr Glu Phe Asp Arg Leu Phe Glu Gly Thr Gly Ala Arg 60 65 70	362
ctc cgc gga atg ccg gag aca ctg ggg cag gta gca aaa gcc ctg gag Leu Arg Gly Met Pro Glu Thr Leu Gly Gln Val Ala Lys Ala Leu Glu 75 80 85 90	410
aag tat gca gcc ccc tcc aag gag gag gaa ggt gga ggt gat ggg cac Lys Tyr Ala Ala Pro Ser Lys Glu Glu Glu Gly Gly Gly Asp Gly His 95 100 105	458
tcc gaa gcg gcc gag aaa gca gcc caa gtt ggg tta ctg ttt ctt aaa Ser Glu Ala Ala Glu Lys Ala Ala Gln Val Gly Leu Leu Phe Leu Lys 110 115 120	506
ctg tta ggg aaa gtt gag act gct aag aat tcc ctg gtc ggc cct gca Leu Leu Gly Lys Val Glu Thr Ala Lys Asn Ser Leu Val Gly Pro Ala 125 130 135	554
tgg cag acg ggc ctg cat cac ttg gca gga ccc gtt tat att ttt gcc Trp Gln Thr Gly Leu His His Leu Ala Gly Pro Val Tyr Ile Phe Ala 140 145 150	602
atc aca cac agc ttg gag caa cca tgg acc act ccg aga tct cgg gaa Ile Thr His Ser Leu Glu Gln Pro Trp Thr Thr Pro Arg Ser Arg Glu 155 160 165 170	650
gtt gct agg gag gtg ctc acc tca ctg ctt caa gtt act gaa tgc ggt Val Ala Arg Glu Val Leu Thr Ser Leu Leu Gln Val Thr Glu Cys Gly 175 180 185	698
tct gtg gca gga ttc cta cat gga gaa aat gaa gat gag aaa ggg aga Ser Val Ala Gly Phe Leu His Gly Glu Asn Glu Asp Glu Lys Gly Arg 190 195 200	746
ctt tcg gtg ata cta ggg ctt ctc aaa ccc gac ttg tat aag gaa tcc Leu Ser Val Ile Leu Gly Leu Leu Lys Pro Asp Leu Tyr Lys Glu Ser 205 210 215	794
tgg aag aat aac cct gcc atc aaa cat gtt ttc tca tgg act ctg caa Trp Lys Asn Asn Pro Ala Ile Lys His Val Phe Ser Trp Thr Leu Gln 220 225 230	842
cag gtc act cgg ccc tgg ctg agc cag cat ctg gaa agg gta ctt ccc Gln Val Thr Arg Pro Trp Leu Ser Gln His Leu Glu Arg Val Leu Pro 235 240 245 250	890
gca tca ttg gtc att tca gat gac tat cag act gag aac aaa atc ctg Ala Ser Leu Val Ile Ser Asp Asp Tyr Gln Thr Glu Asn Lys Ile Leu 255 260 265	938
ggt gta cac tgt ctc cat cac att gtg ctt aat gtg cca gct gct gat Gly Val His Cys Leu His His Ile Val Leu Asn Val Pro Ala Ala Asp 270 275 280	986

ttg ctc cag tat aac aga gcc cag gtc cta tac cat gcc att tcc aac	1034
Leu Leu Gln Tyr Asn Arg Ala Gln Val Leu Tyr His Ala Ile Ser Asn	
285 290 295	
cac ctg tac aca cca gag cac cac ctc att cag gct gtg ctc ctg tgt	1082
His Leu Tyr Thr Pro Glu His His Leu Ile Gln Ala Val Leu Leu Cys	
300 305 310	
ctg ctg gat tta ttc ccc atc ctg gag aaa acc ctg cac tgg aaa gga	1130
Leu Leu Asp Leu Phe Pro Ile Leu Glu Lys Thr Leu His Trp Lys Gly	
315 320 325 330	
gat gga gct cga ccc acc acc cat tgt gat gag gtc ctg cgg ctg atc	1178
Asp Gly Ala Arg Pro Thr Thr His Cys Asp Glu Val Leu Arg Leu Ile	
335 340 345	
ctg acc cac atg gag cca gag cac cgc ctt ctt tta cgc agg acc tac	1226
Leu Thr His Met Glu Pro Glu His Arg Leu Leu Leu Arg Arg Thr Tyr	
350 355 360	
gca aga aac ctg ccg gct ttc gtg aac agg ttg ggg atc cta act gtc	1274
Ala Arg Asn Leu Pro Ala Phe Val Asn Arg Leu Gly Ile Leu Thr Val	
365 370 375	
cgg cac tta aag agg ctg gag aga gtc atc att ggt tat ctg gag gtt	1322
Arg His Leu Lys Arg Leu Glu Arg Val Ile Ile Gly Tyr Leu Glu Val	
380 385 390	
tat gat gga cct gag gag gaa gct aga ctg aag ata ttg gaa acc cta	1370
Tyr Asp Gly Pro Glu Glu Glu Ala Arg Leu Lys Ile Leu Glu Thr Leu	
395 400 405 410	
aaa ctt ctc atg caa cat act tgg ccc aga gtt tcc tgc aga ctt gtg	1418
Lys Leu Leu Met Gln His Thr Trp Pro Arg Val Ser Cys Arg Leu Val	
415 420 425	
gtc tta ctg aag gcc ctc ttg aaa ctg att tgt gat gta gca agg gat	1466
Val Leu Leu Lys Ala Leu Leu Lys Leu Ile Cys Asp Val Ala Arg Asp	
430 435 440	
cca aac ctt aca cct gag tct gtt aag agc gcc ctg cta cag gag gcc	1514
Pro Asn Leu Thr Pro Glu Ser Val Lys Ser Ala Leu Leu Gln Glu Ala	
445 450 455	
aca gac tgc ctg att ctc ctg gac cgc tgt tct caa gga cgg gta aag	1562
Thr Asp Cys Leu Ile Leu Leu Asp Arg Cys Ser Gln Gly Arg Val Lys	
460 465 470	
ggt ctc ctg gcc aaa att ccc caa agc tgt gaa gac aga aaa gtg gtg	1610
Gly Leu Leu Ala Lys Ile Pro Gln Ser Cys Glu Asp Arg Lys Val Val	
475 480 485 490	
aac tat atc aga aaa gtg cag cag gtt tct gaa ggc gca ccc tac aat	1658
Asn Tyr Ile Arg Lys Val Gln Gln Val Ser Glu Gly Ala Pro Tyr Asn	
495 500 505	
gga act taa gacttgt attactttcc caagaggaaa ggattttctt cccatcccaa	1714

Gly Thr *

tttgtatgaa tggagttatt taagaaaaaa agatatTTTT acacgaaaaa aaaaaaaaaa 1773

<210> 141
<211> 2242
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (100)..(942)

<220>
<221> misc_feature
<222> (1)...(2242)
<223> n = a,t,c or g

<400> 141
gaatgccttt tagtgccttg cttcctgaac tagctcacag tagccccggcg gccagggca 60
atccgaccac atttcactct caccgctgta ggaatccag atg cag gcc aag tac 114
Met Gln Ala Lys Tyr
1 5
agc agc acg agg gac atg ctg gat gat gat ggg gac acc acc atg agc 162
Ser Ser Thr Arg Asp Met Leu Asp Asp Asp Gly Asp Thr Thr Met Ser
10 15 20
ctg cat tct caa gcc tct gcc aca act cgg cat cca gag ccc cgg cgc 210
Leu His Ser Gln Ala Ser Ala Thr Thr Arg His Pro Glu Pro Arg Arg
25 30 35
aca gag cac agg gct ccc tct tca acg tgg cga cca gtg gcc ctg acc 258
Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg Pro Val Ala Leu Thr
40 45 50
ctg ctg act ttg tgc ttg gtg ctg ctg ata ggg ctg gca gcc ctg ggg 306
Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly Leu Ala Ala Leu Gly
55 60 65
ctt ttg ttt ttt cag tac tac cag ctc tcc aat act ggt caa gac acc 354
Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn Thr Gly Gln Asp Thr
70 75 80 85
att tct caa atg gaa gaa aga tta gga aat acg tcc caa gag ttg caa 402
Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr Ser Gln Glu Leu Gln
90 95 100
tct ctt caa gtc cag aat ata aag ctt gca gga agt ctg cag cat gtg 450
Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly Ser Leu Gln His Val
105 110 115

gct gaa aaa ctc tgt cgt gag ctg tat aac aaa gct gga gca cac agg	498
Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys Ala Gly Ala His Arg	
120 125 130	
tgc agc cct tgt aca gaa caa tgg aaa tgg cat gga gac aat tgc tac	546
Cys Ser Pro Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr	
135 140 145	
cag ttc tat aaa gac agc aaa agt tgg gag gac tgt aaa tat ttc tgc	594
Gln Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys	
150 155 160 165	
ctt agt gaa aac tct acc atg ctg aag ata aac aaa caa gaa gac ctg	642
Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp Leu	
170 175 180	
gaa ttt gcc gcg tct cag agc tac tct gag ttt ttc tac tct tat tgg	690
Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp	
185 190 195	
aca ggg ctt ttg cgc cct gac agt ggc aag gcc tgg ctg tgg atg gat	738
Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu Trp Met Asp	
200 205 210	
gga acc cct ttc act tct gaa ctg ttc cat att ata ata gat gtc acc	786
Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile Ile Ile Asp Val Thr	
215 220 225	
agc cca aga agc aga gac tgt gtg gcc atc ctt aat ggg atg atc ttc	834
Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu Asn Gly Met Ile Phe	
230 235 240 245	
tca aag gac tgc aaa gaa ttg aag cgt tgt gtc tgt gag aga agg gca	882
Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys Val Cys Glu Arg Arg Ala	
250 255 260	
gga atg gtg aag cca gag agc ctc cat gtc ccc cct gaa aca tta ggc	930
Gly Met Val Lys Pro Glu Ser Leu His Val Pro Pro Glu Thr Leu Gly	
265 270 275	
gaa ggt gac tga ttc gccctctgca actacaaata gcagagtgcg ccaggcggtg	985
Glu Gly Asp *	
280	
ccaaagcaag ggctagttaga gacattggga aatggaacat aatcaggaaa gactatctct	1045
ctgactagta caaatgggt tctcgtgttt cctgttcagg atcaccagca tttctgagct	1105
tgggtttatg cacgtattta acagtcacaa gaagtcttat ttacatgccca ccaaccaacc	1165
tcagaaaccc ataatgtcat ctgccttctt ggcttagaga taacttttag ctctctttct	1225
tctcaatgtc taatatcacc tccctgtttt catgtcttcc ttacacttgg tggaataaga	1285
aactttttga agtagaggaa atacattgag gtaacatcct tttctctgac agtcaagtag	1345
tccatcagaa attggcagtc acttcccaga ttgtaccagc aaatacacia ggaattcttt	1405


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ttgtttgttt cagttcatac tagtcccttc ccaatccatc agtaaagacc ccatctgcct 1465
tgtccatgcc gtttcccaac agggatgtca cttgatatga gaatctcaaa tctcaatgcc 1525
ttataagcat tccttctgt gtccattaag actctgataa ttgtctcccc tccataggaa 1585
tttctcccag gaaagaaata tatccccatc tccgtttcat atcagaacta ccgccccga 1645
tattcccttc agagagatta aagaccagaa aaaagtgagc ctcttcatct gcacctgtaa 1705
tagtttcagt tcctattttc ttccattgac ccatatttat acctttcagg tactgaagat 1765
ttaataataa taaatgtaaa tactgtgaag tgtgtgtgat ttacaatgg acttatgggt 1825
gggtgggaaaa ttcagcatgg aaatgctttt caaaatatga tagcgggtcat tattttgatt 1885
gtgccttact gaaagttttt gggaattta caagagtact gattacatga ttatctggag 1945
aaaataagat gtctttgaaa tacatgttgg cttcaagaaa acagttttaa cgttttccta 2005
aaatgaaatc ttttgagggtg agcttatggc atcaacacat ggttgatgag gaagctgagt 2065
tgcattagtg cacatgattt ccagtcaggt catgggaaat gaacagagac agtgacatct 2125
ttgtagctgc tcctttgtga ggcacttctt tcttgagatg actccatgca caaatataac 2185
agggatcatt gggaatgaca ccatcacagc caccaagntt attgggttac tgataat 2242

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<210> 142
<211> 2323
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (100)..(1023)

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<220>
<221> misc_feature
<222> (1)...(2323)
<223> n = a,t,c or g

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<400> 142
gaatgccttt tagtgccttg ctctctgaac tagctcacag tagcccggcg gccagggca 60

atccgaccac atttcactct caccgctgta ggaatccag atg cag gcc aag tac 114
Met Gln Ala Lys Tyr
1 5

agc agc acg agg gac atg ctg gat gat gat ggg gac acc acc atg agc 162
Ser Ser Thr Arg Asp Met Leu Asp Asp Asp Gly Asp Thr Thr Met Ser
10 15 20

```

ctg cat tct caa gcc tct gcc aca act cgg cat cca gag ccc cgg cgc	210
Leu His Ser Gln Ala Ser Ala Thr Thr Arg His Pro Glu Pro Arg Arg	
25 30 35	
aca gag cac agg gct ccc tct tca acg tgg cga cca gtg gcc ctg acc	258
Thr Glu His Arg Ala Pro Ser Ser Thr Trp Arg Pro Val Ala Leu Thr	
40 45 50	
ctg ctg act ttg tgc ttg gtg ctg ctg ata ggg ctg gca gcc ctg ggg	306
Leu Leu Thr Leu Cys Leu Val Leu Leu Ile Gly Leu Ala Ala Leu Gly	
55 60 65	
ctt ttg ttt ttt cag tac tac cag ctg tcc aat act ggt caa gac acc	354
Leu Leu Phe Phe Gln Tyr Tyr Gln Leu Ser Asn Thr Gly Gln Asp Thr	
70 75 80 85	
att tct caa atg gaa gaa aga tta gga aat acg tcc caa gag ttg caa	402
Ile Ser Gln Met Glu Glu Arg Leu Gly Asn Thr Ser Gln Glu Leu Gln	
90 95 100	
tct ctt caa gtc cag aat ata aag ctt gca gga agt ctg cag cat gtg	450
Ser Leu Gln Val Gln Asn Ile Lys Leu Ala Gly Ser Leu Gln His Val	
105 110 115	
gct gaa aaa ctg tgt cgt gag ctg tat aac aaa gct gga ggc tat aca	498
Ala Glu Lys Leu Cys Arg Glu Leu Tyr Asn Lys Ala Gly Gly Tyr Thr	
120 125 130	
aga aac atg gtg cca gca tct gct tct tct gag agc ctg agg cag ctt	546
Arg Asn Met Val Pro Ala Ser Ala Ser Ser Glu Ser Leu Arg Gln Leu	
135 140 145	
cca cac atg ggg gaa agt gca gca gca cac agg tgc agc cct tgt aca	594
Pro His Met Gly Glu Ser Ala Ala Ala His Arg Cys Ser Pro Cys Thr	
150 155 160 165	
gaa caa tgg aaa tgg cat gga gac aat tgc tac cag ttc tat aaa gac	642
Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr Gln Phe Tyr Lys Asp	
170 175 180	
agc aaa agt tgg gag gac tgt aaa tat ttc tgc ctt agt gaa aac tct	690
Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys Leu Ser Glu Asn Ser	
185 190 195	
acc atg ctg aag ata aac aaa caa gaa gac ctg gaa ttt gcc gcg tct	738
Thr Met Leu Lys Ile Asn Lys Gln Glu Asp Leu Glu Phe Ala Ala Ser	
200 205 210	
cag agc tac tct gag ttt ttc tac tct tat tgg aca ggg ctt ttg cgc	786
Gln Ser Tyr Ser Glu Phe Phe Tyr Ser Tyr Trp Thr Gly Leu Leu Arg	
215 220 225	
cct gac agt ggc aag gcc tgg ctg tgg atg gat gga acc cct ttc act	834
Pro Asp Ser Gly Lys Ala Trp Leu Trp Met Asp Gly Thr Pro Phe Thr	
230 235 240 245	
tct gaa ctg ttc cat att ata ata gat gtc acc agc cca aga agc aga	882

Ser	Glu	Leu	Phe	His	Ile	Ile	Ile	Asp	Val	Thr	Ser	Pro	Arg	Ser	Arg	
				250					255					260		
gac	tgt	gtg	gcc	atc	ctt	aat	ggg	atg	atc	ttc	tca	aag	gac	tgc	aaa	930
Asp	Cys	Val	Ala	Ile	Leu	Asn	Gly	Met	Ile	Phe	Ser	Lys	Asp	Cys	Lys	
			265					270					275			
gaa	ttg	aag	cgt	tgt	gtc	tgt	gag	aga	agg	gca	gga	atg	gtg	aag	cca	978
Glu	Leu	Lys	Arg	Cys	Val	Cys	Glu	Arg	Arg	Ala	Gly	Met	Val	Lys	Pro	
		280						285				290				
gag	agc	ctc	cat	gtc	ccc	cct	gaa	aca	tta	ggc	gaa	ggg	gac	tga	ttc	1026
Glu	Ser	Leu	His	Val	Pro	Pro	Glu	Thr	Leu	Gly	Glu	Gly	Asp	*		
	295					300					305					
gccctctgca	actacaaata	gcagagt	gag	ccaggc	gggtg	ccaaagcaag	ggctagt	ttga								1086
gacattggga	aatggaacat	aatcaggaaa	gactatctct	ctgactagta	caaaatgggt											1146
tctcgtgttt	cctgttcagg	atcaccagca	tttctgagct	tgggtttatg	cacgtattta											1206
acagtcacaa	gaagtcttat	ttacatgcc	ccaaccaacc	tcagaaaccc	ataatgtcat											1266
ctgccttctt	ggcttagaga	taacttttag	ctctctttct	tctcaatgtc	taatatcacc											1326
tccctgtttt	catgtcttcc	ttacacttgg	tgggaataaga	aactttttga	agtagaggaa											1386
atacattgag	gtaacatcct	tttctctgac	agtcaagtag	tccatcagaa	attggcagtc											1446
acttcccaga	ttgtaccagc	aaatacacaa	ggaattcttt	ttgtttgttt	cagttcatac											1506
tagtcccttc	ccaatccatc	agtaaagacc	ccatctgcct	tgtccatgcc	gtttcccaac											1566
agggatgtca	cttgatatga	gaatctcaaa	tctcaatgcc	ttataagcat	tccttcctgt											1626
gtccattaag	actctgataa	ttgtctcccc	tccataggaa	tttctcccag	gaaagaaata											1686
tatccccatc	tccgtttcat	atcagaacta	ccgtccccga	tattcccttc	agagagatta											1746
aagaccagaa	aaaagtgagc	ctcttcatct	gcacctgtaa	tagtttcagt	tcctattttc											1806
ttccattgac	ccatatttat	acctttcagg	tactgaagat	ttaataataa	taaatgtaaa											1866
tactgtgaag	tgtgtgtgat	tttacaatgg	acttatgggt	ggtgggaaaa	ttcagcatgg											1926
aaatgctttt	caaaatatga	tagcgggtcat	tatttttgatt	gtgccttact	gaaagttttt											1986
ggggaattta	caagagtact	gattacatga	ttatctggag	aaaataagat	gtctttgaaa											2046
tacatgttgg	cttcaagaaa	acagttttta	cgttttccta	aaatgaaatc	ttttgagggtg											2106
agcttatggc	atcaacacat	ggttgatgag	gaagctgagt	tgcattagtg	cacatgattt											2166
ccagtcaggt	catgggaaat	gaacagagac	agtgacatct	ttgtagctgc	tcctttgtga											2226
ggcacttctt	tcttgagatg	actccatgca	caaataaac	agggatcatt	gggaatgaca											2286

ccatcacagc caccaagntt attgggttac tgataat

2323

<210> 143
<211> 971
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (72)..(767)

<400> 143

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cggccgcgctc gacagacaga cgggagcagt gcttttccta gagtagagta tgctctataa      60

atgtctactg a atg ttg act ggt gtt gga tgt ctt gtc tcc tca gaa tct      110
      Met Leu Thr Gly Val Gly Cys Leu Val Ser Ser Glu Ser
              1              5              10

ctg agc tgc gtg cag tgt aat tca tgg gaa aaa tcc tgt gtc aac agc      158
Leu Ser Cys Val Gln Cys Asn Ser Trp Glu Lys Ser Cys Val Asn Ser
      15              20              25

att gcc tct gaa tgt ccc tca cat gcc aac acc agc tgt atc agc tcc      206
Ile Ala Ser Glu Cys Pro Ser His Ala Asn Thr Ser Cys Ile Ser Ser
      30              35              40              45

tca gcc agc tcc tct cta gag aca cca gtc aga tta tac cag aat atg      254
Ser Ala Ser Ser Ser Leu Glu Thr Pro Val Arg Leu Tyr Gln Asn Met
              50              55              60

ttc tgc tca gcg gag aac tgc agt gag gag aca cac att aca gcc ttc      302
Phe Cys Ser Ala Glu Asn Cys Ser Glu Glu Thr His Ile Thr Ala Phe
              65              70              75

act gtc cac gtg tct gct gaa gaa cac ttt cat ttt gta agc cag tgc      350
Thr Val His Val Ser Ala Glu Glu His Phe His Phe Val Ser Gln Cys
              80              85              90

tgc caa gga aag gaa tgc agc aac acc agc gat gcc ctg gac cct ccc      398
Cys Gln Gly Lys Glu Cys Ser Asn Thr Ser Asp Ala Leu Asp Pro Pro
      95              100              105

ctg aag aac gtg tcc agc aac gca gag tgc cct gct tgt tat gaa tct      446
Leu Lys Asn Val Ser Ser Asn Ala Glu Cys Pro Ala Cys Tyr Glu Ser
110              115              120              125

aat gga act tcc tgt cgt ggg aag ccc tgg aaa tgc tat gaa gaa gaa      494
Asn Gly Thr Ser Cys Arg Gly Lys Pro Trp Lys Cys Tyr Glu Glu Glu
              130              135              140

cag tgt gtc ttt cta gtt gca gaa ctt aag aat gac att gag tct aag      542
Gln Cys Val Phe Leu Val Ala Glu Leu Lys Asn Asp Ile Glu Ser Lys
              145              150              155

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agc ctc gtc ctg aaa ggc tgt tcc aac gtc agt aac gcc acc tgt cag      590
Ser Leu Val Leu Lys Gly Cys Ser Asn Val Ser Asn Ala Thr Cys Gln
      160                      165                      170

ttc ctg tct ggt gaa aac aag act ctt gga gga gtc atc ttt cga aag      638
Phe Leu Ser Gly Glu Asn Lys Thr Leu Gly Gly Val Ile Phe Arg Lys
      175                      180                      185

ttt gag tgt gca aat gta aac agc tta acc ccc acg tct gca cca acc      686
Phe Glu Cys Ala Asn Val Asn Ser Leu Thr Pro Thr Ser Ala Pro Thr
      190                      195                      200                      205

act tcc cac aac gtg ggc tcc aaa gct tcc ctc tac ctc ttg gcc ctt      734
Thr Ser His Asn Val Gly Ser Lys Ala Ser Leu Tyr Leu Leu Ala Leu
      210                      215                      220

gcc agc ctc ctt ctt cgg gga ctg ctg ccc tga ggtcctgg ggctgcactt      785
Ala Ser Leu Leu Leu Arg Gly Leu Leu Pro *
      225                      230

tgcccagcac cccatttctg cttctctgag gtccagagca cccctgctgg tgctgacacc      845

ctctttccct gctctgcccc gtttaactgc ccagtaagtg ggagtcacag gtctccaggc      905

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aaaaaa                                                                971

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<210> 144
<211> 1689
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (354)..(1370)

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<220>
<221> misc_feature
<222> (1)...(1689)
<223> n = a,t,c or g

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<400> 144
cctgaatgct ttacgtaccg gcccggaatt cccgggtcga cccacgcgtc cgctcggcca      60

ccgaagccac cctgccctgg tgaaagggtc cccgcaccgc ccggtgctcc ccatctgcct      120

ggcgttgtgc gcagagctgg aaagcatggc tgttataaat gaattctgat tttggggagc      180

agatgccaac ttagagcctc gtaccaatct ctctgtcttt aaaagatgag gtgacttggt      240

gattttcctg gaaaattata ggtgcccagc taagacctga atgccatcac cctccccagg      300

gctctgcagt tttctcgtgg tgaacccttg atggatttgt tgttgcttga gaa atg      356

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[illegible]

gcg	atg	atc	gaa	ttg	ggg	ttt	gga	aga	cag	aat	ttt	cat	cca	tta	aag	404
Ala	Met	Ile	Glu	Leu	Gly	Phe	Gly	Arg	Gln	Asn	Phe	His	Pro	Leu	Lys	
			5				10			15						
agg	aag	agt	tca	ttg	ctg	ttg	aaa	ctc	ata	gct	gtt	gtc	ttt	gct	gtg	452
Arg	Lys	Ser	Ser	Leu	Leu	Leu	Lys	Leu	Ile	Ala	Val	Val	Phe	Ala	Val	
			20				25			30						
ctt	cta	ttt	tgt	gaa	ttt	tta	atc	tat	tac	tta	gcg	atc	ttt	cag	tgt	500
Leu	Leu	Phe	Cys	Glu	Phe	Leu	Ile	Tyr	Tyr	Leu	Ala	Ile	Phe	Gln	Cys	
			35				40			45						
aat	tgg	cct	gaa	gtg	aaa	acc	aca	gcc	tct	gat	ggg	gaa	cag	acc	aca	548
Asn	Trp	Pro	Glu	Val	Lys	Thr	Thr	Ala	Ser	Asp	Gly	Glu	Gln	Thr	Thr	
			50				55			60			65			
cgt	gag	cct	gtg	ctc	aaa	gcc	atg	ttt	ttg	gct	gac	acc	cat	ttg	ctt	596
Arg	Glu	Pro	Val	Leu	Lys	Ala	Met	Phe	Leu	Ala	Asp	Thr	His	Leu	Leu	
			70						75			80				
ggg	gaa	ttc	cta	ggc	cac	tgg	ctg	gac	aaa	tta	cga	agg	gaa	tgg	cag	644
Gly	Glu	Phe	Leu	Gly	His	Trp	Leu	Asp	Lys	Leu	Arg	Arg	Glu	Trp	Gln	
			85						90			95				
atg	gag	aga	gcg	ttc	cag	aca	gct	ctg	tgg	ttg	ctg	cag	ccg	gaa	gtc	692
Met	Glu	Arg	Ala	Phe	Gln	Thr	Ala	Leu	Trp	Leu	Leu	Gln	Pro	Glu	Val	
			100						105			110				
gtc	ttc	atc	ctg	ggg	gat	atc	ttt	gat	gaa	ggg	aag	tgg	agc	acc	cct	740
Val	Phe	Ile	Leu	Gly	Asp	Ile	Phe	Asp	Glu	Gly	Lys	Trp	Ser	Thr	Pro	
			115						120			125				
gag	gcc	tgg	gcg	gat	gat	gtg	gag	cgg	ttt	cag	aaa	atg	ttc	aga	cac	788
Glu	Ala	Trp	Ala	Asp	Asp	Val	Glu	Arg	Phe	Gln	Lys	Met	Phe	Arg	His	
			130						135			140			145	
cca	agt	cat	gta	cag	ctg	aag	gta	gtt	gct	gga	aac	cat	gac	att	ggc	836
Pro	Ser	His	Val	Gln	Leu	Lys	Val	Val	Ala	Gly	Asn	His	Asp	Ile	Gly	
			150						155			160				
ttc	cat	tat	gag	atg	aac	aca	tac	aaa	gta	gaa	cgc	ttt	gag	aaa	gtg	884
Phe	His	Tyr	Glu	Met	Asn	Thr	Tyr	Lys	Val	Glu	Arg	Phe	Glu	Lys	Val	
			165						170			175				
ttc	agc	tct	gaa	aga	ctg	ttt	tct	tgg	aaa	ggc	att	aac	ttt	gtg	atg	932
Phe	Ser	Ser	Glu	Arg	Leu	Phe	Ser	Trp	Lys	Gly	Ile	Asn	Phe	Val	Met	
			180						185			190				
gtc	aac	agc	gtg	gcg	ctg	aac	ggg	gat	ggc	tgt	ggc	atc	tgc	tct	gaa	980
Val	Asn	Ser	Val	Ala	Leu	Asn	Gly	Asp	Gly	Cys	Gly	Ile	Cys	Ser	Glu	
			195						200			205				
aca	gaa	gca	gag	ctc	att	gaa	gtt	tct	cac	aga	ctg	aac	tgc	tcc	cga	1028
Thr	Glu	Ala	Glu	Leu	Ile	Glu	Val	Ser	His	Arg	Leu	Asn	Cys	Ser	Arg	

210	215	220	225	
gag gca cgt ggc tcc agc cgg tgt gga cct ggg cct ctg ctg ccc acg				1076
Glu Ala Arg Gly Ser Ser Arg Cys Gly Pro Gly Pro Leu Leu Pro Thr	230	235	240	
tct gcc cct gtc ctc ctg cag cat tat cct ctg tat cgg aga agt gat				1124
Ser Ala Pro Val Leu Leu Gln His Tyr Pro Leu Tyr Arg Arg Ser Asp	245	250	255	
gct aac tgt tct ggg gaa gac gct gct cct gca gag gaa agg gac atc				1172
Ala Asn Cys Ser Gly Glu Asp Ala Ala Pro Ala Glu Glu Arg Asp Ile	260	265	270	
cca ttt aag gag aac tat gac gtg ctt tca cgg gag gca tca caa aag				1220
Pro Phe Lys Glu Asn Tyr Asp Val Leu Ser Arg Glu Ala Ser Gln Lys	275	280	285	
ctg ctg tgg tgg ctc cag ccg cgc ctg gtt ctc agt ggc cac acg cac				1268
Leu Leu Trp Trp Leu Gln Pro Arg Leu Val Leu Ser Gly His Thr His	290	295	300	305
agc gcc tgc gag gtg cac cac ggg ggc cga gtc ccc gag ctc agc gtc				1316
Ser Ala Cys Glu Val His His Gly Gly Arg Val Pro Glu Leu Ser Val	310	315	320	
cca tct ttc agt tgg agg aac aga aac aac ccc agt ttc atc atg gta				1364
Pro Ser Phe Ser Trp Arg Asn Arg Asn Asn Pro Ser Phe Ile Met Val	325	330	335	
ccg tga aagtttattt ttgtctgaaa gctttcataa gtatttaaata caacacagta				1420
Pro *				
atcaactatt taattgctgc aatcgggtcaa aatttacaaa agccacacac aaatttctct				1480
ccttctacac gtagctccat aactgcccc ttgccaaaca cccttccggg aaccaatcag				1540
catgacattc ctgggcagtt aatgtgagaa gcgagggcag ggcaccgtcc nagtggactt				1600
tatccttcag ggaggggcgt atcctctctc ttacactctg tgtgtggtta aatttctaaa				1660
gaacaccatt taatccatag ctatatcag				1689

<210> 145
 <211> 480
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (104) .. (298)

 <400> 145

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 ttttaagtttt ttttctttat tactgatctt atgcaatttg att atg ttc ctt ggt 115
 Met Phe Leu Gly
 1
 gta gct ttt cag tgt ttc ttc tgc ttt tgg ttt gtt gag ctt ttt gga 163
 Val Ala Phe Gln Cys Phe Phe Cys Phe Trp Phe Val Glu Leu Phe Gly
 5 10 15 20
 ttt gtg ggt tta cag tta tta tca aat ttg gaa aaa ttt cag ccc tta 211
 Phe Val Gly Leu Gln Leu Leu Ser Asn Leu Glu Lys Phe Gln Pro Leu
 25 30 35
 tgt ctt caa ata ttt ttt ctg tct ccc tgc ccc atc cgt agt ctt tat 259
 Cys Leu Gln Ile Phe Phe Leu Ser Pro Cys Pro Ile Arg Ser Leu Tyr
 40 45 50
 ata ttt gat cat cta aag ttg tct cac agc tca cag tga cactgcttgt 308
 Ile Phe Asp His Leu Lys Leu Ser His Ser Ser Gln *
 55 60 65
 ttttccagtc tttttttccc tctaggtgtt tcattttgaa caattgctat tgctatgtct 368
 tcaagatcct taatcttttc ttctgtagtg ccacatctta ccagtgaaac ttttcacctc 428
 agacatggta ttttttattt ctagaaatta ggactttttt tacatttccc ac 480

<210> 146
 <211> 557
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (158) .. (520)

<400> 146

agagcagaag tgtgaagagt ggaggagcca gtatgaggct ctgaaggagg actggaggac 60
 ccttgggacc cagcacaggg agctggagag ccaactccac gtgcttcagt ccaaactgca 120
 ggtaccaggc actgggggtg gggaggggaag acagggt atg ggg agg agg gat ggt 175
 Met Gly Arg Arg Asp Gly
 1 5
 gat gaa aga agc tgt tct gga tta ggg act cca aag gca gct gac agc 223
 Asp Glu Arg Ser Cys Ser Gly Leu Gly Thr Pro Lys Ala Ala Asp Ser
 10 15 20
 atc tgg ctt tca gtt cct cag tca cca cta ctt tgt acc aaa ttc act 271
 Ile Trp Leu Ser Val Pro Gln Ser Pro Leu Leu Cys Thr Lys Phe Thr
 25 30 35


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gtt ttg gct ctg aaa tct aat ttt gag ttt agc aag gat gtc tgc att      319
Val Leu Ala Leu Lys Ser Asn Phe Glu Phe Ser Lys Asp Val Cys Ile
    40                      45                      50

gct cat gca aat gaa cta agc gtt cat tgg aat gac acc atc acc acc      367
Ala His Ala Asn Glu Leu Ser Val His Trp Asn Asp Thr Ile Thr Thr
    55                      60                      65                      70

caa atg aaa aga act ggc tgg aat att cat cag cct act aat gtc atc      415
Gln Met Lys Arg Thr Gly Trp Asn Ile His Gln Pro Thr Asn Val Ile
                      75                      80                      85

tcc caa ccc act ctc caa act cca tcc caa aaa agc atc cag ttc aga      463
Ser Gln Pro Thr Leu Gln Thr Pro Ser Gln Lys Ser Ile Gln Phe Arg
                      90                      95                      100

att gcc cac tgt tgg caa aga aag aat gtc act aat tta ttt aca ggg      511
Ile Ala His Cys Trp Gln Arg Lys Asn Val Thr Asn Leu Phe Thr Gly
    105                      110                      115

agc aga tag cagggactta cagatgaacc aggcctgcg atttttg      557
Ser Arg *
    120

<210> 147
<211> 1190
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (172)..(1071)

<400> 147
gggaggggtct gaaccgataa ccctgcggta ccgctccgga attcccgggt cgaccacgc      60

gtccgggggct acacagccag gtgtcagatg tgtctctgct gatctgagtc tgcctgtggc      120

atggacctgc atcttcctg aagcatctcc agggctgaaa aatcactgac c atg gca      177
                               Met Ala
                               1

cca tgg tct cat cca tct gca cag ctg cag cca gtg gga gga gac gcc      225
Pro Trp Ser His Pro Ser Ala Gln Leu Gln Pro Val Gly Gly Asp Ala
    5                      10                      15

gtg agc cct gcc ctc atg gtt ctg ctc tgc ctc ggg ctg agt ctg ggc      273
Val Ser Pro Ala Leu Met Val Leu Leu Cys Leu Gly Leu Ser Leu Gly
    20                      25                      30

ccc agg acc cac gtg cag gca ggg aac ctc tcc aaa gcc acc ctc tgg      321
Pro Arg Thr His Val Gln Ala Gly Asn Leu Ser Lys Ala Thr Leu Trp
    35                      40                      45                      50

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gct gag cca ggc tct gtg atc agc cgg ggg aac tct gtg acc atc cgg	369
Ala Glu Pro Gly Ser Val Ile Ser Arg Gly Asn Ser Val Thr Ile Arg	
55 60 65	
tgt cag ggg acc ctg gag gcc cag gaa tac cgt ctg gtt aaa gag gga	417
Cys Gln Gly Thr Leu Glu Ala Gln Glu Tyr Arg Leu Val Lys Glu Gly	
70 75 80	
agc cca gaa ccc tgg gac aca cag aac cca ctg gag ccc aag aac aag	465
Ser Pro Glu Pro Trp Asp Thr Gln Asn Pro Leu Glu Pro Lys Asn Lys	
85 90 95	
gcc aga ttc tcc atc cca tcc atg aca gag cac cat gca ggg aga tac	513
Ala Arg Phe Ser Ile Pro Ser Met Thr Glu His His Ala Gly Arg Tyr	
100 105 110	
cgc tgt tac tac tac agc cct gca ggc tgg tca gag ccc agc gac ccc	561
Arg Cys Tyr Tyr Tyr Ser Pro Ala Gly Trp Ser Glu Pro Ser Asp Pro	
115 120 125 130	
ctg gag ctg gtg gtg aca gga ttc tac aac aaa ccc acc ctc tca gcc	609
Leu Glu Leu Val Val Thr Gly Phe Tyr Asn Lys Pro Thr Leu Ser Ala	
135 140 145	
ctg ccc agt cct gtg gtg acc tca gga gag aac gtg acc ctc cag tgt	657
Leu Pro Ser Pro Val Val Thr Ser Gly Glu Asn Val Thr Leu Gln Cys	
150 155 160	
ggc tca cgg ctg aga ttc gac agg ttc att ctg act gag gaa gga gac	705
Gly Ser Arg Leu Arg Phe Asp Arg Phe Ile Leu Thr Glu Glu Gly Asp	
165 170 175	
cac aag ctc tcc tgg acc ttg gac tca cag ctg acc ccc agt ggg cag	753
His Lys Leu Ser Trp Thr Leu Asp Ser Gln Leu Thr Pro Ser Gly Gln	
180 185 190	
ttc cag gcc ctg ttc cct gtg ggc cct gtg acc ccc agc cac agg tgg	801
Phe Gln Ala Leu Phe Pro Val Gly Pro Val Thr Pro Ser His Arg Trp	
195 200 205 210	
atg ctc aga tgc tat ggc tct cgc agg cat atc ctg cag gta tgg tca	849
Met Leu Arg Cys Tyr Gly Ser Arg Arg His Ile Leu Gln Val Trp Ser	
215 220 225	
gaa ccc agt gac ctc ctg gag att ccg gtc tca gga gca gct gat aac	897
Glu Pro Ser Asp Leu Leu Glu Ile Pro Val Ser Gly Ala Ala Asp Asn	
230 235 240	
ctc agt ccg tca caa aac aag tct gac tct ggg act gcc tca cac ctt	945
Leu Ser Pro Ser Gln Asn Lys Ser Asp Ser Gly Thr Ala Ser His Leu	
245 250 255	
cag gat tac gca gta gag aat ctc atc cgc atg ggc atg gcc ggc ttg	993
Gln Asp Tyr Ala Val Glu Asn Leu Ile Arg Met Gly Met Ala Gly Leu	
260 265 270	

aac aca gca cca aca gct tcc aag ata gta aca gac tcc aat tcc agg	509
Asn Thr Ala Pro Thr Ala Ser Lys Ile Val Thr Asp Ser Asn Ser Arg	
105 110 115	
gtt tca gaa ccg cat cgc agc atc ttt cct gaa atg cac tca gac tca	557
Val Ser Glu Pro His Arg Ser Ile Phe Pro Glu Met His Ser Asp Ser	
120 125 130	
gcc agc aaa gac gtg cct ggc cgc atc ctg ctg gat ata gac aat gat	605
Ala Ser Lys Asp Val Pro Gly Arg Ile Leu Leu Asp Ile Asp Asn Asp	
135 140 145 150	
acc gag agc act gcc ctg tga ag aaagcccttt cccagccctc caccacttcc	658
Thr Glu Ser Thr Ala Leu *	
155	
accctggcga gtggagcagg ggcaggcgaa cctctttctt tgcagaccga acagtgaaaa	718
gctttcagtg gaggacaaag gagggcctca ctgtgcggga cctggccttc tgcacggccc	778
aaggagaacc tggaggccac cactaaagct gaatgacctg tgtcttgaag aagttggctt	838
tctttacatg ggaaggaaat catgccaaaa aaatccaaaa caaagaagta cctggagtgg	898
agagagtatt cctgctgaaa cgcgcatagg aagcttttgt ccctgctggt aatgcgggca	958
gcacctacag caacttgga tgagtaagaa gcagtgcgtt aactatctat ttaataaaat	1018
gcgctcatta tgcaagtcgc ctactctctg ctacctggac gttcattctt atgtattagg	1078
agggaggctg cgctccttca gacttgctgc agaatcattt tgtatcatgt atggctctgtg	1138
tctccccagt cccctcagaa ccatgcccat ggatgggtgac tgctggctct gtcacctcat	1198
caaactggat gtgacctatg ccgcctcggt ggattgtcgg aatgtagaca gaaatgtact	1258
gt	1260

<210> 149
 <211> 1929
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (208)..(1395)

<400> 149	
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tccttcctct gtctattaca caccatctgc tcatactatc tgggtactcac tcaagaaatc	120
caagatgatg catggctgga caaaatctac agacgctatg cctggataaa acgccagctt	180

Thr Thr Ser Ser Gly Gly Leu Thr Ile Ser Ser Leu Leu Lys Glu Lys
 220 225 230

gag ggc tca gaa gta gcc aag ttc act ctg gag gag ctc tgc ctc atc 951
 Glu Gly Ser Glu Val Ala Lys Phe Thr Leu Glu Glu Leu Cys Leu Ile
 235 240 245

tgt aac atc ctg agc acg gca gag tac tgt ctg gcc acc acc cag cag 999
 Cys Asn Ile Leu Ser Thr Ala Glu Tyr Cys Leu Ala Thr Thr Gln Gln
 250 255 260

cta gaa gaa aaa ctc aaa gaa aaa gtg gat gta agt ctg att gaa cga 1047
 Leu Glu Glu Lys Leu Lys Glu Lys Val Asp Val Ser Leu Ile Glu Arg
 265 270 275 280

atc aat ctg act gga gag atg gac acg ttc agc acc gtc atc tcc agc 1095
 Ile Asn Leu Thr Gly Glu Met Asp Thr Phe Ser Thr Val Ile Ser Ser
 285 290 295

agt att cag ctg ctg gtt cag gat ctg gat gct gcc tgt gat cct gcc 1143
 Ser Ile Gln Leu Leu Val Gln Asp Leu Asp Ala Ala Cys Asp Pro Ala
 300 305 310

ctg act gcc atg agc aag atg cag tgg cag aac gtg gag cac gtt ggt 1191
 Leu Thr Ala Met Ser Lys Met Gln Trp Gln Asn Val Glu His Val Gly
 315 320 325

gac cag agc ccc tac gtc acc tct gtc att ctg cac atc aag cag aac 1239
 Asp Gln Ser Pro Tyr Val Thr Ser Val Ile Leu His Ile Lys Gln Asn
 330 335 340

gtc ccc atc atc cgt gac aac ctg gct tcc aca cgc aag tac ttc act 1287
 Val Pro Ile Ile Arg Asp Asn Leu Ala Ser Thr Arg Lys Tyr Phe Thr
 345 350 355 360

cag ttc tgc gtt aaa ttt gca aac tcc ttc att ccc aaa ttc atc acc 1335
 Gln Phe Cys Val Lys Phe Ala Asn Ser Phe Ile Pro Lys Phe Ile Thr
 365 370 375

cac ctc ttc aag tgc aag cca att agc atg gtg gga gca gaa cag gtg 1383
 His Leu Phe Lys Cys Lys Pro Ile Ser Met Val Gly Ala Glu Gln Val
 380 385 390

aga tgg acg tag tat caggcatttg cctggcagct tttgtttag atcaagcaca 1438
 Arg Trp Thr *
 395

tattcttcta gtccagatct acttggcagg aataaaattg atgatgtccc ctgtttgggg 1498

acagtataat gactcacccg gaaggtttct taattcggtc ttccatttat ttttaaaaat 1558

tttgtttgaa cgctactaa gttctgggtg caggggtataa cacagcaagc accatggaaa 1618

ggtccttgct cctagtgtc acactccaat aagaagaagt ggctgggccc ggcacagcgg 1678

ctcacgtgt aaccccagca tttcgggagg cctgggcagg cagatcacct ggggtaagga 1738

atttgagagc agcctggcca acatggtgaa atcccatctc tactaaaaat acaaaaatta 1798
gctgggcatg ggggcaggct accggggagg ctgaggcagg agaatcactt gaacccggga 1858
ggtggaggtt gcagtgagcc gatatcacac cactgcactc cagcctgggt gacaaagtga 1918
gactccatct c 1929

<210> 150
<211> 1230
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (70)..(555)

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aaaaaagttg gtgtatcatc ctccatcctc caaggtctct ggatctctta tagcacagaa 60
ggtctttcc atg gca ctg gcg tct tta cga aat ctc tac act cca aat 108
Met Ala Leu Ala Ser Leu Arg Asn Leu Tyr Thr Pro Asn
1 5 10
ata aag gtc agc cga ctg ctg att ttg gga ggt gcc aat att aat tac 156
Ile Lys Val Ser Arg Leu Leu Ile Leu Gly Gly Ala Asn Ile Asn Tyr
15 20 25
cgg aca gag gtt tta aat aat gct cca att cta tgt gtt cag tcc cat 204
Arg Thr Glu Val Leu Asn Asn Ala Pro Ile Leu Cys Val Gln Ser His
30 35 40 45
ctt ggt tac aca gaa atg gta gcc ctg ctg ctg gag ttc ggg gcc aac 252
Leu Gly Tyr Thr Glu Met Val Ala Leu Leu Leu Glu Phe Gly Ala Asn
50 55 60
gtg gat gcc tct tct gaa agt ggc ctg act ccc ctg gga tat gct gca 300
Val Asp Ala Ser Ser Glu Ser Gly Leu Thr Pro Leu Gly Tyr Ala Ala
65 70 75
gca gca ggg tac ctg agc att gtg gtg ctg ctg tgc aag aaa cgg gcc 348
Ala Ala Gly Tyr Leu Ser Ile Val Val Leu Leu Cys Lys Lys Arg Ala
80 85 90
aag gtg gat cat ttg gat aag aac ggg cag tgt gct ttg gtt cat gct 396
Lys Val Asp His Leu Asp Lys Asn Gly Gln Cys Ala Leu Val His Ala
95 100 105
gca ctc cga ggt cat ctg gag gtt gtc aag ttt ttg att cag tgt gac 444
Ala Leu Arg Gly His Leu Glu Val Val Lys Phe Leu Ile Gln Cys Asp
110 115 120 125
tgg acg atg gcc ggc cag cag caa gga gta ttt aag aag agc cat gcc 492
Trp Thr Met Ala Gly Gln Gln Gln Gly Val Phe Lys Lys Ser His Ala

130	135	140	
atc caa cag gcc ctc att gct gca gcc agc atg ggt tat act gag gta			540
Ile Gln Gln Ala Leu Ile Ala Ala Ala Ser Met Gly Tyr Thr Glu Val			
145	150	155	
aga agt agg caa tag gattgttttt tcaagctctg tattgaagga cccaggaaac			595
Arg Ser Arg Gln *			
160			
caggagaaaa gattgcacga agacaaaatt gccaaccaaa ttaatgtgaa ttcgtgatcg			655
ctgctctgaa taataaggag attaaactcc atgaagcact ttactcaaat gccaaagtcc			715
ctcaaattat aggtatagaa aggtgcgagt tggaaaggac cgtggaaatg atataattat			775
tctccatggt ttcctccctg tttaacagac agtggcacca aggctcaaag agatgaatta			835
ttgaggtgta gtcacatggt tagataatgt ggcacaggaa cagcataaca tttagaatct			895
cagaaggacc agatttgagt cccagcctcg ctattcatta actctagccc ttgaacaatt			955
tacctatctc ttagaagttt agtttcccat cagcaaagtg aagctaataa actcctttat			1015
acaaggctgt tgtaagggat gcttggtaaa ctgttaaaca ttatacagtt tatttattaa			1075
tgataataac aataatagtg gcaaatgtag ggaattggta gtgtgctagg aaatgtttaa			1135
caaccaactg tgaagagggg tgtgggggtg aacaggggtg tgtgtttgtg tgtgcatacg			1195
tttattataa attttactga tagaatgtgt tgccg			1230

<210> 151
 <211> 1335
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (91)..(1257)

<400> 151		
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gagggagccc gagccaggcc atctccaacc	atg ttc gac gag gcc tcg gcc	111
	Met Phe Asp Glu Ala Ser Ala	
	1 5	
atc act tcc tac gag aag ttt cta acc ccc gag gag ccc ttt cca ctc		159
Ile Thr Ser Tyr Glu Lys Phe Leu Thr Pro Glu Glu Pro Phe Pro Leu		
10 15 20		
ctg gga cct cct cgc ggg gtg ggc acc tgc ccg agc gag gag ccg ggc		207
Leu Gly Pro Pro Arg Gly Val Gly Thr Cys Pro Ser Glu Glu Pro Gly		

25	30	35	
tgc ctg gac atc agc gac ttc ggc tgc cag ctg tcc tcc tgc cat cgc			255
Cys Leu Asp Ile Ser Asp Phe Gly Cys Gln Leu Ser Ser Cys His Arg			
40	45	50	55
acc gac ccg ctc cac cgc ttc cac acc aac agg tgg aac cta act tct			303
Thr Asp Pro Leu His Arg Phe His Thr Asn Arg Trp Asn Leu Thr Ser			
	60	65	70
tgt gga aca agt gtt gcc agc tca gaa ggc agt gag gag ctg ttt tca			351
Cys Gly Thr Ser Val Ala Ser Ser Glu Gly Ser Glu Glu Leu Phe Ser			
	75	80	85
tct gtg tct gtt gga gat caa gat gat tgc tat tcc ctg tta gat gat			399
Ser Val Ser Val Gly Asp Gln Asp Asp Cys Tyr Ser Leu Leu Asp Asp			
	90	95	100
cag gac ttc act tct ttt gat tta ttt cct gag ggg agt gtc tgc agt			447
Gln Asp Phe Thr Ser Phe Asp Leu Phe Pro Glu Gly Ser Val Cys Ser			
	105	110	115
gat gtc tct tct tct att agc act tac tgg gat tgg tca gat agc gag			495
Asp Val Ser Ser Ser Ile Ser Thr Tyr Trp Asp Trp Ser Asp Ser Glu			
	120	125	130
ttt gaa tgg cag tta cca ggc agt gac att gcc agt ggg agt gat gta			543
Phe Glu Trp Gln Leu Pro Gly Ser Asp Ile Ala Ser Gly Ser Asp Val			
	140	145	150
ctt tct gat gtc ata ccc agt att cca agt tca cct tgc ctg ctt cct			591
Leu Ser Asp Val Ile Pro Ser Ile Pro Ser Ser Pro Cys Leu Leu Pro			
	155	160	165
aaa aag aaa aac aag cac cgg aat tta gat gaa ctc cct tgg agt gca			639
Lys Lys Lys Asn Lys His Arg Asn Leu Asp Glu Leu Pro Trp Ser Ala			
	170	175	180
atg aca aat gat gag cag gtg gaa tat att gag tat ctg agt cgg aaa			687
Met Thr Asn Asp Glu Gln Val Glu Tyr Ile Glu Tyr Leu Ser Arg Lys			
	185	190	195
gtg agt act gag atg ggt ctt cgg gag caa ctt gat att att aag atc			735
Val Ser Thr Glu Met Gly Leu Arg Glu Gln Leu Asp Ile Ile Lys Ile			
	200	205	210
att gat cct tct gct cag atc tcc cct aca gac agg gag ttt att att			783
Ile Asp Pro Ser Ala Gln Ile Ser Pro Thr Asp Arg Glu Phe Ile Ile			
	220	225	230
gaa ctt aac tgt ctc aca gat gaa aaa ctg aag cag gtc aga aac tat			831
Glu Leu Asn Cys Leu Thr Asp Glu Lys Leu Lys Gln Val Arg Asn Tyr			
	235	240	245
atc aag gaa cat agc cct cgc caa cgg cct gca aga gag gcc tgg aag			879
Ile Lys Glu His Ser Pro Arg Gln Arg Pro Ala Arg Glu Ala Trp Lys			
	250	255	260

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aga agc aac ttt agt tgt gca agc acc agt gga gtg agc ggt gcc agt      927
Arg Ser Asn Phe Ser Cys Ala Ser Thr Ser Gly Val Ser Gly Ala Ser
265                               270                               275

gcc agc gcc agc agc agc agt gcc agc atg gtc agt tct gca agc agc      975
Ala Ser Ala Ser Ser Ser Ser Ala Ser Met Val Ser Ser Ala Ser Ser
280                               285                               290                               295

agt ggg tcc agt gtt gga aac tct gct tca aac tcc agt gcc aac atg      1023
Ser Gly Ser Ser Val Gly Asn Ser Ala Ser Asn Ser Ser Ala Asn Met
300                               305                               310

agt cga gca cac agt gac agc aac ctg tct gca agt gca gca gag cgg      1071
Ser Arg Ala His Ser Asp Ser Asn Leu Ser Ala Ser Ala Ala Glu Arg
315                               320                               325

att cgg gat tca aaa aag cga tcc aag cag cgg aag tta cag cag aag      1119
Ile Arg Asp Ser Lys Lys Arg Ser Lys Gln Arg Lys Leu Gln Gln Lys
330                               335                               340

gcc ttc cgc aag agg cag ctg aag gag cag agg cag gcc cgg aag gag      1167
Ala Phe Arg Lys Arg Gln Leu Lys Glu Gln Arg Gln Ala Arg Lys Glu
345                               350                               355

agg ctc agt ggg ctc ttc ctt aac gaa gag gtg ctg tcc ttg aaa gtg      1215
Arg Leu Ser Gly Leu Phe Leu Asn Glu Glu Val Leu Ser Leu Lys Val
360                               365                               370                               375

act gag gaa gac cat gaa gca gat gtt gat gtt ttg atg taa taagggt      1264
Thr Glu Glu Asp His Glu Ala Asp Val Asp Val Leu Met *
380                               385

gaatttatca acgttctttg tgagcattaa aatactccat ccttatgggt ttacatgcaa      1324

aaaaaaaaa a                                                                1335

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<210> 152
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (203)..(1582)

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gatgcaggaa ttcatctaatt tttcactgcc gggcgaggtg tgagagccct agcatctgaa      180

agtggtcgac ttgcgagttg tt atg gag aaa act tgt ata gat gca ctt cct      232

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	Met	Glu	Lys	Thr	Cys	Ile	Asp	Ala	Leu	Pro	
	1				5					10	
ctt act atg aat tct tca gaa aag caa gag act gta tgt att ttt gga											280
Leu Thr Met Asn Ser Ser Glu Lys Gln Glu Thr Val Cys Ile Phe Gly											
				15					20		25
act ggt gat ttt gga aga tca ctg gga ttg aaa atg ctc cag tgt ggt											328
Thr Gly Asp Phe Gly Arg Ser Leu Gly Leu Lys Met Leu Gln Cys Gly											
				30					35		40
tat tct gtt gtt ttt gga agt cga aac ccc cag aag acc acc cta ctg											376
Tyr Ser Val Val Phe Gly Ser Arg Asn Pro Gln Lys Thr Thr Leu Leu											
				45					50		55
ccc agt ggt gca gaa gtc ttg agc tat tca gaa gca gcc aag aag tct											424
Pro Ser Gly Ala Glu Val Leu Ser Tyr Ser Glu Ala Ala Lys Lys Ser											
				60					65		70
ggc atc ata atc ata gca atc cac aga gag cat tat gat ttt ctc aca											472
Gly Ile Ile Ile Ile Ala Ile His Arg Glu His Tyr Asp Phe Leu Thr											
				75					80		85
gaa tta act gag gtt ctc aat gga aaa ata ttg gta gac atc agc aac											520
Glu Leu Thr Glu Val Leu Asn Gly Lys Ile Leu Val Asp Ile Ser Asn											
				95					100		105
aac ctc aaa atc aat caa tat cca gaa tct aat gca gag tac ctt gct											568
Asn Leu Lys Ile Asn Gln Tyr Pro Glu Ser Asn Ala Glu Tyr Leu Ala											
				110					115		120
cat ttg gtg cca gga gcc cac gtg gta aaa gca ttt aac acc atc tca											616
His Leu Val Pro Gly Ala His Val Val Lys Ala Phe Asn Thr Ile Ser											
				125					130		135
gcc tgg gct ctc cag tca gga gca ctg gat gca agt cgg cag gtg ttt											664
Ala Trp Ala Leu Gln Ser Gly Ala Leu Asp Ala Ser Arg Gln Val Phe											
				140					145		150
gtg tgt gga aat gac agc aaa gcc aag caa aga gtg atg gat att gtt											712
Val Cys Gly Asn Asp Ser Lys Ala Lys Gln Arg Val Met Asp Ile Val											
				155					160		165
cgt aat ctt gga ctt act cca atg gat caa gga tca ctc atg gca gcc											760
Arg Asn Leu Gly Leu Thr Pro Met Asp Gln Gly Ser Leu Met Ala Ala											
				175					180		185
aaa gaa att gaa aag tac ccc ctg cag cta ttt cca atg tgg agg ttc											808
Lys Glu Ile Glu Lys Tyr Pro Leu Gln Leu Phe Pro Met Trp Arg Phe											
				190					195		200
ccc ttc tat ttg tct gct gtg ctg tgt gtc ttc ttg ttt ttc tat tgt											856
Pro Phe Tyr Leu Ser Ala Val Leu Cys Val Phe Leu Phe Phe Tyr Cys											
				205					210		215
gtt ata aga gac gta atc tac cct tat gtt tat gaa aag aaa gat aat											904
Val Ile Arg Asp Val Ile Tyr Pro Tyr Val Tyr Glu Lys Lys Asp Asn											


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cac tag aaaaagcatt gaatggaaaa tcaatattta aaacaaagtt caatttagct 1632
His *
460

ggatttctga actatggttt tgaatgttta aagaagaatg atgggtacag ttaggaaagt 1692
ttttttctta caccgtgact gagggaaaca ttgcttgctt ttgagaaatt gactgacata 1752
ctggaagaga acaccatttt atctcagggt agtgaagaat cagtgcaggt ccctgactct 1812
tattttccca gagggcatgg agctgagatt gagactagcc ttgtggtttc aactaaaga 1872
gtttccttgt tatgggcaac atgcatgacc taatgtcttg caaaatccaa tagaagtatt 1932
gcagcttcct tctctggctc aagggtgag ttaagtgaag ggaaaaacag cacaatgggtg 1992
accactgata aaggctttat taggtatatc tgaggaagtg ggacacatga aatgtaaaaa 2052
gggaatgagg tttttgttgt tttttggaag taaaggcaaa cataaatatt accatgatga 2112
attctagtga aatgaccctt tgactttgct tttcttaata cagatattta ctgagaggaa 2172
ctatttttat aacacaagaa aaatttacia ttgattaaaa gtatccatgt cttggataca 2232
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<210> 153
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<212> DNA
<213> Homo sapiens

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<222> (306) .. (2174)

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ggccagagcc caccctcctg ctcatgaggg cagacaggcc tttccaggga cacagtcctt 120
cttctcccca ggaccccagg gccaactccc cctgccggcc ctctgccatc aaattggcag 180
tggtccagg ggagtcacct ggggatgggg gaccactgtt ggggacctct ctgcgtgcac 240
ccctgtagtt ggggaagcag gacagggggc tggggagacg gaagggcgcc aggggttag 300
agagg      atg gtg gac gtt gtt gga ctt gaa agg gaa aca ggc cct cgg 347
            Met Val Asp Val Val Gly Leu Glu Arg Glu Thr Gly Pro Arg
            1             5             10

gga agc ccc tgg cca ggc ctg cct ctc ccc tcc ctg gtg ggc cca gcg 395
Gly Ser Pro Trp Pro Gly Leu Pro Leu Pro Ser Leu Val Gly Pro Ala
15             20             25             30

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tat gga ctg tcg gaa cag gct ggg gtg acc ccg gag gcc tgg gcc caa	1115
Tyr Gly Leu Ser Glu Gln Ala Gly Val Thr Pro Glu Ala Trp Ala Gln	
255 260 265 270	
ctg agc cct gcc ctg ctc caa cag cag ctg agt gga gcc tgc acc tcc	1163
Leu Ser Pro Ala Leu Leu Gln Gln Gln Leu Ser Gly Ala Cys Thr Ser	
275 280 285	
cag tcc agg ccc ccc gtc cag gac cag ctc agc cag tca gag agg tat	1211
Gln Ser Arg Pro Pro Val Gln Asp Gln Leu Ser Gln Ser Glu Arg Tyr	
290 295 300	
ctg tac ggc tcc ctg gcc acg ctg ctc atc tgc ctc tgc gcg gtc ttt	1259
Leu Tyr Gly Ser Leu Ala Thr Leu Leu Ile Cys Leu Cys Ala Val Phe	
305 310 315	
ggc ctc ctg ctg ctg acc tgc act ggc tgc agg ggg gtc gcc cac tac	1307
Gly Leu Leu Leu Leu Thr Cys Thr Gly Cys Arg Gly Val Ala His Tyr	
320 325 330	
atc ctg cag acc ttc ctg agc ctg gca gtg ggt gca ctc act ggg gac	1355
Ile Leu Gln Thr Phe Leu Ser Leu Ala Val Gly Ala Leu Thr Gly Asp	
335 340 345 350	
gct gtc ctg cat ctg acg ccc aag gtg ctg ggg ctg cat aca cac agc	1403
Ala Val Leu His Leu Thr Pro Lys Val Leu Gly Leu His Thr His Ser	
355 360 365	
gaa gag ggc ctc agc cca cag ccc acc tgg cgc ctc ctg gct atg ctg	1451
Glu Glu Gly Leu Ser Pro Gln Pro Thr Trp Arg Leu Leu Ala Met Leu	
370 375 380	
gcc ggg ctc tac gcc ttc ttc ctg ttt gag aac ctc ttc aat ctc ctg	1499
Ala Gly Leu Tyr Ala Phe Phe Leu Phe Glu Asn Leu Phe Asn Leu Leu	
385 390 395	
ctg ccc agg gac ccg gag gac ctg gag gac ggg ccc tgc ggc cac agc	1547
Leu Pro Arg Asp Pro Glu Asp Leu Glu Asp Gly Pro Cys Gly His Ser	
400 405 410	
agc cat agc cac ggg ggc cac agc cac ggt gtg tcc ctg cag ctg gca	1595
Ser His Ser His Gly Gly His Ser His Gly Val Ser Leu Gln Leu Ala	
415 420 425 430	
ccc agc gag ctc cgg cag ccc aag ccc ccc cac gag ggc tcc cgc gca	1643
Pro Ser Glu Leu Arg Gln Pro Lys Pro Pro His Glu Gly Ser Arg Ala	
435 440 445	
gac ctg gtg gcg gag gag agc ccg gag ctg ctg aac cct gag ccc agg	1691
Asp Leu Val Ala Glu Glu Ser Pro Glu Leu Leu Asn Pro Glu Pro Arg	
450 455 460	
aga ctg agc cca gag ttg agg cta ctg ccc tat atg atc act ctg ggc	1739
Arg Leu Ser Pro Glu Leu Arg Leu Leu Pro Tyr Met Ile Thr Leu Gly	
465 470 475	
gac gcc gtg cac aac ttc gcc gac ggg ctg gcc gtg ggc gcc gcc ttc	1787

Asp	Ala	Val	His	Asn	Phe	Ala	Asp	Gly	Leu	Ala	Val	Gly	Ala	Ala	Phe		
480						485					490						
gcg	tcc	tcc	tgg	aag	acc	ggg	ctg	gcc	acc	tgc	ctg	gcc	gtg	ttc	tgc	1835	
Ala	Ser	Ser	Trp	Lys	Thr	Gly	Leu	Ala	Thr	Ser	Leu	Ala	Val	Phe	Cys		
495					500					505					510		
cac	gag	ttg	cca	cac	gag	ctg	ggg	gac	ttc	gcc	gcc	ttg	ctg	cac	gcg	1883	
His	Glu	Leu	Pro	His	Glu	Leu	Gly	Asp	Phe	Ala	Ala	Leu	Leu	His	Ala		
				515					520					525			
ggg	ctg	tcc	gtg	cgc	caa	gca	ctg	ctg	ctg	aac	ctg	gcc	tcc	gcg	ctc	1931	
Gly	Leu	Ser	Val	Arg	Gln	Ala	Leu	Leu	Leu	Asn	Leu	Ala	Ser	Ala	Leu		
			530					535					540				
acg	gcc	ttc	gct	ggt	ctc	tac	gtg	gca	ctc	gcg	gtt	gga	gtc	agc	gag	1979	
Thr	Ala	Phe	Ala	Gly	Leu	Tyr	Val	Ala	Leu	Ala	Val	Gly	Val	Ser	Glu		
		545					550					555					
gag	agc	gag	gcc	tgg	atc	ctg	gca	gtg	gcc	acc	ggc	ctg	ttc	ctc	tac	2027	
Glu	Ser	Glu	Ala	Trp	Ile	Leu	Ala	Val	Ala	Thr	Gly	Leu	Phe	Leu	Tyr		
	560					565					570						
gta	gca	ctc	tgc	gac	atg	ctc	ccg	gcg	atg	ttg	aaa	gta	cgg	gac	ccg	2075	
Val	Ala	Leu	Cys	Asp	Met	Leu	Pro	Ala	Met	Leu	Lys	Val	Arg	Asp	Pro		
575					580					585					590		
cgg	ccc	tgg	ctc	ctc	ttc	ctg	ctg	cac	aac	gtg	ggc	ctg	ctg	ggc	ggc	2123	
Arg	Pro	Trp	Leu	Leu	Phe	Leu	Leu	His	Asn	Val	Gly	Leu	Leu	Gly	Gly		
				595					600					605			
ttg	acc	gtc	ctg	ctg	ctg	ctg	tcc	ctg	tac	gag	gat	gac	atc	acc	ttc	2171	
Trp	Thr	Val	Leu	Leu	Leu	Leu	Ser	Leu	Tyr	Glu	Asp	Asp	Ile	Thr	Phe		
			610					615					620				
tga	tacc	ctgccctagt	ccccacatt	tgacttaaga	tcccacacct	cacaaaccta										2228	
*																	
cagcccagaa	accagaagcc	cctatagagg	cccaggtccc	aactccagta	aagacactct											2288	
tgtccttgga	aaaaaaaaaa	aa														2310	

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 <213> Homo sapiens

<220>
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 <222> (136)..(1170)

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ccgcgggctg ggacc atg ggc tgc ttc ttc tcc aag aga cgg aag gct gac	171
Met Gly Cys Phe Phe Ser Lys Arg Arg Lys Ala Asp	
1 5 10	
aag gag tcg cgg ccc gag aac gag gag gag cgg cca aag cag tac agc	219
Lys Glu Ser Arg Pro Glu Asn Glu Glu Glu Arg Pro Lys Gln Tyr Ser	
15 20 25	
tgg gat cag cgc gag aag gtt gat cca aaa gac tac atg ttc agt gga	267
Trp Asp Gln Arg Glu Lys Val Asp Pro Lys Asp Tyr Met Phe Ser Gly	
30 35 40	
ctg aag gat gaa aca gta ggt cgc tta cct ggg acg gta gca gga caa	315
Leu Lys Asp Glu Thr Val Gly Arg Leu Pro Gly Thr Val Ala Gly Gln	
45 50 55 60	
cag ttt ctc att caa gac tgt gag aac tgt aac atc tat att ttt gat	363
Gln Phe Leu Ile Gln Asp Cys Glu Asn Cys Asn Ile Tyr Ile Phe Asp	
65 70 75	
cac tct gct aca gtt acc att gat gac tgt act aac tgc ata att ttt	411
His Ser Ala Thr Val Thr Ile Asp Asp Cys Thr Asn Cys Ile Ile Phe	
80 85 90	
ctg gga ccc gtg aaa ggc agc gtg ttt ttc cgg aat tgc aga gat tgc	459
Leu Gly Pro Val Lys Gly Ser Val Phe Phe Arg Asn Cys Arg Asp Cys	
95 100 105	
aag tgc aca tta gcc tgc caa caa ttt cgt gtg cga gat tgt aga aag	507
Lys Cys Thr Leu Ala Cys Gln Gln Phe Arg Val Arg Asp Cys Arg Lys	
110 115 120	
ctg gaa gtc ttt ttg tgt tgt gcc act caa ccc atc att gag tct tcc	555
Leu Glu Val Phe Leu Cys Cys Ala Thr Gln Pro Ile Ile Glu Ser Ser	
125 130 135 140	
tca aat atc aaa ttt gga tgt ttt caa tgg tac tat cct gaa tta gct	603
Ser Asn Ile Lys Phe Gly Cys Phe Gln Trp Tyr Tyr Pro Glu Leu Ala	
145 150 155	
ttc cag ttc aaa gat gca ggg cta agt atc ttc gac aat aca tgg agt	651
Phe Gln Phe Lys Asp Ala Gly Leu Ser Ile Phe Asp Asn Thr Trp Ser	
160 165 170	
aac att cat gac ttt aca cct gtg tca gga gaa ctc aac tgg agc ctt	699
Asn Ile His Asp Phe Thr Pro Val Ser Gly Glu Leu Asn Trp Ser Leu	
175 180 185	
ctt cca gaa gat gct gtg gtt cag gac tat gtt cct ata cct act acc	747
Leu Pro Glu Asp Ala Val Gln Asp Tyr Val Pro Ile Pro Thr Thr	
190 195 200	
gaa gag ctc aaa gct gtt cgt gtt tcc aca gaa gcc aat aga agc att	795
Glu Glu Leu Lys Ala Val Arg Val Ser Thr Glu Ala Asn Arg Ser Ile	

205	210	215	220	
gtt cca ata tcc cgg ggt cag aga cag aag agc agc gat gaa tca tgc				843
Val Pro Ile Ser Arg Gly Gln Arg Gln Lys Ser Ser Asp Glu Ser Cys				
225		230	235	
tta gtg gta tta ttt gct ggt gat tac act att gca aat gcc aga aaa				891
Leu Val Val Leu Phe Ala Gly Asp Tyr Thr Ile Ala Asn Ala Arg Lys				
240		245	250	
cta att gat gag atg gtt ggt aaa ggc ttt ttc cta gtt cag aca aag				939
Leu Ile Asp Glu Met Val Gly Lys Gly Phe Phe Leu Val Gln Thr Lys				
255		260	265	
gaa gtg tcc atg aaa gct gag gat gct caa agg gtt ttt cgg gaa aaa				987
Glu Val Ser Met Lys Ala Glu Asp Ala Gln Arg Val Phe Arg Glu Lys				
270		275	280	
gca cct gac ttc ctt cct ctt ctg aac aaa ggt cct gtt att gcc ttg				1035
Ala Pro Asp Phe Leu Pro Leu Leu Asn Lys Gly Pro Val Ile Ala Leu				
285		290	295	300
gag ttt aat ggg gat ggt gct gta gaa gta tgt caa ctt att gta aac				1083
Glu Phe Asn Gly Asp Gly Ala Val Glu Val Cys Gln Leu Ile Val Asn				
305		310	315	
gag ata ttc aat ggg acc aag atg ttt gta tct gaa agc aag gag aca				1131
Glu Ile Phe Asn Gly Thr Lys Met Phe Val Ser Glu Ser Lys Glu Thr				
320		325	330	
ggt ttc tgg aga tgt aga cac gct cta aca ctt ggc tga tatacagatg				1180
Gly Phe Trp Arg Cys Arg His Ala Leu Thr Leu Gly *				
335		340	345	
ggaatatgaa gtgcaatgtg gaaccggac ttggtataag acctttccca ctt				1233

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<220>
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ccttttgtag tcttgatgaa taatttcatt ttctcaagt ttatgacact cggaacgtca	180
agaactggag gtttgtgcaa tttgagaccg gtcggcactg tgcagagatc agagtactaa	240

gagacagaga ttaaa atg gct tcc aga gga aag aca gag aca agc aaa tta 291
Met Ala Ser Arg Gly Lys Thr Glu Thr Ser Lys Leu
1 5 10

aag cag aat tta gaa gaa cag ttg gat aga ctc atg caa caa tta caa 339
Lys Gln Asn Leu Glu Glu Gln Leu Asp Arg Leu Met Gln Gln Leu Gln
15 20 25

gat ctg gag gaa tgc aga gag gaa ctt gat aca gat gaa tat gaa gaa 387
Asp Leu Glu Glu Cys Arg Glu Glu Leu Asp Thr Asp Glu Tyr Glu Glu
30 35 40

acc aaa aag gaa act ctg gag caa cta agt gaa ttt aat gat tca cta 435
Thr Lys Lys Glu Thr Leu Glu Gln Leu Ser Glu Phe Asn Asp Ser Leu
45 50 55 60

aag aaa att atg tct gga aat atg act ttg gta gat gaa cta agt gga 483
Lys Lys Ile Met Ser Gly Asn Met Thr Leu Val Asp Glu Leu Ser Gly
65 70 75

atg cag ctg gct att cag gca gct atc agc cag gcc ttt aaa acc cca 531
Met Gln Leu Ala Ile Gln Ala Ala Ile Ser Gln Ala Phe Lys Thr Pro
80 85 90

gag gtc atc aga ttg ttt gca aag aaa caa cca ggt cag ctt cgg aca 579
Glu Val Ile Arg Leu Phe Ala Lys Lys Gln Pro Gly Gln Leu Arg Thr
95 100 105

agg tta gca gag atg gat aga gat ctg atg gta gga aag ctg gaa aga 627
Arg Leu Ala Glu Met Asp Arg Asp Leu Met Val Gly Lys Leu Glu Arg
110 115 120

gac ctg tac act caa cag aaa gtg gag ata cta aca gct ctt agg aaa 675
Asp Leu Tyr Thr Gln Gln Lys Val Glu Ile Leu Thr Ala Leu Arg Lys
125 130 135 140

ctt gga gag aag ctg act gca gat gat gag gcc ttc ttg tca gca aat 723
Leu Gly Glu Lys Leu Thr Ala Asp Asp Glu Ala Phe Leu Ser Ala Asn
145 150 155

gca ggt gct ata ctc agc cag ttt gag aaa gtc tct aca gac ctt gga 771
Ala Gly Ala Ile Leu Ser Gln Phe Glu Lys Val Ser Thr Asp Leu Gly
160 165 170

cgg ccc cca agt tac atg aac tac ctg cta gac tca cac ccc agc aaa 819
Arg Pro Pro Ser Tyr Met Asn Tyr Leu Leu Asp Ser His Pro Ser Lys
175 180 185

aat att gat gtc ccc agc aag att agc ttc ctg tta aag atc cag gac 867
Asn Ile Asp Val Pro Ser Lys Ile Ser Phe Leu Leu Lys Ile Gln Asp
190 195 200

ctg tga atacatgcgt aactgcaaga atggaagcaa aggatgaacc caagttaaag 923
Leu *
205

cccagcaciaa gaatatgatg taagcgcttt tgggaaatgc agagattttc ttttctcttc 983

aaataataaa ttacatctaa aaattaaaaa aaaaaaaa

1021

<210> 156
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<212> DNA
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gaa ggg aca gaa cag aca cta gat gcg gag gag gag cag gag gaa tcc	96
Glu Gly Thr Glu Gln Thr Leu Asp Ala Glu Glu Glu Gln Glu Glu Ser	
20 25 30	

gaa gaa gcg gcc tgt ggc agc aag aag cgg gta gtg cca ggt att gtg	144
Glu Glu Ala Ala Cys Gly Ser Lys Lys Arg Val Val Pro Gly Ile Val	
35 40 45	

tac ctg ggc cat atc ccg ccg cgc ttc cgg ccc ctg cac gtc cgc aac	192
Tyr Leu Gly His Ile Pro Pro Arg Phe Arg Pro Leu His Val Arg Asn	
50 55 60	

ctt ctc agc gcc tat ggc gag gtc gga cgc gtc ttc ttt cag gct gag	240
Leu Leu Ser Ala Tyr Gly Glu Val Gly Arg Val Phe Phe Gln Ala Glu	
65 70 75 80	

gac cgg ttc gtg aga cgc aag aag aag gca gca gca gct gcc gga gga	288
Asp Arg Phe Val Arg Arg Lys Lys Lys Ala Ala Ala Ala Ala Gly Gly	
85 90 95	

aaa aag cgg tcc tac acc aag gac tac acc gag gga tgg gtg gag ttc	336
Lys Lys Arg Ser Tyr Thr Lys Asp Tyr Thr Glu Gly Trp Val Glu Phe	
100 105 110	

cgt gac aag cgc ata gcc aag cgc gtg gcg gcc agt cta cac aac acg	384
Arg Asp Lys Arg Ile Ala Lys Arg Val Ala Ala Ser Leu His Asn Thr	
115 120 125	

cct atg ggt gcc cgc agg cgc agc ccc ttc cgt tat gat ctt tgg aac	432
Pro Met Gly Ala Arg Arg Arg Ser Pro Phe Arg Tyr Asp Leu Trp Asn	
130 135 140	

ctc aag tac ttg cac cgt ttc acc tgg tcc cac ctc agc gag cac ctc	480
Leu Lys Tyr Leu His Arg Phe Thr Trp Ser His Leu Ser Glu His Leu	
145 150 155 160	

gcc ttt gag cgc cag gtg cgc agg cag cgc ttg aga gcg gag gtt gct	528
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Ala Phe Glu Arg Gln Val Arg Arg Gln Arg Leu Arg Ala Glu Val Ala	
165 170 175	
caa gcc aag cgt gag acc gac ttc tat ctt caa agt gtg gaa cgg gga	576
Gln Ala Lys Arg Glu Thr Asp Phe Tyr Leu Gln Ser Val Glu Arg Gly	
180 185 190	
caa cgc ttt ctt gcg gcc gat ggg gac cct gct cgc cca gat ggc tcc	624
Gln Arg Phe Leu Ala Ala Asp Gly Asp Pro Ala Arg Pro Asp Gly Ser	
195 200 205	
tgg aca ttt gcc cag cgt cct act gag cag gaa ctg agg gcc cgt aaa	672
Trp Thr Phe Ala Gln Arg Pro Thr Glu Gln Glu Leu Arg Ala Arg Lys	
210 215 220	
gca gca cgg cca ggg gga cgt gaa cgg gct cgc ctg gca act gcc cag	720
Ala Ala Arg Pro Gly Gly Arg Glu Arg Ala Arg Leu Ala Thr Ala Gln	
225 230 235 240	
gac aag gcc cgc tcc aac aaa ggg ctc ctg gcc agg atc ttt gga gcc	768
Asp Lys Ala Arg Ser Asn Lys Gly Leu Leu Ala Arg Ile Phe Gly Ala	
245 250 255	
ccg cca ccc tca gag agc atg gag gga cct tcc ctt gtc agg gac tcc	816
Pro Pro Pro Ser Glu Ser Met Glu Gly Pro Ser Leu Val Arg Asp Ser	
260 265 270	
tga gggc ctgggtggcc ccttccatct cctggccctg ctctgcttcc tgtctacctc	873
*	
atactagaat gatcgtgact acccgggcag acatttttact gtgtttctca gaccaagtgt	933
ctactgatgg cccaaacatg gagttttgtg ggcttccact gtccccactc cgaactcctg	993
tatgtgcctg gctgagtcac ctaattcata ctgtcatact agcataatta tgactattgc	1053
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cttctgccc ccagaaaggg cctttatttc caactaggag gataatgcct agtcaggca	1173
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cctggcacc accttactgt ttaacctgga ttttttttcc tatttaattt ttgtctaata	1473
tattagccca gtttatcaat cagttatctt aagtcagcat tttctaagcc attgtttgag	1533
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 <213> Homo sapiens

<220>
 <221> CDS
 <222> (228)..(911)

<400> 157

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gcggcggcag cgctccaact ggctcctcgc tccgggctcc gccgtcgagc cgggagagag      120
cctccgccag cggccaggca ccagccagac gacgccagcg accccggcct ctcggcggca      180
ccgcgctaac tcaggggctg cataggcacc cagagccgaa ctccaag  atg gga ggc      236
                                     Met Gly Gly
                                     1

aag ctc agc aag aag aag aag ggc tac aat gtg aac gac gag aaa gcc      284
Lys Leu Ser Lys Lys Lys Lys Gly Tyr Asn Val Asn Asp Glu Lys Ala
      5                                10                                15

aag gag aaa gac aag aag gcc gag ggc gcg gcg acg gaa gag gag ggg      332
Lys Glu Lys Asp Lys Lys Ala Glu Gly Ala Ala Thr Glu Glu Glu Gly
      20                                25                                30                                35

acc ccg aag gag agt gag ccc cag gcg gcc gca gag ccc gcc gag gcc      380
Thr Pro Lys Glu Ser Glu Pro Gln Ala Ala Ala Glu Pro Ala Glu Ala
                                40                                45                                50

aag gag ggc aag gag aag ccc gac cag gac gcc gag ggc aag gcc gag      428
Lys Glu Gly Lys Glu Lys Pro Asp Gln Asp Ala Glu Gly Lys Ala Glu
                                55                                60                                65

gag aag gag ggc gag aag gac gcg gcg gct gcc aag gag gag gcc ccg      476
Glu Lys Glu Gly Glu Lys Asp Ala Ala Ala Ala Lys Glu Glu Ala Pro
      70                                75                                80

aag gcg gag ccc gag aag acg gag ggc gcg gca gag gcc aag gct gag      524
Lys Ala Glu Pro Glu Lys Thr Glu Gly Ala Ala Glu Ala Lys Ala Glu
      85                                90                                95

ccc ccg aag gcg ccc gag cag gag cag gcg gcc ccc ggc ccc gct gcg      572
Pro Pro Lys Ala Pro Glu Gln Glu Gln Ala Ala Pro Gly Pro Ala Ala
      100                                105                                110                                115

ggc ggc gag gcc ccc aaa gct gct gag gcc gcc gcg gcc ccg gcc gag      620
Gly Gly Glu Ala Pro Lys Ala Ala Glu Ala Ala Ala Ala Pro Ala Glu
                                120                                125                                130

agc gcg gcc cct gcc gcc ggg gag gag ccc agc aag gag gaa ggg gaa      668
Ser Ala Ala Pro Ala Ala Gly Glu Glu Pro Ser Lys Glu Glu Gly Glu
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<221> CDS
 <222> (417)..(1403)

<400> 158

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gggtcaccac cctgggcgac ccggaggtgg cgcctccgcc ggccgcagct ggagaggagc      180
gtgtcccaaa gccggggggag caggacttga gcaggcacgc ggggtcaccg ccgggcagcg      240
tggaggagcc atctcctgga ggagaaaact cacctggtgg cggaggctcc ccttgtttgt      300
cctcccggag cctggcgtgg ggttcttctg cggaagaga gagtgcgcgc ggagatagca      360

gtgtggaac gcgcgaggag tcggagggca cgggcggcca gcgctcagcc tgcgcc      416
atg ggt ggt ccc ggg acc aag agc ggg gag cct ttg tgt cct ccg tta      464
Met Gly Gly Pro Gly Thr Lys Ser Gly Glu Pro Leu Cys Pro Pro Leu
  1             5             10             15

ctg tgt aat cag gac aaa gaa acc ttg act ctg ctc att cag gtg cct      512
Leu Cys Asn Gln Asp Lys Glu Thr Leu Thr Leu Leu Ile Gln Val Pro
             20             25             30

cgg atc cag ccg caa agt ctt caa gga gat ttg aat ccc ctc tgg tac      560
Arg Ile Gln Pro Gln Ser Leu Gln Gly Asp Leu Asn Pro Leu Trp Tyr
             35             40             45

aaa tta cgc ttc tcc gca caa gac tta gtt tat tcc ttc ttt ttg caa      608
Lys Leu Arg Phe Ser Ala Gln Asp Leu Val Tyr Ser Phe Phe Leu Gln
             50             55             60

ttt gct cca gag aat aaa ttg agt acc aca gaa cct gtg att agc att      656
Phe Ala Pro Glu Asn Lys Leu Ser Thr Thr Glu Pro Val Ile Ser Ile
             65             70             75             80

tct tca aac aat gca gtg ata gaa ctg gca aaa tct cca gag agc cat      704
Ser Ser Asn Asn Ala Val Ile Glu Leu Ala Lys Ser Pro Glu Ser His
             85             90             95

gga cat tgg aga gag tgg tat tat ggt gta aac aac gat tct ttg gag      752
Gly His Trp Arg Glu Trp Tyr Tyr Gly Val Asn Asn Asp Ser Leu Glu
             100             105             110

gaa agg tta ttt gtc aat gaa gaa aat gtt aat gag ttt ctt gaa gag      800
Glu Arg Leu Phe Val Asn Glu Glu Asn Val Asn Glu Phe Leu Glu Glu
             115             120             125

gtc ctg agc tct cca ttc aaa cag tct atg tcc ttg acc cca cca tta      848
Val Leu Ser Ser Pro Phe Lys Gln Ser Met Ser Leu Thr Pro Pro Leu
             130             135             140

att gaa gtt ctt caa gtt act gat aat aag att caa att aat gca aag      896
Ile Glu Val Leu Gln Val Thr Asp Asn Lys Ile Gln Ile Asn Ala Lys
             145             150             155             160

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ttg caa gaa tgt agt aac tct gat cag cta caa gga aag gag gaa aga Leu Gln Glu Cys Ser Asn Ser Asp Gln Leu Gln Gly Lys Glu Glu Arg 165 170 175	944
gta aat gaa gaa agt cat cta act gaa aag gaa tat ata gaa cat tgt Val Asn Glu Glu Ser His Leu Thr Glu Lys Glu Tyr Ile Glu His Cys 180 185 190	992
aac acc cct aca act gat tct gat tca tct ata gca gtt aaa gca cta Asn Thr Pro Thr Thr Asp Ser Asp Ser Ser Ile Ala Val Lys Ala Leu 195 200 205	1040
caa ata gat agc ttt ggt tta gtt aca tgc ttt caa caa gag tct ctt Gln Ile Asp Ser Phe Gly Leu Val Thr Cys Phe Gln Gln Glu Ser Leu 210 215 220	1088
gat gtt tct caa atg ata ctt gga aaa tct cag caa cct gag tca aaa Asp Val Ser Gln Met Ile Leu Gly Lys Ser Gln Gln Pro Glu Ser Lys 225 230 235 240	1136
atg caa tct gaa ttt ata aaa gaa aaa agt gct act tgt tca aat gag Met Gln Ser Glu Phe Ile Lys Glu Lys Ser Ala Thr Cys Ser Asn Glu 245 250 255	1184
gaa aaa ggt aac tta aac gag tca gta ata act gaa gag aaa gaa aca Glu Lys Gly Asn Leu Asn Glu Ser Val Ile Thr Glu Glu Lys Glu Thr 260 265 270	1232
gat gga gat cac cta tct tca tta ctg aac aaa act acg gtt cac aat Asp Gly Asp His Leu Ser Ser Leu Leu Asn Lys Thr Thr Val His Asn 275 280 285	1280
ata cct gga ttc gac agc ata aaa gaa acc aat atg cag gat ggt agt Ile Pro Gly Phe Asp Ser Ile Lys Glu Thr Asn Met Gln Asp Gly Ser 290 295 300	1328
gtg cag gtc att aaa gat cat gtg acc aat tgt gca ttc agt ttt cag Val Gln Val Ile Lys Asp His Val Thr Asn Cys Ala Phe Ser Phe Gln 305 310 315 320	1376
aat tct ttg cta tat gat ttg gat taa ttcta tataattttg gacttttaaa Asn Ser Leu Leu Tyr Asp Leu Asp *	1428
325	
tattaagggtt aaaaaataacc tgtatctaaa attgattctg ttaactgttg tcttaaaact	1488
aaagggtatta aagtataaaa ttaaaatttg caa	1521

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 <213> Homo sapiens
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<221> CDS

<222> (417)..(1259)

<400> 159

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gggtcaccac	cctgggcgac	ccggaggtgg	cgctcccgcc	ggccgcagct	ggagaggagc	180
gtgtcccaaa	gccgggggag	caggacttga	gcaggcacgc	ggggtcaccg	ccgggcagcg	240
tggaggagcc	atctcctgga	ggagaaaact	cacctggtgg	cggaggctcc	ccttgtttgt	300
cctcccggag	cctggcgtgg	ggttcttctg	cggaagaga	gagtgcgcgc	ggagatagca	360
gtgtggaaac	gcgcgaggag	tcggagggca	cgggcgccca	gcgctcagcc	tgcgcc	416
atg ggt ggt	ccc ggg acc	aag agc ggg	gag cct ttg	tgt cct ccg	tta	464
Met Gly Gly	Pro Gly Thr	Lys Ser Gly	Glu Pro Leu	Cys Pro Pro	Leu	
1	5	10	15			
ctg tgt aat	cag gac aaa	gaa acc ttg	act ctg ctc	att cag gtg	cct	512
Leu Cys Asn	Gln Asp Lys	Glu Thr Leu	Thr Leu Leu	Ile Gln Val	Pro	
	20	25	30			
cgg atc cag	ccg caa agt	ctt caa gga	gat ttg aat	ccc ctc tgg	tac	560
Arg Ile Gln	Pro Gln Ser	Leu Gln Gly	Asp Leu Asn	Pro Leu Trp	Tyr	
	35	40	45			
aaa tta cgc	ttc tcc gca	caa gac tta	gtt tat tcc	ttc ttt ttg	caa	608
Lys Leu Arg	Phe Ser Ala	Gln Asp Leu	Val Tyr Ser	Phe Phe Leu	Gln	
	50	55	60			
ttt gct cca	gag aat aaa	ttg agt acc	aca gaa cct	gtg att agc	att	656
Phe Ala Pro	Glu Asn Lys	Leu Ser Thr	Thr Glu Pro	Val Ile Ser	Ile	
	65	70	75	80		
tct tca aac	aat gca gtg	ata gaa ctg	gca aaa tct	cca gag agc	cat	704
Ser Ser Asn	Asn Ala Val	Ile Glu Leu	Ala Lys Ser	Pro Glu Ser	His	
	85	90	95			
gga cat tgg	aga gag tgg	tat tat ggt	gta aac aac	gat tct ttg	gag	752
Gly His Trp	Arg Glu Trp	Tyr Tyr Gly	Val Asn Asn	Asp Ser Leu	Glu	
	100	105	110			
ttg caa gaa	tgt agt aac	tct gat cag	cta caa gga	aag gag gaa	aga	800
Leu Gln Glu	Cys Ser Asn	Ser Asp Gln	Leu Gln Gly	Lys Glu Glu	Arg	
	115	120	125			
gta aat gaa	gaa agt cat	cta act gaa	aag gaa tat	ata gaa cat	tgt	848
Val Asn Glu	Glu Ser His	Leu Thr Glu	Lys Glu Tyr	Ile Glu His	Cys	
	130	135	140			
aac acc cct	aca act gat	tct gat tca	tct ata gca	gtt aaa gca	cta	896
Asn Thr Pro	Thr Thr Asp	Ser Asp Ser	Ser Ser Ile	Ala Val Lys	Ala Leu	
	145	150	155	160		

caa ata gat agc ttt ggt tta gtt aca tgc ttt caa caa gag tct ctt	944
Gln Ile Asp Ser Phe Gly Leu Val Thr Cys Phe Gln Gln Glu Ser Leu	
165 170 175	
gat gtt tct caa atg ata ctt gga aaa tct cag caa cct gag tca aaa	992
Asp Val Ser Gln Met Ile Leu Gly Lys Ser Gln Gln Pro Glu Ser Lys	
180 185 190	
atg caa tct gaa ttt ata aaa gaa aaa agt gct act tgt tca aat gag	1040
Met Gln Ser Glu Phe Ile Lys Glu Lys Ser Ala Thr Cys Ser Asn Glu	
195 200 205	
gaa aaa ggt aac tta aac gag tca gta ata act gaa gag aaa gaa aca	1088
Glu Lys Gly Asn Leu Asn Glu Ser Val Ile Thr Glu Glu Lys Glu Thr	
210 215 220	
gat gga gat cac cta tct tca tta ctg aac aaa act acg gtt cac aat	1136
Asp Gly Asp His Leu Ser Ser Leu Leu Asn Lys Thr Thr Val His Asn	
225 230 235 240	
ata cct gga ttc gac agc ata aaa gaa acc aat atg cag gat ggt agt	1184
Ile Pro Gly Phe Asp Ser Ile Lys Glu Thr Asn Met Gln Asp Gly Ser	
245 250 255	
gtg cag gtc att aaa gat cat gtg acc aat tgt gca ttc agt ttt cag	1232
Val Gln Val Ile Lys Asp His Val Thr Asn Cys Ala Phe Ser Phe Gln	
260 265 270	
aat tct ttg cta tat gat ttg gat taa ttcta tataattttg gacttttaaa	1284
Asn Ser Leu Leu Tyr Asp Leu Asp *	
275 280	
tattaagggtt aaaaaatacc tgtatctaaa attgattctg ttaactgttg tcttaaaaact	1344
aaagggtatta aagtataaaa ttaaaatttg caa	1377

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 <213> Homo sapiens

<220>
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 <222> (510) .. (1112)

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ttgactgcaa ggccagccca cgccgagggt ccaagcatcg ggatatgccg ccagcacctg	180
gctgctgcag caccgcgctg gacatgagcg ctccgccccaa cccgacggcg tcagctggcg	240

cgcgcgccccg	cgaccgacgt	gcgcaggcg	ccacgggccc	cgagccgcc	attgctctcc	300
tgccacggag	gggagcgctt	ggtggcagtc	cgcgggcccc	gacggaaggc	tgaggcgacg	360
cctcgacgac	agcggaccgg	agctgcaggg	gcaacacatt	cagggcgggg	tgccccattt	420
aggcctggct	gaccggagta	agaaactaca	acccccgaag	tgccttgcg	ctcaaggtta	480
cgagggcagt	gaccacccac	cctggagcc	atg gtc cac gcc ttc ctc att cac			533
			Met Val His Ala Phe Leu Ile His			
			1	5		
acc ttg agg gcc ccg aat act gag gac acg ggc ctt tgc cga gtg ctg						581
Thr Leu Arg Ala Pro Asn Thr Glu Asp Thr Gly Leu Cys Arg Val Leu						
10		15		20		
tac tcc tgc gtc ttc ggt gct gag aag tca cct gat gac cca cgg ccg						629
Tyr Ser Cys Val Phe Gly Ala Glu Lys Ser Pro Asp Asp Pro Arg Pro						
25		30		35		40
cat ggt gcc gag agg gac agg ctt ctc cgg aag gaa cag att tta gct						677
His Gly Ala Glu Arg Asp Arg Leu Leu Arg Lys Glu Gln Ile Leu Ala						
		45		50		55
gtg gcc agg cag gta gag tca atg tgt cgg ctg cag cag cag gca tct						725
Val Ala Arg Gln Val Glu Ser Met Cys Arg Leu Gln Gln Gln Ala Ser						
		60		65		70
ggc cgg ccc ccc atg gac ctg cag ccg caa tcc tca gat gag caa gtg						773
Gly Arg Pro Pro Met Asp Leu Gln Pro Gln Ser Ser Asp Glu Gln Val						
		75		80		85
ccg ctg cac gag gcc cca cgt ggg gct ttc cgc ctg gca gca gag aac						821
Pro Leu His Glu Ala Pro Arg Gly Ala Phe Arg Leu Ala Ala Glu Asn						
		90		95		100
cct ttc cag gag cca cgg acg gtg gtg tgg ctg ggc gtg ctc tcg tta						869
Pro Phe Gln Glu Pro Arg Thr Val Val Trp Leu Gly Val Leu Ser Leu						
105			110		115	120
ggc ttt gcc ctg gtg ctg gat gcc cat gag aac ctg cta ctg gct gag						917
Gly Phe Ala Leu Val Leu Asp Ala His Glu Asn Leu Leu Leu Ala Glu						
		125		130		135
ggc acg ctc cgg ctg ctg aca cgc ctc ctc ctt gac cac ctc cgg ctg						965
Gly Thr Leu Arg Leu Leu Thr Arg Leu Leu Leu Asp His Leu Arg Leu						
		140		145		150
ctg gcg ccc agc acc agc ctt ctg ctg cgg gct gac cgc att gag ggc						1013
Leu Ala Pro Ser Thr Ser Leu Leu Leu Arg Ala Asp Arg Ile Glu Gly						
		155		160		165
atc ctc acc cgc ttc ctg cca cat ggt cag ctg ctt ttc ctc aac gac						1061
Ile Leu Thr Arg Phe Leu Pro His Gly Gln Leu Leu Phe Leu Asn Asp						
		170		175		180
cag ttt gtc caa ggc ctg gag aag gaa ttc agt gcc gct tgg ccc cgc						1109

Gln Phe Val Gln Gly Leu Glu Lys Glu Phe Ser Ala Ala Trp Pro Arg
 185 190 195 200

tga ttcc tcgttgggat ggtgcttctg agggcaggca gagggtagac acacagccag 1166
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atgaagcttg gcattccct cctaccacgc agctctgatg tgctgctata ccaggacaag 1226

tgggtgacac aagcctgcag aaagggggct gggcagaggg tggaggaggt cctgcctgtc 1286

ctcaggtttag tggaaccaca gaacttcctg agcctagagc tgctgtgtta cttagaccgc 1346

tgccgtgagg cagccacgct tgtccttgaa cccaccttcc tccatccctg ccagccgata 1406

gtgctaggggt gaggagctgc ctggagctca ccccgctctt cttccaaacc cacagccacc 1466

atgcctggcc tcaatctttt cttttaaaca attattccta tattttattg taatgcagtt 1526

aaccgtgttt gtcagattca atactctgtg acccgtaac caagtctctg tatgtttatt 1586

actgcaattc aagtggccct gtatt 1611

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<211> 568

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (193)..(555)

<400> 161

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accgccgccc agtcgcgcgg aggcggaggc ttgggtgctg tcaagattca gcttcacccc 180

taaccacccg cc atg gcc gag gaa ggc att gct gct gga ggt gta atg 228
 Met Ala Glu Glu Gly Ile Ala Ala Gly Gly Val Met
 1 5 10

gac gtt aat act gct tta caa gag gtt ctg aag act gcc ctc atc cac 276
 Asp Val Asn Thr Ala Leu Gln Glu Val Leu Lys Thr Ala Leu Ile His
 15 20 25

gat ggc cta gca cgt gga att cgc gaa gct gcc aaa gcc tta gac aag 324
 Asp Gly Leu Ala Arg Gly Ile Arg Glu Ala Ala Lys Ala Leu Asp Lys
 30 35 40

cgc caa gcc cat ctt tgt gtg ctt gca tcc aac tgt gat gag cct atg 372
 Arg Gln Ala His Leu Cys Val Leu Ala Ser Asn Cys Asp Glu Pro Met
 45 50 55 60

tat gtc aag ttg gtg gag gcc ctt tgt gct gaa cac caa atc aac cta	420
Tyr Val Lys Leu Val Glu Ala Leu Cys Ala Glu His Gln Ile Asn Leu	
65 70 75	
att aag gtt gat gac aac aag aaa cta gga gaa tgg gta ggc ctt tgt	468
Ile Lys Val Asp Asp Asn Lys Lys Leu Gly Glu Trp Val Gly Leu Cys	
80 85 90	
aaa att gac aga gag ggg tgt att gcg gcc gct cta gag gat cca agc	516
Lys Ile Asp Arg Glu Gly Cys Ile Ala Ala Ala Leu Glu Asp Pro Ser	
95 100 105	
tta cgt acg cgt gca tgc gac gtc ata gct ctt cta tag tgtcacctaa	565
Leu Arg Thr Arg Ala Cys Asp Val Ile Ala Leu Leu *	
110 115 120	
att	568

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 <212> DNA
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 <222> (784) .. (1473)

<400> 162	
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aggaaacttc tggttaccaa ttccatctgc ctcttctca gtgactcctg acgagctgct	180
catttacaca cacctgctcc cccccccacc ccacagtctg gattgcgaaa cctaccgcac	240
cccaccccca gtgcaggaag aaggtagacc tgggtctgggg tggggacaga gagtctggga	300
gggggtgggtg gctggcagtc tcgggtggctg gcgacgcctc ttccgctctt ccttcctggg	360
aggaggcggg caaggcgaag cctctccgct cagtcgatgg tttccttcag gacgtctcat	420
agaggtgtgg gtgagatccc aggtctgggc cgcaatttct agccacgctg cccaaccttc	480
aggcaagcag tcaggttcca cagctacccc accacactct cagagtcgag gggaacaaga	540
agagggagtg gtctgtaaat gcgtcgggac aagagtgccc tcctaactcc acctggagct	600
ggcgtcaggg cgatctctgg atgccagacc cataagcctg gcctgtctgt gaggaggctg	660
cgtctggctc ccgctctcac agccattgca gtacattgag ctccatagag acagcgccgg	720
ggcaagtgag agccggacgg gcaactgggcg actctgtgcc tcgctgagga aaaataacta	780

aac atg ggc aaa gga gat cct aag aag ccg aga ggc aaa atg tca tca Met Gly Lys Gly Asp Pro Lys Lys Pro Arg Gly Lys Met Ser Ser 1 5 10 15	828
tat gca ttt ttt gtg caa act tgt cgg gag gag cat aag aag aag cac Tyr Ala Phe Phe Val Gln Thr Cys Arg Glu Glu His Lys Lys Lys His 20 25 30	876
cca gat gct tca gtc aac ttc tca gag ttt tct aag aag tgc tca gag Pro Asp Ala Ser Val Asn Phe Ser Glu Phe Ser Lys Lys Cys Ser Glu 35 40 45	924
agg tgg aag acc atg tct gct aaa gag aaa gga aaa ttt gaa gat atg Arg Trp Lys Thr Met Ser Ala Lys Glu Lys Gly Lys Phe Glu Asp Met 50 55 60	972
gca aag gcg gac aag gcc cgt tat gaa aga gaa atg aaa acc tat atc Ala Lys Ala Asp Lys Ala Arg Tyr Glu Arg Glu Met Lys Thr Tyr Ile 65 70 75	1020
cct ccc aaa ggg gag aca aaa aag aag ttc aag gat ccc aat gca ccc Pro Pro Lys Gly Glu Thr Lys Lys Lys Phe Lys Asp Pro Asn Ala Pro 80 85 90 95	1068
aag agg cct cct tcg gcc ttc ttc ctc ttc tgc tct gag tat cgc cca Lys Arg Pro Pro Ser Ala Phe Phe Leu Phe Cys Ser Glu Tyr Arg Pro 100 105 110	1116
aaa atc aaa gga gaa cat cct ggc ctg tcc att ggt gat gtt gcg aag Lys Ile Lys Gly Glu His Pro Gly Leu Ser Ile Gly Asp Val Ala Lys 115 120 125	1164
aaa ctg gga gag atg tgg aat aac act gct gca gat gac aag cag cct Lys Leu Gly Glu Met Trp Asn Asn Thr Ala Ala Asp Asp Lys Gln Pro 130 135 140	1212
tat gaa aag aag gct gcg aag ctg aag gaa aaa tac gaa aag gat att Tyr Glu Lys Lys Ala Ala Lys Leu Lys Glu Lys Tyr Glu Lys Asp Ile 145 150 155	1260
gct gca tat cga gct aaa gga aag cct gat gca gca aaa aag gga gtt Ala Ala Tyr Arg Ala Lys Gly Lys Pro Asp Ala Ala Lys Lys Gly Val 160 165 170 175	1308
gtc aag gct gaa aaa agc aaa aaa aag aag gaa gag gag gaa gat gag Val Lys Ala Glu Lys Ser Lys Lys Lys Lys Glu Glu Glu Glu Asp Glu 180 185 190	1356
gaa gat gaa gag gat gag gag gag gag gaa gat gaa gaa gat gaa gat Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu Asp Glu Glu Asp Glu Asp 195 200 205	1404
gaa gaa gaa gaa gat gat gat atg atg aat aag ttg gtt cta gcg cag Glu Glu Glu Glu Asp Asp Asp Met Met Asn Lys Leu Val Leu Ala Gln 210 215 220	1452

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ttt ttt ttt tct tgt cta taa ag catttaaccc cctgttaca caactcactc 1505
Phe Phe Phe Ser Cys Leu *
225 230

cttttaaaga aaaaaattga aatgtaaggc tgtgtaagat ttgttttttaa actgtacagt 1565

gtctttttttt gtatagttaa cacactaccg aatgtgtctt tagatagccc tgtcctgggtg 1625

gtatttttcaa tagccactaa ccttgccctgg tacagtatgg gggttgtaaa ttggcatgga 1685

aatttaaagc aggttcttgt tgggtgcacag cacaaattag ttatatatgg ggatggtagt 1745

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gaataccact ctgtaattgc aaaaaaaaaa aa 1837

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<210> 163
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<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (269)..(718)

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gcggcatggc tggcccaagg tgccgaggcg cactagccct gggggtgctt ccgtgtctgc 180

gccctgagac atttttggcg ccggccccag cctgagcggg gacggcggcc gggagggcgc 240

ggcccggggtt cccgttcccc gcggagcc atg cgg tac aac gag aag gag ctg 292
Met Arg Tyr Asn Glu Lys Glu Leu
1 5

cag gct ctg tcc cgg cag ccg gcc gag atg gcg gcc gag ctg ggc atg 340
Gln Ala Leu Ser Arg Gln Pro Ala Glu Met Ala Ala Glu Leu Gly Met
10 15 20

agg ggc ccc aag aag ggc agc gtg ctg aag cgg cgg ctg gtg aag ctg 388
Arg Gly Pro Lys Lys Gly Ser Val Leu Lys Arg Arg Leu Val Lys Leu
25 30 35 40

gtg gtg aat ttc ctc ttc tac ttt cgg aca gac gag gcc gag ccc gtc 436
Val Val Asn Phe Leu Phe Tyr Phe Arg Thr Asp Glu Ala Glu Pro Val
45 50 55

gga gcc ctg ctg ctg gag cgc tgc aga gtc gtc cgg gaa gag ccc ggc 484
Gly Ala Leu Leu Leu Glu Arg Cys Arg Val Val Arg Glu Glu Pro Gly
60 65 70

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[illegible]

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<212> DNA
<213> Homo sapiens
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Met Ala Ala Ala Ala Ala Glu Thr Pro Glu Val Leu Arg Glu
1 5 10

tgc ggt tgc aag ggc atc cgg acc tgt ctg atc tgc gag cgg cag cgc 98
Cys Gly Cys Lys Gly Ile Arg Thr Cys Leu Ile Cys Glu Arg Gln Arg
15 20 25 30

ggc agt gac ccg ccc tgg gag ctg ccc cca gcg aaa aca tac cgt ttc 146
Gly Ser Asp Pro Pro Trp Glu Leu Pro Pro Ala Lys Thr Tyr Arg Phe
35 40 45

att tac tgc tcc gac acc ggc tgg gcc gtg ggc aca gag gag tct gac 194
Ile Tyr Cys Ser Asp Thr Gly Trp Ala Val Gly Thr Glu Glu Ser Asp
50 55 60

ttt gag ggc tgg gcc ttc ccc ttc cca gga gtg atg ctg atc gag gac 242
Phe Glu Gly Trp Ala Phe Pro Phe Pro Gly Val Met Leu Ile Glu Asp
65 70 75

ttt gtg acc cgg gag gaa gaa gcc gag ttg gtg cgg ctc atg gac cgt 290
Phe Val Thr Arg Glu Glu Glu Ala Glu Leu Val Arg Leu Met Asp Arg
80 85 90

gac ccc tgg aag ctc tcc cag tct gga cgg agg aag cag gac tat ggc 338
Asp Pro Trp Lys Leu Ser Gln Ser Gly Arg Arg Lys Gln Asp Tyr Gly
95 100 105 110

ccc aaa gtc aac ttt cgg aaa cag aag cta aag acc gag ggc ttc tgc 386
Pro Lys Val Asn Phe Arg Lys Gln Lys Leu Lys Thr Glu Gly Phe Cys
115 120 125

ggc ctc ccc agc ttc agc cgg gag gtg gtg cgg agg atg ggc ctc tac 434
Gly Leu Pro Ser Phe Ser Arg Glu Val Val Arg Arg Met Gly Leu Tyr
130 135 140

ccg ggg ctg gag ggc ttc cgg ccc gtc gag cag tgc aac ctg gac tac 482
Pro Gly Leu Glu Gly Phe Arg Pro Val Glu Gln Cys Asn Leu Asp Tyr
145 150 155

tgc ccc gag cgg ggc tct gcc att gac ccc cac ctg gac gac gcc tgg 530
Cys Pro Glu Arg Gly Ser Ala Ile Asp Pro His Leu Asp Asp Ala Trp
160 165 170

ctg tgg ggg gag cgg ctg gtc agc ctc aac ctc ctg tcc ccc acc gtg 578
Leu Trp Gly Glu Arg Leu Val Ser Leu Asn Leu Leu Ser Pro Thr Val
175 180 185 190

ctg tcc atg tgt cgg gag gcg ccc ggg agc ctg ctc ctc tgc tcg gcc 626
Leu Ser Met Cys Arg Glu Ala Pro Gly Ser Leu Leu Leu Cys Ser Ala
195 200 205

ccg tcg gct gcc ccg gag gcc ttg gtg gac agc gtg ata gca ccc agc 674
Pro Ser Ala Ala Pro Glu Ala Leu Val Asp Ser Val Ile Ala Pro Ser
210 215 220

aag aaa aca gtt tct tgt ttt gtg aac ttc acc aga cta cag cag atc	198
Lys Lys Thr Val Ser Cys Phe Val Asn Phe Thr Arg Leu Gln Gln Ile	
40 45 50	
aca aat att caa gct gaa atc tac cag aaa aac ctg gaa att gaa ctc	246
Thr Asn Ile Gln Ala Glu Ile Tyr Gln Lys Asn Leu Glu Ile Glu Leu	
55 60 65	
ctg aaa cta gaa aaa gat aca gca gat gtt gtt cat cct ttc ttt ttg	294
Leu Lys Leu Glu Lys Asp Thr Ala Asp Val Val His Pro Phe Phe Leu	
70 75 80 85	
gct cag aag tgt cat act ctg caa agc atg aat aat cat ttg gaa gca	342
Ala Gln Lys Cys His Thr Leu Gln Ser Met Asn Asn His Leu Glu Ala	
90 95 100	
gtg ctg aaa gag aag aga tcc ctt agg caa aga ctg ttg aaa ccc atg	390
Val Leu Lys Glu Lys Arg Ser Leu Arg Gln Arg Leu Leu Lys Pro Met	
105 110 115	
tgc cag gaa aac tta cct att gaa gct gtt tat cac aga tat atg gta	438
Cys Gln Glu Asn Leu Pro Ile Glu Ala Val Tyr His Arg Tyr Met Val	
120 125 130	
cat ttg ctg gag ttg gct gtg act ttc att gag aga tta gaa acc cac	486
His Leu Leu Glu Leu Ala Val Thr Phe Ile Glu Arg Leu Glu Thr His	
135 140 145	
ctt gaa aca att aga aat att cct cat tta gct gca aat cta aag aaa	534
Leu Glu Thr Ile Arg Asn Ile Pro His Leu Ala Ala Asn Leu Lys Lys	
150 155 160 165	
atg aac cag gct tta gca aag atg gat ata ttg gtg act gag aca gaa	582
Met Asn Gln Ala Leu Ala Lys Met Asp Ile Leu Val Thr Glu Thr Glu	
170 175 180	
gaa ctg gca gag aat ata ctc aag tgg cgt aaa caa caa aac gaa gtt	630
Glu Leu Ala Glu Asn Ile Leu Lys Trp Arg Lys Gln Gln Asn Glu Val	
185 190 195	
tcg tct tgt atc ccc aaa ata tta gct gaa gaa agt tat ctt tat aaa	678
Ser Ser Cys Ile Pro Lys Ile Leu Ala Glu Glu Ser Tyr Leu Tyr Lys	
200 205 210	
cat gat att ata atg cct cct tta cct ttt act tct aaa gtt cat gtc	726
His Asp Ile Ile Met Pro Pro Leu Pro Phe Thr Ser Lys Val His Val	
215 220 225	
caa act att aat gcc aag tag tc atcaacttta tttttgctta attatgtgta	779
Gln Thr Ile Asn Ala Lys *	
230 235	
gtcatatgaa gtctatttct agttgactgt aacatgggta ttaatagtct ttgctgctgg	839
taatactgaa agaacctgct ttatattgga gtatcaagat ctcaggttca ttaagaccaa	899

actgactttt cctttgtttt tcatatattt ttattctacc tttcagtaaa actagagaag 959

ctaaaaaata gccatgacaa tttattaata taagtgaatt aaccattaaa aaaaaaaaaa 1018

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<211> 925

<212> DNA

<213> Homo sapiens

<220>

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<222> (40) .. (654)

<400> 166

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Met Ala Ala Ala Asn
1 5

ccg tgg gac ccg gcg tcc gcg cct aac ggc gct ggg cta gtg cta ggc 102
Pro Trp Asp Pro Ala Ser Ala Pro Asn Gly Ala Gly Leu Val Leu Gly
10 15 20

cac ttc ata gct tgc ggg atg gtc aat cag aaa aac ctg gaa att gaa 150
His Phe Ile Ala Ser Gly Met Val Asn Gln Lys Asn Leu Glu Ile Glu
25 30 35

ctc ctg aaa cta gaa aaa gat aca gca gat gtt gtt cat cct ttc ttt 198
Leu Leu Lys Leu Glu Lys Asp Thr Ala Asp Val Val His Pro Phe Phe
40 45 50

ttg gct cag aag tgt cat act ctg caa agc atg aat aat cat ttg gaa 246
Leu Ala Gln Lys Cys His Thr Leu Gln Ser Met Asn Asn His Leu Glu
55 60 65

gca gtg ctg aaa gag aag aga tcc ctt agg caa aga ctg ttg aaa ccc 294
Ala Val Leu Lys Glu Lys Arg Ser Leu Arg Gln Arg Leu Leu Lys Pro
70 75 80 85

atg tgc cag gaa aac tta cct att gaa gct gtt tat cac aga tat atg 342
Met Cys Gln Glu Asn Leu Pro Ile Glu Ala Val Tyr His Arg Tyr Met
90 95 100

gta cat ttg ctg gag ttg gct gtg act ttc att gag aga tta gaa acc 390
Val His Leu Leu Glu Leu Ala Val Thr Phe Ile Glu Arg Leu Glu Thr
105 110 115

cac ctt gaa aca att aga aat att cct cat tta gct gca aat cta aag 438
His Leu Glu Thr Ile Arg Asn Ile Pro His Leu Ala Ala Asn Leu Lys
120 125 130

aaa atg aac cag gct tta gca aag atg gat ata ttg gtg act gag aca 486
Lys Met Asn Gln Ala Leu Ala Lys Met Asp Ile Leu Val Thr Glu Thr
135 140 145

gaa gaa ctg gca gag aat ata ctc aag tgg cgt aaa caa caa aac gaa 534
 Glu Glu Leu Ala Glu Asn Ile Leu Lys Trp Arg Lys Gln Gln Asn Glu
 150 155 160 165

gtt tgc tct tgt atc ccc aaa ata tta gct gaa gaa agt tat ctt tat 582
 Val Ser Ser Cys Ile Pro Lys Ile Leu Ala Glu Glu Ser Tyr Leu Tyr
 170 175 180

aaa cat gat att ata atg cct cct tta cct ttt act tct aaa gtt cat 630
 Lys His Asp Ile Ile Met Pro Pro Leu Pro Phe Thr Ser Lys Val His
 185 190 195

gtc caa act att aat gcc aag tag tcatcaactt tatttttgct taattatgtg 684
 Val Gln Thr Ile Asn Ala Lys *
 200 205

tagtcatatg aagtctatatt ctagttagact gtaacatggg tattaatagt ctttgctgct 744

ggtaataactg aaagaacctg ctttatattg gagtatcaag atctcagggtt cattaagacc 804

aaactgactt ttcttttggt tttcatatat ttttattcta ccttttcagta aaactagaga 864

agctaaaaaa tagccatgac aatttattaa tataagtga ttaaccatta aaaaaaaaaa 924

a 925

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 <211> 1058
 <212> DNA
 <213> Homo sapiens

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 <222> (190)..(828)

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 ggggtggtga ggcccagaggc agctcttggt cagcttctgg aatttctgag cagccctcgt 180
 cagtacaag atg gac ccc gta gtc ttg agt tac atg gac agt cta ctg 228
 Met Asp Pro Val Val Leu Ser Tyr Met Asp Ser Leu Leu
 1 5 10

cgg caa tca gat gtc tca cta ttg gat ccg cca agc tgg ctc aat gac 276
 Arg Gln Ser Asp Val Ser Leu Leu Asp Pro Pro Ser Trp Leu Asn Asp
 15 20 25

cat att att ggg ttt gcg ttt gag tac ttt gcc aac agt cag ttt cat 324
 His Ile Ile Gly Phe Ala Phe Glu Tyr Phe Ala Asn Ser Gln Phe His
 30 35 40 45

gac tgc tct gat cac gtc agt ttc atc agc cct gaa gtc acc cag ttc	372
Asp Cys Ser Asp His Val Ser Phe Ile Ser Pro Glu Val Thr Gln Phe	
50 55 60	
atc aag tgc act agc aac cca gca gag att gcc atg ttc ctt gaa cca	420
Ile Lys Cys Thr Ser Asn Pro Ala Glu Ile Ala Met Phe Leu Glu Pro	
65 70 75	
ctg gac ctc ccc aac aag aga gtt gta ttt tta gcc atc aat gat aac	468
Leu Asp Leu Pro Asn Lys Arg Val Val Phe Leu Ala Ile Asn Asp Asn	
80 85 90	
tcc aac cag gca gct gga gga acc cac tgg agt tta ttg gtc tac ctc	516
Ser Asn Gln Ala Ala Gly Gly Thr His Trp Ser Leu Leu Val Tyr Leu	
95 100 105	
caa gat aaa aat agc ttt ttt cat tat gat tcc cat agc agg agc aac	564
Gln Asp Lys Asn Ser Phe Phe His Tyr Asp Ser His Ser Arg Ser Asn	
110 115 120 125	
tca gtt cac gca aag cag gta gca gag aaa ctg gag gct ttc tta ggc	612
Ser Val His Ala Lys Gln Val Ala Glu Lys Leu Glu Ala Phe Leu Gly	
130 135 140	
aga aaa gga gac aaa ctg gcc ttt gtg gaa gag aaa gcc cct gcc caa	660
Arg Lys Gly Asp Lys Leu Ala Phe Val Glu Glu Lys Ala Pro Ala Gln	
145 150 155	
caa aac agc tat gac tgt ggg atg tac gtg ata tgt aac act gag gcc	708
Gln Asn Ser Tyr Asp Cys Gly Met Tyr Val Ile Cys Asn Thr Glu Ala	
160 165 170	
ttg tgt cag aac ttc ttt agg caa cag aca gaa tca ctg ctg cag cta	756
Leu Cys Gln Asn Phe Phe Arg Gln Gln Thr Glu Ser Leu Leu Gln Leu	
175 180 185	
ctc acc cct gca tac atc aca aag aag agg gga gaa tgg aaa gat ctc	804
Leu Thr Pro Ala Tyr Ile Thr Lys Lys Arg Gly Glu Trp Lys Asp Leu	
190 195 200 205	
att gcc aca ctt gct aaa aag tag ctattgaagt atatttgcga cttttgaagg	858
Ile Ala Thr Leu Ala Lys Lys *	
210	
ctcctctttc tgcccttccc catttggttg atggctgcaa tctcagtgcc tgagggaaga	918
tgccctagtag aggaaagctt aatactcttt ttcctgaaag aatatcatcc tctgcattat	978
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tgaaattgta caccaaaacc	1058

<210> 168

<211> 7643

<212> DNA
 <213> Homo sapiens

<220>
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 <222> (99)..(5618)

<400> 168

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                                   Met Lys Pro Val Leu
                                   1          5

cag tcc ctc tac cac cga gtg ctg ctc tac ccc cca ccc cag cac cgg      161
Gln Ser Leu Tyr His Arg Val Leu Leu Tyr Pro Pro Pro Gln His Arg
              10              15              20

gtg gaa gcc atc aaa ata atg aaa gag ata ctt ggg agc cca cag cgt      209
Val Glu Ala Ile Lys Ile Met Lys Glu Ile Leu Gly Ser Pro Gln Arg
              25              30              35

ctc tgt gac ttg gca gga ccc agc tcc act gaa tca gag tcc aga aaa      257
Leu Cys Asp Leu Ala Gly Pro Ser Ser Thr Glu Ser Glu Ser Arg Lys
              40              45              50

aga tca att tca aaa aga aag tct cat ctg gat ctc ctc aaa ctc atc      305
Arg Ser Ile Ser Lys Arg Lys Ser His Leu Asp Leu Leu Lys Leu Ile
              55              60              65

atg gat ggc atg acc gaa gca tgc atc aag ggt ggc atc gaa gct tgc      353
Met Asp Gly Met Thr Glu Ala Cys Ile Lys Gly Gly Ile Glu Ala Cys
              70              75              80              85

tat gca gcc gtg tcc tgt gtc tgc acc ttg ctg ggt gcc ctg gat gag      401
Tyr Ala Ala Val Ser Cys Val Cys Thr Leu Leu Gly Ala Leu Asp Glu
              90              95              100

ctc agc cag ggg aag ggc ttg agc gaa ggt cag gtg caa ctg ctg ctt      449
Leu Ser Gln Gly Lys Gly Leu Ser Glu Gly Gln Val Gln Leu Leu Leu
              105              110              115

ctg cgc ctt gag gag ctg aag gat ggg gct gag tgg agc cga gat tcc      497
Leu Arg Leu Glu Glu Leu Lys Asp Gly Ala Glu Trp Ser Arg Asp Ser
              120              125              130

atg gag atc aat gag gct gac ttc cgc tgg cag cgg cga gtg ctg tcc      545
Met Glu Ile Asn Glu Ala Asp Phe Arg Trp Gln Arg Arg Val Leu Ser
              135              140              145

tca gaa cac acg ccg tgg gag tca ggg aac gag agg agc ctt gac atc      593
Ser Glu His Thr Pro Trp Glu Ser Gly Asn Glu Arg Ser Leu Asp Ile
              150              155              160              165

agc atc agt gtc acc aca gac aca ggc cag acc act ctc gag gga gag      641
Ser Ile Ser Val Thr Thr Asp Thr Gly Gln Thr Thr Leu Glu Gly Glu
              170              175              180

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ttg ggt cag act aca ccc gag gac cat tcg gga aac cac aag aac agt	689
Leu Gly Gln Thr Thr Pro Glu Asp His Ser Gly Asn His Lys Asn Ser	
185 190 195	
ctc aag tcg cca gcc atc cca gag ggt aag gag acg ctg agc aaa gta	737
Leu Lys Ser Pro Ala Ile Pro Glu Gly Lys Glu Thr Leu Ser Lys Val	
200 205 210	
ttg gaa aca gag gcg gta gac cag cca gat gtc gtg cag aga agc cac	785
Leu Glu Thr Glu Ala Val Asp Gln Pro Asp Val Val Gln Arg Ser His	
215 220 225	
acg gtc cct tac cct gac ata act aac ttc ctg tca gta gac tgc agg	833
Thr Val Pro Tyr Pro Asp Ile Thr Asn Phe Leu Ser Val Asp Cys Arg	
230 235 240 245	
aca agg tcc tat gga tct agg tat agt gag agc aat ttt agc gtt gat	881
Thr Arg Ser Tyr Gly Ser Arg Tyr Ser Glu Ser Asn Phe Ser Val Asp	
250 255 260	
gac caa gac ctt tct agg aca gag ttt gat tcc tgt gat cag tac tct	929
Asp Gln Asp Leu Ser Arg Thr Glu Phe Asp Ser Cys Asp Gln Tyr Ser	
265 270 275	
atg gca gca gaa aag gac tcg ggc agg tcc gac gtg tca gac att ggg	977
Met Ala Ala Glu Lys Asp Ser Gly Arg Ser Asp Val Ser Asp Ile Gly	
280 285 290	
tcg gac aac tgt tca cta gcc gat gaa gag cag aca ccc cgg gac tgc	1025
Ser Asp Asn Cys Ser Leu Ala Asp Glu Glu Gln Thr Pro Arg Asp Cys	
295 300 305	
cta ggc cac cgg tcc ctg cga act gcc gcc ctg tct cta aaa ctg ctg	1073
Leu Gly His Arg Ser Leu Arg Thr Ala Ala Leu Ser Leu Lys Leu Leu	
310 315 320 325	
aag aac cag gag gcg gat cag cac agc gcc agg ctg ttc ata cag tcc	1121
Lys Asn Gln Glu Ala Asp Gln His Ser Ala Arg Leu Phe Ile Gln Ser	
330 335 340	
ctg gaa ggc ctc ctc cct cgg ctc ctg gct ctc tcc aat gta gag gag	1169
Leu Glu Gly Leu Leu Pro Arg Leu Leu Ala Leu Ser Asn Val Glu Glu	
345 350 355	
gtg gac acc gct ctg cag aac ttt gcc tct act ttc tgc tca ggc atg	1217
Val Asp Thr Ala Leu Gln Asn Phe Ala Ser Thr Phe Cys Ser Gly Met	
360 365 370	
atg cac tct cct ggc ttt gac ggg aat agc agc ctc agc ttc cag atg	1265
Met His Ser Pro Gly Phe Asp Gly Asn Ser Ser Leu Ser Phe Gln Met	
375 380 385	
ctg atg aac gca gac agc ctc tac aca gct gca cac tgc gcc ctg ctc	1313
Leu Met Asn Ala Asp Ser Leu Tyr Thr Ala Ala His Cys Ala Leu Leu	
390 395 400 405	

ctc aac ctg aag ctc tcc cac ggt gac tac tac agg aag cgg ccg acc Leu Asn Leu Lys Leu Ser His Gly Asp Tyr Tyr Arg Lys Arg Pro Thr 410 415 420	1361
ctg gcg cca ggc gtg atg aag gac ttc atg aag cag gtg cag acc agc Leu Ala Pro Gly Val Met Lys Asp Phe Met Lys Gln Val Gln Thr Ser 425 430 435	1409
ggc gtg ctg atg gtc ttc tct cag gcc tgg att gag gag ctc tac cat Gly Val Leu Met Val Phe Ser Gln Ala Trp Ile Glu Glu Leu Tyr His 440 445 450	1457
cag gtg ctc gac agg aac atg ctt gga gag gct ggc tat tgg ggc agc Gln Val Leu Asp Arg Asn Met Leu Gly Glu Ala Gly Tyr Trp Gly Ser 455 460 465	1505
cca gaa gat aac agc ctt ccc ctc atc aca atg ctg acc gat att gac Pro Glu Asp Asn Ser Leu Pro Leu Ile Thr Met Leu Thr Asp Ile Asp 470 475 480 485	1553
ggc tta gag agc agt gcc att ggt ggc cag ctg atg gcc tcg gct gct Gly Leu Glu Ser Ser Ala Ile Gly Gly Gln Leu Met Ala Ser Ala Ala 490 495 500	1601
aca gag tct cct ttc gcc cag agc agg aga att gat gac tcc aca gtg Thr Glu Ser Pro Phe Ala Gln Ser Arg Arg Ile Asp Asp Ser Thr Val 505 510 515	1649
gca ggc gtg gca ttt gct cgc tat att ctg gtg ggc tgc tgg aag aac Ala Gly Val Ala Phe Ala Arg Tyr Ile Leu Val Gly Cys Trp Lys Asn 520 525 530	1697
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aac cag aag gag cgg gac gcc atc tgc atg agc ctc gac ggg ctg cgg Asn Gln Lys Glu Arg Asp Ala Ile Cys Met Ser Leu Asp Gly Leu Arg 570 575 580	1841
aaa gcc gca cgg ctg agc tgc gct cta ggc gtt gct gct aac tgc gcc Lys Ala Ala Arg Leu Ser Cys Ala Leu Gly Val Ala Ala Asn Cys Ala 585 590 595	1889
tca gcc ctt gcc cag atg gca gct gcc tcc tgt gtc caa aaa aaa aaa Ser Ala Leu Ala Gln Met Ala Ala Ala Ser Cys Val Gln Lys Lys Lys 600 605 610	1937
gaa gag agg gag gcc caa gaa ccc agt gat gcc atc aca caa gtg aaa Glu Glu Arg Glu Ala Gln Glu Pro Ser Asp Ala Ile Thr Gln Val Lys 615 620 625	1985
cta aaa gtg gag cag aaa ctg gag cag att ggg aag gtg cag ggg gtg	2033

Leu Lys Val Glu Gln Lys Leu Glu Gln Ile Gly Lys Val Gln Gly Val	
630 635 640 645	
tgg ctg cac act gcc cac gtc ttg tgc atg gag gcc atc ctc agc gta	2081
Trp Leu His Thr Ala His Val Leu Cys Met Glu Ala Ile Leu Ser Val	
650 655 660	
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Gly Leu Glu Met Gly Ser His Asn Pro Asp Cys Trp Pro His Val Phe	
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Arg Val Cys Glu Tyr Val Gly Thr Leu Glu His Asn His Phe Ser Asp	
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Gly Ala Ser Gln Pro Pro Leu Thr Ile Ser Gln Pro Gln Lys Ala Thr	
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Gly Ser Ala Gly Leu Leu Gly Asp Pro Glu Cys Glu Gly Ser Pro Pro	
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Glu His Ser Pro Glu Gln Gly Arg Ser Leu Ser Thr Ala Pro Val Val	
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Gln Pro Leu Ser Ile Gln Asp Leu Val Arg Glu Gly Ser Arg Gly Arg	
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Ala Ser Asp Phe Arg Gly Gly Ser Leu Met Ser Gly Ser Ser Ala Ala	
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Lys Val Val Leu Thr Leu Ser Thr Gln Ala Asp Arg Leu Phe Glu Asp	
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Ala Thr Asp Lys Leu Asn Leu Met Ala Leu Gly Gly Phe Leu Tyr Gln	
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Leu Lys Lys Ala Ser Gln Ser Gln Leu Phe His Ser Val Thr Asp Thr	
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Val Asp Tyr Ser Leu Ala Met Pro Gly Glu Val Lys Ser Thr Gln Asp	
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Arg Lys Ser Ala Leu His Leu Phe Arg Leu Gly Asn Ala Met Leu Arg	
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Glu	Ala	Phe	Leu	Asn	Thr	Asp	Asn	Ile	Gln	Val	Phe	Ala	Asn	Ala	Ala	
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Ser	Thr	Asp	Leu	Cys	Leu	Pro	Ala	Leu	Asp	Tyr	Leu	Arg	Arg	Cys	Ser	
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Gln	Leu	Leu	Al													

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Thr Pro Ser Glu Asp Asp Arg Ser Gln Ser Arg Glu His Met Gly Glu	
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Ser Leu Ser Leu Lys Ala Gly Gly Asp Leu Leu Leu Pro Pro Ser	
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Pro Lys Val Glu Lys Lys Asp Pro Ser Arg Lys Lys Glu Trp Trp Glu	
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1670 1675 1680 1685	
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Lys Leu Met Thr Glu Tyr Lys Lys Arg Lys Gln Gln His Asn Leu Ser	
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Arg Gln Asp Lys Arg Pro Arg Ser Gly Ser Thr Gly Ser Ser Leu Ser	
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Val Ser Val Arg Asp Ala Glu Ala Gln Ile Gln Ala Trp Thr Asn Met	

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Val Leu Thr Val Leu Asn Gln Ile Gln Ile Leu Pro Asp Gln Thr Phe			
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Thr Ala Leu Gln Pro Ala Val Phe Pro Cys Ile Ser Gln Leu Thr Cys			
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His Val Thr Asp Ile Arg Val Arg Gln Ala Val Arg Glu Trp Leu Gly			
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Met Ser Ser Gly Gly Ser Pro Gly Cys Leu Arg
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Asn Pro Arg His Leu Leu Trp Asn Val Cys Leu Val Val Leu Val Cys	
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Cys Ser Val Glu Ser His Arg Thr Lys Arg Lys Ile Leu Gln Leu Phe	
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 ttgcacgtat tcgtcatagg atg ctg tgg ccc ggc gca gga ttg gag gga 170
 Met Leu Trp Pro Gly Ala Gly Leu Glu Gly
 1 5 10
 cat aga cct ggt gga agg cgt ggg gct gcc ctg acc cag gga ttt ggc 218
 His Arg Pro Gly Gly Arg Arg Gly Ala Ala Leu Thr Gln Gly Phe Gly
 15 20 25
 tcc tgt agc gct gct ggg cag agg tcc gca gga gct gca ggt act tct 266
 Ser Cys Ser Ala Ala Gly Gln Arg Ser Ala Gly Ala Ala Gly Thr Ser
 30 35 40

tgg cca act cta gct gct gct tct tgc act gct tcc ggc ggg gtg agg	314
Trp Pro Thr Leu Ala Ala Ala Ser Cys Thr Ala Ser Gly Gly Val Arg	
45 50 55	
acc cac agc tct gat gtg ggc gct tca ggc cat ggt gga gct gag att	362
Thr His Ser Ser Asp Val Gly Ala Ser Gly His Gly Gly Ala Glu Ile	
60 65 70	
cag gtt ggc ttt tcc cct cag ctc cca gct ggc tgg tga acccatcatc	411
Gln Val Gly Phe Ser Pro Gln Leu Pro Ala Gly Trp *	
75 80 85	
atagccaaaa gtactcagca gcagcacctc caggtccaga ggcacctcca gctgcatgca	471
cacacaatga atgaaagact gccaggtgtc cgaaccctgg acatgcagct tgttgagttg	531
caggatgact ctctgttcag ggtccaaggt ctcgttcctg gaatccaggt ccgtgttggg	591
gaggaagaac ttcatcttgg cgttcagcca ttctgggtct ttggtgagca gcctcacaag	651
acagctccac aggttcttgt tgccgagctg gaggccaacg ggggccatga ggagccagcc	711
ttggtctcct cgttcatgat aggtgctcta gggccccac ggagaggggc tcatgggtgt	771
ctgggctatg tgtgccttga gctggattga cagggtgttt ccatagtgca gactccctca	831
gagctcccgg cactcaccct cagcgctcgc ggctcctccg cgc	874

<210> 172
 <211> 1297
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (15)..(1052)

<400> 172	
agccagaggc cccg atg gca aag ggt aaa agc acc acc tta acg cag gac	50
Met Ala Lys Gly Lys Ser Thr Thr Leu Thr Gln Asp	
1 5 10	
atg agc acc agc ctc cag gaa ggc cag gag gac ggg ccg gca gga tgg	98
Met Ser Thr Ser Leu Gln Glu Gly Gln Glu Asp Gly Pro Ala Gly Trp	
15 20 25	
aga gcg aat ctg aag ccc gtg gac agg aga agc cca gct gag agg act	146
Arg Ala Asn Leu Lys Pro Val Asp Arg Arg Ser Pro Ala Glu Arg Thr	
30 35 40	
ctg aag ccc aag gaa cca cgg gcc ctg gca gag ccg agg gcg ggg gag	194
Leu Lys Pro Lys Glu Pro Arg Ala Leu Ala Glu Pro Arg Ala Gly Glu	
45 50 55 60	

gcc ccc agg aag gtc tca ggc agc ttt gct ggg agt gtc cac atc acc	242
Ala Pro Arg Lys Val Ser Gly Ser Phe Ala Gly Ser Val His Ile Thr	
65 70 75	
ctg acc ccc gtg agg cct gac agg acc cca cgc cca gcc agc cca gga	290
Leu Thr Pro Val Arg Pro Asp Arg Thr Pro Arg Pro Ala Ser Pro Gly	
80 85 90	
ccc agc ctc cca gcc agg tcc ccc tcc cca ccc cgc cgc agg aga ctg	338
Pro Ser Leu Pro Ala Arg Ser Pro Ser Pro Pro Arg Arg Arg Leu	
95 100 105	
gcc gtc cct gcc agc ctc gac gtt tgt gac aac tgg ctt cgg ccg gag	386
Ala Val Pro Ala Ser Leu Asp Val Cys Asp Asn Trp Leu Arg Pro Glu	
110 115 120	
ccc cct ggc cag gaa gcc cga gtg cag agc tgg aag gag gag gag aag	434
Pro Pro Gly Gln Glu Ala Arg Val Gln Ser Trp Lys Glu Glu Glu Lys	
125 130 135 140	
aaa cct cac ctt cag ggc aaa cca ggg aga ccc ttg tcc ccg gcc aat	482
Lys Pro His Leu Gln Gly Lys Pro Gly Arg Pro Leu Ser Pro Ala Asn	
145 150 155	
gtc cct gct ctg cct ggc gag acg gtg acc tcc cca gtc agg ctg cac	530
Val Pro Ala Leu Pro Gly Glu Thr Val Thr Ser Pro Val Arg Leu His	
160 165 170	
ccc gac tac ctc tcc ccg gag gag ata cag agg cag ctg cag gac atc	578
Pro Asp Tyr Leu Ser Pro Glu Glu Ile Gln Arg Gln Leu Gln Asp Ile	
175 180 185	
gag agg cgg ctg gac gcc ctg gag ctc cgc ggc gtg gag ctg gag aag	626
Glu Arg Arg Leu Asp Ala Leu Glu Leu Arg Gly Val Glu Leu Glu Lys	
190 195 200	
cga ctg cgg gcg gcc gag gga gat gac gct gag gat agc ctc atg gtg	674
Arg Leu Arg Ala Ala Glu Gly Asp Asp Ala Glu Asp Ser Leu Met Val	
205 210 215 220	
gac tgg ttc tgg ctc att cac gag aag cag ctt ctg ctg aga cag gag	722
Asp Trp Phe Trp Leu Ile His Glu Lys Gln Leu Leu Leu Arg Gln Glu	
225 230 235	
tca gag ctg atg tac aag tcc aag gcc cag cgt ctg gag gag cag cag	770
Ser Glu Leu Met Tyr Lys Ser Lys Ala Gln Arg Leu Glu Glu Gln Gln	
240 245 250	
ctg gac atc gag ggc gag ctg cgc cgg ctc atg gcc aag ccc gag gct	818
Leu Asp Ile Glu Gly Glu Leu Arg Arg Leu Met Ala Lys Pro Glu Ala	
255 260 265	
ctg aag tca ctg cag gag cgg cgg cgg gag cag gag ctg ctg gag cag	866
Leu Lys Ser Leu Gln Glu Arg Arg Glu Gln Glu Leu Leu Glu Gln	
270 275 280	

caa tcg cgc gtt ctt tct tta ctt gtg ctc cac tgg tgg gca gca tgt	361
Gln Ser Arg Val Leu Ser Leu Leu Val Leu His Trp Trp Ala Ala Cys	
65 70 75	
gct ccc gcg tcc aca gct ctg ttt cgc ctt ccg gtc ccc gta gct ctg	409
Ala Pro Ala Ser Thr Ala Leu Phe Arg Leu Pro Val Pro Val Ala Leu	
80 85 90	
cag ggg aac ggg atc tct gcc gcc tcc tcg gcc gct aag cga ccc ggg	457
Gln Gly Asn Gly Ile Ser Ala Ala Ser Ser Ala Ala Lys Arg Pro Gly	
95 100 105	
gct gcc cga cct agc gag tgc gca cga ccg ccc agc gag ggg tag ccg	505
Ala Ala Arg Pro Ser Glu Cys Ala Arg Pro Pro Ser Glu Gly *	
110 115 120	
agtcgaggca gcacgggtcc caaggcagcc aaggctgcgc c	546

<210> 174
 <211> 1009
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (50)..(793)

<400> 174	
gcacgagggc acgagctgta tgagtggtag cctttcccct caaccagca	55
atg gag	
Met Glu	
1	
gag cag ccc cag atg caa gac gcc gac gag ccc gcg gac tcc gga ggg	103
Glu Gln Pro Gln Met Gln Asp Ala Asp Glu Pro Ala Asp Ser Gly Gly	
5 10 15	
gaa ggc cgg gca ggc ggg cca ccg cag gtc gcc ggc gcc cag gcg gcg	151
Glu Gly Arg Ala Gly Gly Pro Pro Gln Val Ala Gly Ala Gln Ala Ala	
20 25 30	
tgc agc gag gac cgc atg acc ctg ctc ctc agg ctg aga gca cag aca	199
Cys Ser Glu Asp Arg Met Thr Leu Leu Leu Arg Leu Arg Ala Gln Thr	
35 40 45 50	
aaa caa caa ctc tta gaa tat aaa tca atg gtt gat gca agt gaa gaa	247
Lys Gln Gln Leu Leu Glu Tyr Lys Ser Met Val Asp Ala Ser Glu Glu	
55 60 65	
aaa act cca gaa caa att atg caa gaa aag caa atc gaa gct aaa att	295
Lys Thr Pro Glu Gln Ile Met Gln Glu Lys Gln Ile Glu Ala Lys Ile	
70 75 80	
gaa gac ctg gaa aat gaa att gaa gag gta aaa gtt gct ttt gag ata	343
Glu Asp Leu Glu Asn Glu Ile Glu Glu Val Lys Val Ala Phe Glu Ile	

85	90	95	
aaa aag ctt gca tta gac agg atg aga ctt tca act gca ctt aaa aaa			391
Lys Lys Leu Ala Leu Asp Arg Met Arg Leu Ser Thr Ala Leu Lys Lys			
100	105	110	
aac ctg gag aaa att agc aga cag tct agt gtg ctc atg gat aac atg			439
Asn Leu Glu Lys Ile Ser Arg Gln Ser Ser Val Leu Met Asp Asn Met			
115	120	125	130
aaa cac cta tta gag cta aat aaa tta ata atg aaa tca cag cag gaa			487
Lys His Leu Leu Glu Leu Asn Lys Leu Ile Met Lys Ser Gln Gln Glu			
135	140	145	
tct tgg gat tta gag gaa aaa ctg ctt gat att aga aag aag aga ttg			535
Ser Trp Asp Leu Glu Glu Lys Leu Leu Asp Ile Arg Lys Lys Arg Leu			
150	155	160	
caa tta aaa caa gct tca gaa agt aag ctt tta gaa ata cag act gaa			583
Gln Leu Lys Gln Ala Ser Glu Ser Lys Leu Leu Glu Ile Gln Thr Glu			
165	170	175	
aag aac aaa cag aag att gat ttg gac agt atg gaa aac tca gag agg			631
Lys Asn Lys Gln Lys Ile Asp Leu Asp Ser Met Glu Asn Ser Glu Arg			
180	185	190	
ata aag atc ata cga caa aac cta cag atg gag ata aaa att act act			679
Ile Lys Ile Ile Arg Gln Asn Leu Gln Met Glu Ile Lys Ile Thr Thr			
195	200	205	210
gtt att caa cat gtg ttc cag aac ctt att ttg ggg agt aaa gtc aat			727
Val Ile Gln His Val Phe Gln Asn Leu Ile Leu Gly Ser Lys Val Asn			
215	220	225	
tgg gca gag gat cct gcc ctt aag gaa att gtt ctg cag ctt gag aag			775
Trp Ala Glu Asp Pro Ala Leu Lys Glu Ile Val Leu Gln Leu Glu Lys			
230	235	240	
aat gtt gac atg atg taa taagaa ttcatttctg acatatttta catttctggc			829
Asn Val Asp Met Met *			
245			
aatctcaact cttatttgga atacttctgt gcatttgtct gtccaccgta attttagaaa			889
agcatatcca taacgtttac agttgtagta cagttgtggt tagttatttg tagtgggatt			949
gaaagtaatt tttttctttt tatatttcta tattcagggtt gggttttttg tgccgttcgc			1009

<210> 175
 <211> 834
 <212> DNA
 <213> Homo sapiens
 <220>

<221> CDS
 <222> (12)..(833)

<400> 175

tttcgtcaag g atg aca tcc att cga gct gta ttt ata ttc ctg tgg ctg	50
Met Thr Ser Ile Arg Ala Val Phe Ile Phe Leu Trp Leu	
1 5 10	
cag ctg gac ttg gtg aat gga gag aat gtg gag cag cat cct tca acc	98
Gln Leu Asp Leu Val Asn Gly Glu Asn Val Glu Gln His Pro Ser Thr	
15 20 25	
ctg agt gtc cag gag gga gac agc gct gtt atc aag tgt act tat tca	146
Leu Ser Val Gln Glu Gly Asp Ser Ala Val Ile Lys Cys Thr Tyr Ser	
30 35 40 45	
gac agt gcc tca aac tac ttc cct tgg tat aag caa gaa ctt gga aaa	194
Asp Ser Ala Ser Asn Tyr Phe Pro Trp Tyr Lys Gln Glu Leu Gly Lys	
50 55 60	
aga cct cag ctt att ata gac att cgt tca aat gtg ggc gaa aag aaa	242
Arg Pro Gln Leu Ile Ile Asp Ile Arg Ser Asn Val Gly Glu Lys Lys	
65 70 75	
gac caa cga att gct gtt aca ttg aac aag aca gcc aaa cat ttc tcc	290
Asp Gln Arg Ile Ala Val Thr Leu Asn Lys Thr Ala Lys His Phe Ser	
80 85 90	
ctg cac atc aca gag acc caa cct gaa gac tcg gct gtc tac ttc tgt	338
Leu His Ile Thr Glu Thr Gln Pro Glu Asp Ser Ala Val Tyr Phe Cys	
95 100 105	
gca gca agt aac ggc cag gca gga act gct ctg atc ttt ggg aag gga	386
Ala Ala Ser Asn Gly Gln Ala Gly Thr Ala Leu Ile Phe Gly Lys Gly	
110 115 120 125	
acc acc tta tca gtg agt tcc aat atc cag aac cct gac cct gcc gtg	434
Thr Thr Leu Ser Val Ser Ser Asn Ile Gln Asn Pro Asp Pro Ala Val	
130 135 140	
tac cag ctg aga gac tct aaa tcc agt gac aag tct gtc tgc cta ttc	482
Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe	
145 150 155	
acc gat ttt gat tct caa aca aat gtg tca caa agt aag gat tct gat	530
Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp	
160 165 170	
gtg tat atc aca gac aaa act gtg cta gac atg agg tct atg gac ttc	578
Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe	
175 180 185	
aag agc aac agt gct gtg gcc tgg agc aac aaa tct gac ttt gca tgt	626
Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys	
190 195 200 205	
gca aac gcc ttc aac aac agc att att cca gaa gac acc ttc ttc ccc	674

Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro	
210 215 220	
agc cca gaa agt tcc tgt gat gtc aag ctg gtc gag aaa agc ttt gaa	722
Ser Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu	
225 230 235	
aca gat acg aac cta aac ttt caa aac ctg tca gtg att ggg ttc cga	770
Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg	
240 245 250	
atc ctc ctc ctg aaa gtg gcc ggg ttt aat ctg ctc atg acg ctg cgg	818
Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg	
255 260 265	
ctg tgg tcc agc tga g	834
Leu Trp Ser Ser *	
270	

<210> 176
 <211> 778
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (34)..(576)

 <220>
 <221> misc_feature
 <222> (1)...(778)
 <223> n = a,t,c or g

<400> 176	
tttcgtagac ctctctgtct tgtagcatct gcc atg aga atc agg ctc ctg tgc	54
Met Arg Ile Arg Leu Leu Cys	
1 5	
tgt gtg gcc ttt tct ctc ctg tgg gca ggt cca gtg att gct ggg atc	102
Cys Val Ala Phe Ser Leu Leu Trp Ala Gly Pro Val Ile Ala Gly Ile	
10 15 20	
acc cag gca cca aca tct cag atc ctg gca gca gga cgg cgc atg aca	150
Thr Gln Ala Pro Thr Ser Gln Ile Leu Ala Ala Gly Arg Arg Met Thr	
25 30 35	
ctg aga tgt acc cag gat atg aga cat aat gcc atg tac tgg tat aga	198
Leu Arg Cys Thr Gln Asp Met Arg His Asn Ala Met Tyr Trp Tyr Arg	
40 45 50 55	
caa gat cta gga ctg ggg cta agg ctc atc cat tat tca aat act gca	246
Gln Asp Leu Gly Leu Gly Leu Arg Leu Ile His Tyr Ser Asn Thr Ala	
60 65 70	

ggt acc act ggc aaa gga gaa gtc cct gat ggt tat agt gtc tcc aga	294
Gly Thr Thr Gly Lys Gly Glu Val Pro Asp Gly Tyr Ser Val Ser Arg	
75 80 85	
gca aac aca gat gat ttc ccc ctg acg ttg gcg tct gct gta ccc tct	342
Ala Asn Thr Asp Asp Phe Pro Leu Thr Leu Ala Ser Ala Val Pro Ser	
90 95 100	
cag aca tct gtg tac ttc tgt gcc agc agt gac ggg gct agc ggg agt	390
Gln Thr Ser Val Tyr Phe Cys Ala Ser Ser Asp Gly Ala Ser Gly Ser	
105 110 115	
ccc cac acc ggg gag ctg ttt ttt gga gaa ggc tct agg ctg acc gta	438
Pro His Thr Gly Glu Leu Phe Phe Gly Glu Gly Ser Arg Leu Thr Val	
120 125 130 135	
ctg gag gac ctg aaa aac gtg ttc cca ccc gag gtc gct gtg ttt gag	486
Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu	
140 145 150	
cca tca gaa gca gag atc tcc cac acc caa aag gcc aca ctg gtg tgc	534
Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys	
155 160 165	
ctg gcc aca ggc ttc tac ccc gac cac gtg gag ctg agc tga ttttttc	583
Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser *	
170 175 180	
atagactatg agcttctaaa aaatcatccc catattcgtc attacattct tgggatcaaa	643
tatactgcat gaaaaaagat gctcagaaaa gtctatgtta agttaatgta gaatatatga	703
atgagtgaag gaaagtgttt tgaaaccatc atagggaata taataagata anattacact	763
agaataaaat gaaac	778

<210> 177
 <211> 708
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (176)..(493)

<400> 177	
gagggcgggg gaggcagatg agtaaattgga tccttacact aagtgtgatg agcagaaacc	60
cagggcgtct ggggcatgag cagggatacc taaccagcc ctgggggctc aatctctccc	120
caccctgca ggagaggctt ggggtgagtt ttgggaataa ggaccatcca gccac atg	178
Met	
1	

acg aag ggg aag gaa aat ccc cat caa ggc aaa aac aca gtc caa ggc	226
Thr Lys Gly Lys Glu Asn Pro His Gln Gly Lys Asn Thr Val Gln Gly	
5 10 15	
tct gag gcc caa att ccg ggg aga ggg gtg aag gtt gtt tgt cgc acc	274
Ser Glu Ala Gln Ile Pro Gly Arg Gly Val Lys Val Val Cys Arg Thr	
20 25 30	
tgg gtt aaa ggg tgg ggg tgg aga gta gga gaa gag gct aca cag gtg	322
Trp Val Lys Gly Trp Gly Trp Arg Val Gly Glu Glu Ala Thr Gln Val	
35 40 45	
aga agg tgt cag atc aca aag ggc ctt gta tgc caa act aag aag act	370
Arg Arg Cys Gln Ile Thr Lys Gly Leu Val Cys Gln Thr Lys Lys Thr	
50 55 60 65	
gaa ctt gac cat gaa gtt agg cag acc ctc tgg aga gtt tta aag caa	418
Glu Leu Asp His Glu Val Arg Gln Thr Leu Trp Arg Val Leu Lys Gln	
70 75 80	
gga gtc gtg tgg atg aac aaa cct gtg atg ggc tgg ggt tac caa gga	466
Gly Val Val Trp Met Asn Lys Pro Val Met Gly Trp Gly Tyr Gln Gly	
85 90 95	
ggg ctt cct gga gga ggt cag act tga gctga gggaaggata ggatttggag	518
Gly Leu Pro Gly Gly Gly Gln Thr *	
100 105	
agctgacatt ctgatgagcg gcttcggtta aagctcacia aaacccttcc ctcccccatg	578
ccctttgaaa tcatttgaat caaagattgc gtgtgttaaa gacatgtttg tctgttatct	638
gaaagctgtg gtttctcttt aacagattca gggcctcatc ctttgactcg gaccaagaag	698
gaattatgag	708

<210> 178
 <211> 1463
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (120)..(1175)

<220>
 <221> misc_feature
 <222> (1)...(1463)
 <223> n = a,t,c or g

<400> 178	
tttcgtgcaa agaaaactgt gagagagaga atttttaaaaa agcagctggg gcctgaggtt	60

tctccccag	taccctgggt	cacctcagcc	cagagctggc	ggcaggcccc	cagccccctc	119
atg tca gag ccc cct gtg tac tgt aac ctg gtg gac ctt cgc cgc tgt	167					
Met Ser Glu Pro Pro Val Tyr Cys Asn Leu Val Asp Leu Arg Arg Cys						
1 5 10 15						
cct cgg tcc cca ccc cca ggc cct gca tgc ccc ctg ctg cag agg ctg	215					
Pro Arg Ser Pro Pro Pro Gly Pro Ala Cys Pro Leu Leu Gln Arg Leu						
20 25 30						
gat gcc tgg gag cag cac ctg gac ccc aac tct gga cgc tgc ttc tac	263					
Asp Ala Trp Glu Gln His Leu Asp Pro Asn Ser Gly Arg Cys Phe Tyr						
35 40 45						
ata aat tca ctg act ggc tgc aag tcc tgg aag ccc ccg cgc cgc agt	311					
Ile Asn Ser Leu Thr Gly Cys Lys Ser Trp Lys Pro Pro Arg Arg Ser						
50 55 60						
cgc agc gag acg aac cct ggc tcc atg gag ggg aca cag acc ctg aag	359					
Arg Ser Glu Thr Asn Pro Gly Ser Met Glu Gly Thr Gln Thr Leu Lys						
65 70 75 80						
agg aac aat gat gtc ctg caa cct cag gca aag ggc ttc aga tct gac	407					
Arg Asn Asn Asp Val Leu Gln Pro Gln Ala Lys Gly Phe Arg Ser Asp						
85 90 95						
aca ggg acc cca gaa ccg ctt gac cca cag ggt tca ctc agc ctc agc	455					
Thr Gly Thr Pro Glu Pro Leu Asp Pro Gln Gly Ser Leu Ser Leu Ser						
100 105 110						
caa cgc acc tcg cag ctt gac cct cca gcc ttg cag gcc cct cga cct	503					
Gln Arg Thr Ser Gln Leu Asp Pro Pro Ala Leu Gln Ala Pro Arg Pro						
115 120 125						
ctg ccg cag ctc ctg gac gac ccc cat gag gtg gaa aag tcg ggt ctg	551					
Leu Pro Gln Leu Leu Asp Asp Pro His Glu Val Glu Lys Ser Gly Leu						
130 135 140						
ctc aac atg acc aag att gcc caa ggg ggg cgc aag ctc agg aag aac	599					
Leu Asn Met Thr Lys Ile Ala Gln Gly Gly Arg Lys Leu Arg Lys Asn						
145 150 155 160						
tgg ggc ccg tct tgg gtg gtg tta acg ggt aac agc ctg gtg ttc tac	647					
Trp Gly Pro Ser Trp Val Val Leu Thr Gly Asn Ser Leu Val Phe Tyr						
165 170 175						
cga gag cca ccg ccg aca gcg ccc tcc tca ggc tgg gga cca gcg ggt	695					
Arg Glu Pro Pro Pro Thr Ala Pro Ser Ser Gly Trp Gly Pro Ala Gly						
180 185 190						
agc cgg ccc gaa agt agc gtg gac ctg cgc ggg gcg gcc ctg gcg cac	743					
Ser Arg Pro Glu Ser Ser Val Asp Leu Arg Gly Ala Ala Leu Ala His						
195 200 205						
ggc cgc cac ctg tcc agc cgc cgc aac gtc ctg cac atc cgc acg atc	791					
Gly Arg His Leu Ser Ser Arg Arg Asn Val Leu His Ile Arg Thr Ile						
210 215 220						

cct ggc cac gag ttc ctg ctg cag tgc gac cac gag aca gag ctg cga 839
Pro Gly His Glu Phe Leu Leu Gln Ser Asp His Glu Thr Glu Leu Arg
225 230 235 240

gcc tgg cac cgc gcg ctg cgg act gtc atc gag cgg ctg gat cgg gag 887
Ala Trp His Arg Ala Leu Arg Thr Val Ile Glu Arg Leu Asp Arg Glu
245 250 255

aac ccc ctg gag ctg cgt ctg tgc ggc tct gga ccc gcg gag ctg agc 935
Asn Pro Leu Glu Leu Arg Leu Ser Gly Ser Gly Pro Ala Glu Leu Ser
260 265 270

gcc ggg gag gac gaa gaa gag gag tgc gag ctg gtg tcc aag ccg ctg 983
Ala Gly Glu Asp Glu Glu Glu Glu Ser Glu Leu Val Ser Lys Pro Leu
275 280 285

ctg cgc ctc agc agc cgc cgg agc tcc att cgg ggg ccc gaa ggc acc 1031
Leu Arg Leu Ser Ser Arg Arg Ser Ser Ile Arg Gly Pro Glu Gly Thr
290 295 300

gag cag aac cgc gtg cgc aac aaa cta aag cgg ctc atc gcg aag aga 1079
Glu Gln Asn Arg Val Arg Asn Lys Leu Lys Arg Leu Ile Ala Lys Arg
305 310 315 320

ccg ccc tta caa agc ctg cag gag cgg ggt ctg ctc cga ggt gag ggg 1127
Pro Pro Leu Gln Ser Leu Gln Glu Arg Gly Leu Leu Arg Gly Glu Gly
325 330 335

gct ggg cca ggt tca tgg ata aga aaa ctc cag cga ggc tca gag tag 1175
Ala Gly Pro Gly Ser Trp Ile Arg Lys Leu Gln Arg Gly Ser Glu *
340 345 350

agcttcccag aactagacca caaccttctg tgactgctgc tttcccacta cccagattg 1235

tttaggggag aagctggggg gacctgtacc cctttgccag attgtttgaa gcangggaag 1295

ggaggtggag tgtatttcct tgcccaggcc tggcacaggc agccaggagg accagcctca 1355

cttaaggata aagacctatg ctgagaagag ctctgtgag tgacgctggc acttggttc 1415

cgcctcactc tacttcccca gaccaggtgt tcggctggca gatggaat 1463

<210> 179
<211> 678
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (122)..(478)

<400> 179
agtgcggtgg aattctggtt aaaaaaagta cagaatgcaa aaggatatgg cataaaaggc 60


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caagtcgaa aagggctact agtgttctag gtgtctttcc agaaagatta tgcgcatata      120

a    atg tgc aca ctt gca tgt gtg cac aca cat aca cac act ctc ata      166
    Met Cys Thr Leu Ala Cys Val His Thr His Thr His Thr Leu Ile
        1             5             10             15

tac cta aaa tac gaa tgg gag cac atg aca cac aca ttc tgc ctg ctg      214
Tyr Leu Lys Tyr Glu Trp Glu His Met Thr His Thr Phe Cys Leu Leu
        20             25             30

ctt tgt ctg tgc ata att tta tct tcc agg tca tct gtg ctg gtg tct      262
Leu Cys Leu Cys Ile Ile Leu Ser Ser Arg Ser Ser Val Leu Val Ser
        35             40             45

atc agt ctg cta gtc ttt ccc cgc cat gtg gcc att gtt cca gtc ccc      310
Ile Ser Leu Leu Val Phe Pro Arg His Val Ala Ile Val Pro Val Pro
        50             55             60

tcc tat gca cac cca ggt ttc tct agg acc atg tta tcc cag agc cag      358
Ser Tyr Ala His Pro Gly Phe Ser Arg Thr Met Leu Ser Gln Ser Gln
        65             70             75

gtg gac agg aca caa agg gct agg ggt caa tgg ggg tgt tct cgc ctc      406
Val Asp Arg Thr Gln Arg Ala Arg Gly Gln Trp Gly Cys Ser Arg Leu
        80             85             90             95

cag tct gcc ctg cca gcc ccc agt cgt ggg tgg acc tgc cat cag ctt      454
Gln Ser Ala Leu Pro Ala Pro Ser Arg Gly Trp Thr Cys His Gln Leu
        100            105            110

gct ctg ccc act ccc cag gcc tga gctgctggcg aaacaggcaa gtgactgcac      508
Ala Leu Pro Thr Pro Gln Ala *
        115

tgcccatggc cggtcaccag cctcagggtga accccaggag gggttcctac ctagcactca      568

tcatttcctc aacttcacta ctgtgtcgcc ctgtgggaca gggaagtcca agtcggggaa      628

aaagcctgtg gggagggggtt ggtgggagat ggggagccca tatggcccag      678

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<210> 180
<211> 599
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (189)..(512)

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cctttccaaa tttgtaattc tctgactata agaaatctgg ctccctgctct ttccctgctg      120

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ccactgaatt gtatagaggc ggagtcctcg gtgcattcaa gatccggctt cactcgtaac 180

ccactgcc atg gcc gag gaa ggc agt gct gct gga ggt gta atg gac att 230
Met Ala Glu Glu Gly Ser Ala Ala Gly Gly Val Met Asp Ile
1 5 10

aat act gtt tta cag gag gtg ctg aag acc gcc ctc atc cat gat ggc 278
Asn Thr Val Leu Gln Glu Val Leu Lys Thr Ala Leu Ile His Asp Gly
15 20 25 30

cta gca tat gaa att tgc aaa gct gcc aaa gcc tca gac aag tgc caa 326
Leu Ala Tyr Glu Ile Cys Lys Ala Ala Lys Ala Ser Asp Lys Cys Gln
35 40 45

gcc cat ctt tgt gtg ctg tgt gtg ctt gca tcc aac tgt gat gag cct 374
Ala His Leu Cys Val Leu Cys Val Leu Ala Ser Asn Cys Asp Glu Pro
50 55 60

atg tat gtc aag ttg gtg gag gcc ctt tgt gct gaa cac caa atc aac 422
Met Tyr Val Lys Leu Val Glu Ala Leu Cys Ala Glu His Gln Ile Asn
65 70 75

cta att aag gtt gat gac cag aaa cta ggg gaa tcg gta ggc ctc tgt 470
Leu Ile Lys Val Asp Asp Gln Lys Leu Gly Glu Ser Val Gly Leu Cys
80 85 90

aaa act gac aga gag ggg aaa ccg tgt aaa gtg gtt ggt tga agttgta 519
Lys Thr Asp Arg Glu Gly Lys Pro Cys Lys Val Val Gly *
95 100 105

tagtagttac gaactatggc aaggagtctc aggccaagga tatcattgaa gagtacttca 579

aatgcaagaa atgaacaagt 599

<210> 181
<211> 1396
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (68)..(1039)

<400> 181

tttcgtagtt cttagtccgt gcggtggaat tcccggccgc gctccgaacg gcgcctcccg 60

ccccacc atg gcc aac agc gcg agc cgc aac gac ttc gag tgg gtc tac 109
Met Gly Asn Ser Ala Ser Arg Asn Asp Phe Glu Trp Val Tyr
1 5 10

acc gac cag ccg cac acg cag cgg cgc aag gag ata ctg gcc aag tac 157
Thr Asp Gln Pro His Thr Gln Arg Arg Lys Glu Ile Leu Ala Lys Tyr
15 20 25 30

Asn Val Gly Tyr His Val Glu His His Asp Phe Pro Ser Ile Pro Gly
 255 260 265 270
 tac aac ctg ccg ctg gtg cgg aag atc gcg ccc gag tac tac gac cac 925
 Tyr Asn Leu Pro Leu Val Arg Lys Ile Ala Pro Glu Tyr Tyr Asp His
 275 280 285
 ctg ccg cag cac cac tcc tgg gtg aag gtg ctc tgg gat ttt gtg ttt 973
 Leu Pro Gln His Ser Trp Val Lys Val Leu Trp Asp Phe Val Phe
 290 295 300
 gag gac tcc ctg ggg ccc tat gcc agg gtg aag cgg gtg tac agg ctg 1021
 Glu Asp Ser Leu Gly Pro Tyr Ala Arg Val Lys Arg Val Tyr Arg Leu
 305 310 315
 gca aaa gat ggt ctg tga gcccgg gctgcctcct ggtggtggcc attgtccccc 1075
 Ala Lys Asp Gly Leu *
 320
 atcggccccct cagccttgca cccagcact gagaagctac atttccttcc tgtgctctgg 1135
 actgctgccc ttgtccccga ggagtgtccc gcgcagccac acctggcaac agcagtgtgg 1195
 gctgcagggc tccgtctgca cgtggacttg ccctggacct tgagtgtggc cctccctttc 1255
 tgggcctccc caggtgagggc ctggccctgc cccaccatga cctgggtgct ctgagccac 1315
 gggtccacg gagctgactt ctccgggggtg cctgtgcctt acattaaacc cggcgtttgt 1375
 ttcacagcca aaaaaaaaaa a 1396

<210> 182
 <211> 2728
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (22)..(2688)

<400> 182
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 Met Ala Gly Ala Ala Ala Glu Ser Gly Arg
 1 5 10
 gag ctg tgg acc ttc gcg ggt tcc cgg gac ccg agc gca ccg cgg cta 99
 Glu Leu Trp Thr Phe Ala Gly Ser Arg Asp Pro Ser Ala Pro Arg Leu
 15 20 25
 gcc tac ggc tac ggc ccg ggc agc ctg cgc gag ctg cgg gcg cgc gag 147
 Ala Tyr Gly Tyr Gly Pro Gly Ser Leu Arg Glu Leu Arg Ala Arg Glu
 30 35 40
 ttc agc cgc ctg gca gga act gtc tat ctt gac cat gca ggt gcc acc 195

Phe	Ser	Arg	Leu	Ala	Gly	Thr	Val	Tyr	Leu	Asp	His	Ala	Gly	Ala	Thr		
		45					50					55					
ttg	ttc	tcc	cag	agc	cag	ctc	gaa	agc	ttc	act	agt	gat	ctc	atg	gaa	243	
Leu	Phe	Ser	Gln	Ser	Gln	Leu	Glu	Ser	Phe	Thr	Ser	Asp	Leu	Met	Glu		
	60					65					70						
aac	act	tat	ggg	aat	cct	cac	agc	cag	aac	atc	agc	agc	aag	ctc	acc	291	
Asn	Thr	Tyr	Gly	Asn	Pro	His	Ser	Gln	Asn	Ile	Ser	Ser	Lys	Leu	Thr		
	75				80					85					90		
cat	gac	act	gtg	gag	cag	gtg	cgc	tac	aga	atc	ctg	gcg	cac	ttc	cac	339	
His	Asp	Thr	Val	Glu	Gln	Val	Arg	Tyr	Arg	Ile	Leu	Ala	His	Phe	His		
			95						100					105			
acc	acc	gca	gaa	gac	tac	act	gtg	atc	ttc	act	gcc	ggg	agc	acg	gct	387	
Thr	Thr	Ala	Glu	Asp	Tyr	Thr	Val	Ile	Phe	Thr	Ala	Gly	Ser	Thr	Ala		
			110					115					120				
gct	ctc	aaa	ctg	gtg	gca	gag	gcc	ttt	cca	tgg	gtg	tcc	cag	ggc	cca	435	
Ala	Leu	Lys	Leu	Val	Ala	Glu	Ala	Phe	Pro	Trp	Val	Ser	Gln	Gly	Pro		
		125					130					135					
gag	agc	agt	ggg	agt	cgc	ttc	tgt	tac	ctc	acc	gac	agc	cac	acc	tcc	483	
Glu	Ser	Ser	Gly	Ser	Arg	Phe	Cys	Tyr	Leu	Thr	Asp	Ser	His	Thr	Ser		
	140					145					150						
gta	gtg	ggg	atg	agg	aac	gtg	acc	atg	gct	ata	aat	gtc	ata	tcc	atc	531	
Val	Val	Gly	Met	Arg	Asn	Val	Thr	Met	Ala	Ile	Asn	Val	Ile	Ser	Ile		
	155				160					165					170		
ccg	gtc	agg	cca	gag	gac	ctg	tgg	tct	gca	gag	gaa	cgt	ggg	gct	tca	579	
Pro	Val	Arg	Pro	Glu	Asp	Leu	Trp	Ser	Ala	Glu	Glu	Arg	Gly	Ala	Ser		
			175						180					185			
gcc	agc	aac	cca	gac	tgc	cag	ctg	ccg	cat	ctc	ttc	tgc	tac	cca	gct	627	
Ala	Ser	Asn	Pro	Asp	Cys	Gln	Leu	Pro	His	Leu	Phe	Cys	Tyr	Pro	Ala		
		190						195					200				
cag	agt	aac	ttt	tct	gga	gtc	aga	tac	ccc	ctg	tcc	tgg	ata	gaa	gag	675	
Gln	Ser	Asn	Phe	Ser	Gly	Val	Arg	Tyr	Pro	Leu	Ser	Trp	Ile	Glu	Glu		
		205					210					215					
gtc	aag	tct	ggg	cgg	ttg	cgc	cct	gtg	agc	acg	cct	ggg	aag	tgg	ttt	723	
Val	Lys	Ser	Gly	Arg	Leu	Arg	Pro	Val	Ser	Thr	Pro	Gly	Lys	Trp	Phe		
	220					225					230						
gtg	ctg	ctg	gat	gca	gcc	tcc	tac	gtg	agc	acc	tcg	cct	ttg	gac	ctg	771	
Val	Leu	Leu	Asp	Ala	Ala	Ser	Tyr	Val	Ser	Thr	Ser	Pro	Leu	Asp	Leu		
	235				240					245				250			
tca	gct	cac	cag	gcc	gac	ttt	gtc	ccc	atc	tcc	ttc	tat	aag	atc	ttc	819	
Ser	Ala	His	Gln	Ala	Asp	Phe	Val	Pro	Ile	Ser	Phe	Tyr	Lys	Ile	Phe		
			255						260					265			
ggg	ttt	cct	aca	ggc	ctg	ggc	gct	ctg	ctg	gtc	cat	aat	cgt	gcg	gct	867	
Gly	Phe	Pro	Thr	Gly	Leu	Gly	Ala	Leu	Leu	Val	His	Asn	Arg	Ala	Ala		

270	275	280	
cct cta ctg agg aag acc tac ttt gga gga ggg aca gcc tct gcg tac			915
Pro Leu Leu Arg Lys Thr Tyr Phe Gly Gly Gly Thr Ala Ser Ala Tyr			
285	290	295	
cta gca gga gaa gac ttc tac atc ccg agg cag tcg gta gct cag agg			963
Leu Ala Gly Glu Asp Phe Tyr Ile Pro Arg Gln Ser Val Ala Gln Arg			
300	305	310	
ttt gaa gat ggc acc atc tca ttc ctt gat gtt atc gcg cta aaa cat			1011
Phe Glu Asp Gly Thr Ile Ser Phe Leu Asp Val Ile Ala Leu Lys His			
315	320	325	330
gga ttt gac acc cta gag cgc ctc aca ggt gga atg gag aat ata aag			1059
Gly Phe Asp Thr Leu Glu Arg Leu Thr Gly Gly Met Glu Asn Ile Lys			
335	340	345	
cag cac acc ttc acc ttg gct cag tat acc tac atg gcc ctg tcc tct			1107
Gln His Thr Phe Thr Leu Ala Gln Tyr Thr Tyr Met Ala Leu Ser Ser			
350	355	360	
ctc cag tac ccc aat gga gcc cct gtg gtg cgg att tac agc gat tct			1155
Leu Gln Tyr Pro Asn Gly Ala Pro Val Val Arg Ile Tyr Ser Asp Ser			
365	370	375	
gag ttc agc agc cct gag gtt cag ggc ccg atc atc aat ttt aat gtg			1203
Glu Phe Ser Ser Pro Glu Val Gln Gly Pro Ile Ile Asn Phe Asn Val			
380	385	390	
ctg gat gac aaa ggg aac atc att ggt tac tcc cag gtg gac aaa atg			1251
Leu Asp Asp Lys Gly Asn Ile Ile Gly Tyr Ser Gln Val Asp Lys Met			
395	400	405	410
gcc agt ctt tac aac atc cac ctg cga act ggc tgc ttc tgt aac act			1299
Ala Ser Leu Tyr Asn Ile His Leu Arg Thr Gly Cys Phe Cys Asn Thr			
415	420	425	
ggg gcc tgc cag agg cac ctg ggc ata agc aac gag atg gtc agg aag			1347
Gly Ala Cys Gln Arg His Leu Gly Ile Ser Asn Glu Met Val Arg Lys			
430	435	440	
cat ttt cag gct ggt cat gtc tgt ggg gac aat atg gac ctc ata gat			1395
His Phe Gln Ala Gly His Val Cys Gly Asp Asn Met Asp Leu Ile Asp			
445	450	455	
ggg cag ccc aca gga tct gtg agg att tca ttt gga tac atg tcg acg			1443
Gly Gln Pro Thr Gly Ser Val Arg Ile Ser Phe Gly Tyr Met Ser Thr			
460	465	470	
ctg gat gat gtc cag gcc ttt ctt agg ttc atc ata gac act cgc ctg			1491
Leu Asp Asp Val Gln Ala Phe Leu Arg Phe Ile Ile Asp Thr Arg Leu			
475	480	485	490
cac tca tca ggg gac tgg cct gtc cct cag gcc cat gct gac acc ggg			1539
His Ser Ser Gly Asp Trp Pro Val Pro Gln Ala His Ala Asp Thr Gly			
495	500	505	

gag act gga gcc cca tca gca gac agc cag gct gat gtt ata cct gct	1587
Glu Thr Gly Ala Pro Ser Ala Asp Ser Gln Ala Asp Val Ile Pro Ala	
510 515 520	
gtc atg ggc aga cgt agc ctc tcg cct cag gaa gat gcc ctc aca ggc	1635
Val Met Gly Arg Arg Ser Leu Ser Pro Gln Glu Asp Ala Leu Thr Gly	
525 530 535	
tcc agg gtt tgg aac aac tcg tct act gtg aat gct gtg cct gtg gcc	1683
Ser Arg Val Trp Asn Asn Ser Ser Thr Val Asn Ala Val Pro Val Ala	
540 545 550	
cca cct gtg tgt gat gtc gcc aga acc cag ccg act cct tca gag aaa	1731
Pro Pro Val Cys Asp Val Ala Arg Thr Gln Pro Thr Pro Ser Glu Lys	
555 560 565 570	
gct gca gga gtc ctg gag ggg gcc ctt ggg cca cat gtt gtc act aac	1779
Ala Ala Gly Val Leu Glu Gly Ala Leu Gly Pro His Val Val Thr Asn	
575 580 585	
ctt tat ctc tat cca atc aaa tcc tgt gct gca ttt gag gtg acc agg	1827
Leu Tyr Leu Tyr Pro Ile Lys Ser Cys Ala Ala Phe Glu Val Thr Arg	
590 595 600	
tgg cct gta gga aac caa ggg ctg cta tat gac cgg agc tgg atg gtt	1875
Trp Pro Val Gly Asn Gln Gly Leu Leu Tyr Asp Arg Ser Trp Met Val	
605 610 615	
gtg aat cac aat ggt gtt tgc ctg agt cag aag cag gaa ccc cgg ctc	1923
Val Asn His Asn Gly Val Cys Leu Ser Gln Lys Gln Glu Pro Arg Leu	
620 625 630	
tgc ctg atc cag ccc ttc atc gac ttg cgg caa agg atc atg gtc atc	1971
Cys Leu Ile Gln Pro Phe Ile Asp Leu Arg Gln Arg Ile Met Val Ile	
635 640 645 650	
aaa gcc aaa ggg atg gag cct ata gag gtg cct ctt gag gaa aat agt	2019
Lys Ala Lys Gly Met Glu Pro Ile Glu Val Pro Leu Glu Glu Asn Ser	
655 660 665	
gaa cgg act cag att cgc caa agc agg gtc tgt gct gac aga gta agt	2067
Glu Arg Thr Gln Ile Arg Gln Ser Arg Val Cys Ala Asp Arg Val Ser	
670 675 680	
act tat gat tgt gga gaa aaa att tca agc tgg ttg tca aca ttt ttt	2115
Thr Tyr Asp Cys Gly Glu Lys Ile Ser Ser Trp Leu Ser Thr Phe Phe	
685 690 695	
ggc cgt cct tgt aat ttg atc aaa caa agt tca aac tct caa agg aat	2163
Gly Arg Pro Cys Asn Leu Ile Lys Gln Ser Ser Asn Ser Gln Arg Asn	
700 705 710	
gca aag aag aaa cat gga aaa gat caa ctt cct ggt aca atg gcc acc	2211
Ala Lys Lys Lys His Gly Lys Asp Gln Leu Pro Gly Thr Met Ala Thr	
715 720 725 730	

ctt tct ctg gtg aat gag gca cag tat ctg ctg atc aac aca tcc agt	2259
Leu Ser Leu Val Asn Glu Ala Gln Tyr Leu Leu Ile Asn Thr Ser Ser	
735 740 745	
att ttg gaa ctt cac cgg caa cta aac acc agt gat gag aat gga aag	2307
Ile Leu Glu Leu His Arg Gln Leu Asn Thr Ser Asp Glu Asn Gly Lys	
750 755 760	
gag gaa tta ttc tca ctg aag gat ctc agc ttg cgt ttt cgt gcc aat	2355
Glu Glu Leu Phe Ser Leu Lys Asp Leu Ser Leu Arg Phe Arg Ala Asn	
765 770 775	
att att atc aat gga aaa agg gct ttt gaa gaa gag aaa tgg gat gag	2403
Ile Ile Ile Asn Gly Lys Arg Ala Phe Glu Glu Glu Lys Trp Asp Glu	
780 785 790	
att tca att ggc tct ttg cgt ttc cag gtt ttg ggg cct tgt cac aga	2451
Ile Ser Ile Gly Ser Leu Arg Phe Gln Val Leu Gly Pro Cys His Arg	
795 800 805 810	
tgc cag atg att tgc atc gac cag caa act ggg caa cga aac cag cat	2499
Cys Gln Met Ile Cys Ile Asp Gln Gln Thr Gly Gln Arg Asn Gln His	
815 820 825	
gtt ttc caa aaa ctt tct gag agt cgt gaa aca aag gtg aac ttt ggc	2547
Val Phe Gln Lys Leu Ser Glu Ser Arg Glu Thr Lys Val Asn Phe Gly	
830 835 840	
atg tac ctg atg cat gca tca ttg gat tta tcc tcc cca tgt ttc ctg	2595
Met Tyr Leu Met His Ala Ser Leu Asp Leu Ser Ser Pro Cys Phe Leu	
845 850 855	
tct gta gga tct cag gtg ctc cct gtg ttg aaa gag aat gtg gaa ggt	2643
Ser Val Gly Ser Gln Val Leu Pro Val Leu Lys Glu Asn Val Glu Gly	
860 865 870	
cat gat tta cct gca tct gag aaa cac cag gat gtt acc tcc taa aaa	2691
His Asp Leu Pro Ala Ser Glu Lys His Gln Asp Val Thr Ser *	
875 880 885	
aaatttttag catacattaa agtttctctt ttaaaaa	2728

<210> 183
 <211> 1265
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (546)..(857)

<400> 183
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gctcggatcc actagtccag tgtggtggaa ttcggcagtc cccaaggggc gcagactctg 120

ctgtgaggtg tgcgaagccc cagccgagcg ggtgtgctcg gcctgcacag tcacttatta 180

ctggtctggg ccgaatcggt caggctgaag aatatctatt ccaagcccag tggacagtcc 240

tcaaataaac tgactgtagt aatgccaccc actctttact gcatcggaat ctgggacttc 300

tctatatagc taagaaaaac tatgaagagg cccgttatca tctggccaat gatatttatt 360

ttgccagttg tgcatttggg acagaggaca ttaggacttc aggaggctac ttccacctgg 420

ctaataatatt ctatgacctt aaaaagttgg acctggcaga cacattgtac accaaggtct 480

ctgagatctg gcatgcatat ttgaacaatc actatcaagt cctctcacag gctcacatcc 540

aacaa atg gat tta ctg ggc aaa cta ttt gag aat gac act ggc ttg 587
Met Asp Leu Leu Gly Lys Leu Phe Glu Asn Asp Thr Gly Leu
1 5 10

gat gaa gcc caa gaa gca gaa gcc att cgc atc ctg act tca atc ttg 635
Asp Glu Ala Gln Glu Ala Glu Ala Ile Arg Ile Leu Thr Ser Ile Leu
15 20 25 30

aac att cga gaa tct aca tct gac aaa gcc ccc caa aaa acc atc ttt 683
Asn Ile Arg Glu Ser Thr Ser Asp Lys Ala Pro Gln Lys Thr Ile Phe
35 40 45

gtt ctg aag atc ctg gtc atg ctt tac tac ctg atg atg aat tct tca 731
Val Leu Lys Ile Leu Val Met Leu Tyr Tyr Leu Met Met Asn Ser Ser
50 55 60

aag gca cag gaa tat ggc atg agg gcc ctc agt cta gcc aaa gaa caa 779
Lys Ala Gln Glu Tyr Gly Met Arg Ala Leu Ser Leu Ala Lys Glu Gln
65 70 75

cag ctt gat gtc cat gag caa agc acc att caa gag tta tta agt ctc 827
Gln Leu Asp Val His Glu Gln Ser Thr Ile Gln Glu Leu Leu Ser Leu
80 85 90

att tca act gaa gac cat ccc att act tag t gacccatgag ctctgcatca 878
Ile Ser Thr Glu Asp His Pro Ile Thr *
95 100

agggttattc caggggctac tgaagatcta atatattcca gccttgcaca actgctttga 938

ggtactgtag actgctgaag tttccaccct cttcccctgg gattgcacac atagctgtta 998

tttttttctt acacagcata ttaaggggaat ataaagcttt aggcatagaa atcactaaaa 1058

actgtgtttg tcatgacctt tgtacttgat ttatcatgac tttgtatgac tgagtaatat 1118

gtagtcagat cactaatatg gtatttgtaa ttaaactaca aatagtttgt catttcccag 1178

aagtcttcca acgatgcatg tttcatacac ttttgctaaa ggagggggtaa aggaggggggt 1238

agggaataaaa gctatatattgg aacaaaaa 1265

<210> 184
 <211> 1288
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (251)..(1246)

<400> 184

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aactacagct tcttggcagc gtcggtgttg gccgcgggag aaggggagac cgcggcggcc      120
cccagtgaga gcggctttcc aggacggtgc gatgtgctgc gcagcgaaga ggcaggaggc      180
cggtttctctg gggtagcggt acaggcgggc gcttactctg tgcgcttgct tccccaaccc      240
tgcaccggcc   atg cgc ccg gcc ttg gcg gtg ggc ctg gtg ttc gca ggc      289
              Met Arg Pro Ala Leu Ala Val Gly Leu Val Phe Ala Gly
              1             5             10

tgc tgc agt aac gtg atc ttc cta gag ctc ctg gcc cgg aag cat cca      337
Cys Cys Ser Asn Val Ile Phe Leu Glu Leu Leu Ala Arg Lys His Pro
              15             20             25

gga tgt ggg aac att gtg aca ttt gca caa ttt tta ttt att gct gtg      385
Gly Cys Gly Asn Ile Val Thr Phe Ala Gln Phe Leu Phe Ile Ala Val
              30             35             40             45

gaa ggc ttc ctc ttt gaa gct gat ttg gga agg aag cca cca gct atc      433
Glu Gly Phe Leu Phe Glu Ala Asp Leu Gly Arg Lys Pro Pro Ala Ile
              50             55             60

cca ata agg tac tat gcc ata atg gtg acc atg ttc ttc acc gtg agc      481
Pro Ile Arg Tyr Tyr Ala Ile Met Val Thr Met Phe Phe Thr Val Ser
              65             70             75

gtg gtg aac aac tat gcc ctg aat ctc aac att gcc atg ccc ctg cat      529
Val Val Asn Asn Tyr Ala Leu Asn Leu Asn Ile Ala Met Pro Leu His
              80             85             90

atg ata ttt aga tcc ggt tct cta att gcc aac acg att cta gga att      577
Met Ile Phe Arg Ser Gly Ser Leu Ile Ala Asn Thr Ile Leu Gly Ile
              95             100            105

atc att ttg aag aaa aga tac agt ata ttc aaa tat acc tcc att gcc      625
Ile Ile Leu Lys Lys Arg Tyr Ser Ile Phe Lys Tyr Thr Ser Ile Ala
              110             115            120            125

ctg gtg tct gtg ggg ata ttt att tgc act ttt atg tca gca aag cag      673
Leu Val Ser Val Gly Ile Phe Ile Cys Thr Phe Met Ser Ala Lys Gln
              130             135            140

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gtg act tcc cag tcc agc ttg agt gag aat gat gga ttc cag gca ttt	721
Val Thr Ser Gln Ser Ser Leu Ser Glu Asn Asp Gly Phe Gln Ala Phe	
145 150 155	
gtg tgg tgg tta cta ggt att ggg gca ttg act ttt gct ctt ctg atg	769
Val Trp Trp Leu Leu Gly Ile Gly Ala Leu Thr Phe Ala Leu Leu Met	
160 165 170	
tca gca agg atg ggg ata ttc caa gag act ctc tac aaa cga ttt ggg	817
Ser Ala Arg Met Gly Ile Phe Gln Glu Thr Leu Tyr Lys Arg Phe Gly	
175 180 185	
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Lys His Ser Lys Glu Ala Leu Phe Tyr Asn His Ala Leu Pro Leu Pro	
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Gly Phe Val Phe Leu Ala Ser Asp Ile Tyr Asp His Ala Val Leu Phe	
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Asn Lys Ser Glu Leu Tyr Glu Ile Pro Val Ile Gly Val Thr Leu Pro	
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Ile Met Trp Phe Tyr Leu Leu Met Asn Ile Ile Thr Gln Tyr Val Cys	
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Ile Arg Gly Val Phe Ile Leu Thr Thr Glu Cys Ala Ser Leu Thr Val	
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Thr Leu Val Val Thr Leu Arg Lys Phe Val Ser Leu Ile Phe Ser Ile	
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Leu Tyr Phe Gln Asn Pro Phe Thr Leu Trp His Trp Leu Gly Thr Leu	
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Phe Val Phe Ile Gly Thr Leu Met Tyr Thr Glu Val Trp Asn Asn Leu	
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tggactcttt caccaggtg ttgccaacc aaaacctgcg aattcaggtc aacaat 836

atg gcc cag gtg ctg cac act cag tca gca gtg atg gat gga gcc cct 884

Met Ala Gln Val Leu His Thr Gln Ser Ala Val Met Asp Gly Ala Pro
1 5 10 15

gac agt gct ctc cgc cag ctg ctg tct cag aag ccc atg gag ccc cca 932

Asp Ser Ala Leu Arg Gln Leu Leu Ser Gln Lys Pro Met Glu Pro Pro
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gca ccg gct atc cct tcc cgc tac cag cag gtg ccc cag cag cct cac 980

Ala Pro Ala Ile Pro Ser Arg Tyr Gln Gln Val Pro Gln Gln Pro His
35 40 45

cct ggt ttc act ggt ggg ctg tcc aaa cca gct ctt cag gtc ggg cag 1028

Pro Gly Phe Thr Gly Gly Leu Ser Lys Pro Ala Leu Gln Val Gly Gln
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His Pro Thr Gln Gly His Leu Tyr Tyr Asp Tyr Gln Gln Pro Leu Ala
65 70 75 80

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Gln Val Pro Val Gln Gly Gly Gln Pro Leu Gln Ala Pro Gln Met Leu
85 90 95

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Gln	Gln	Gln	Gln	Ala	Gly	Gln	Gln	Arg	Ile	Ser	Met	Gln	Glu	Ile	Gln	
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Thr	Gln	Pro	Gln	Gln	Ile	Arg	Pro	Ser	Gln	Pro	Gln	Pro	Pro	Pro	Gln	
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Gln	Gln	Gln	Pro	Gln	Gln	Leu	Gln	Leu	Gln	Gln	Arg	Gln	Gly	Ser	Met	
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cag	ata	cct	cag	tat	tat	cag	ccc	caa	ccc	atg	atg	cag	cac	ttg	caa	1364
Gln	Ile	Pro	Gln	Tyr	Tyr	Gln	Pro	Gln	Pro	Met	Met	Gln	His	Leu	Gln	
				165					170					175		
gag	cag	cag	cag	caa	cag	atg	cac	ctg	cag	cct	cct	tct	tat	cac	agg	1412
Glu	Gln	Gln	Gln	Gln	Gln	Met	His	Leu	Gln	Pro	Pro	Ser	Tyr	His	Arg	
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Asp	Pro	His	Gln	Tyr	Thr	Pro	Glu	Gln	Ala	His	Thr	Val	Gln	Leu	Ile	
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Tyr	Ser	His	Pro	Leu	Tyr	Gln	Gln	Ser	His	Leu	Ser	Gln	His	Gln	Gln	
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cgt	gag	gac	agt	cag	ctg	aag	acc	tac	tct	agt	gac	aga	cag	gcc	cag	1604
Arg	Glu	Asp	Ser	Gln	Leu	Lys	Thr	Tyr	Ser	Ser	Asp	Arg	Gln	Ala	Gln	
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gcc	atg	ctg	agc	tcc	cat	ggg	gac	ctg	ggg	cct	cct	gac	aca	gga	atg	1652
Ala	Met	Leu	Ser	Ser	His	Gly	Asp	Leu	Gly	Pro	Pro	Asp	Thr	Gly	Met	
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Gly	Asp	Pro	Ala	Ser	Ser	Asp	Leu	Thr	Arg	Val	Ser	Ser	Thr	Leu	Pro	
		275					280				285					
cat	cgc	ccc	ctc	cta	tcc	ccc	agt	ggg	atc	cac	ctc	aac	aac	atg	ggg	1748
His	Arg	Pro	Leu	Leu	Ser	Pro	Ser	Gly	Ile	His	Leu	Asn	Asn	Met	Gly	
	290					295					300					
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Pro	Gln	His														

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cac atg cgg tcc cac ggg gga atg agg gcc tcc ccc aac ctc aaa cag His Met Arg Ser His Gly Gly Met Arg Ala Ser Pro Asn Leu Lys Gln 370 375 380	1988
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acg ccc cca ccc atg ctg agc ccg gtg cgc cag ggc tcg ggg ctc ttc Thr Pro Pro Pro Met Leu Ser Pro Val Arg Gln Gly Ser Gly Leu Phe 465 470 475 480	2276
agc aat gtc ctc atc tcc ggc cac ggc cct ggc gcc cac ccg cag ctg Ser Asn Val Leu Ile Ser Gly His Gly Pro Gly Ala His Pro Gln Leu 485 490 495	2324
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Thr Pro Phe Leu Pro Gln Val Phe Ser Ser Arg Gln Ala Leu Asn Gly			
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cat gcc cgc atc cac ggg ggc acc aac cag gtg acc aag gcc cga ggt			3284
His Ala Arg Ile His Gly Gly Thr Asn Gln Val Thr Lys Ala Arg Gly			
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gcc atc ccc tct ggg aag cag aag cct ggt ggc acc cag agt ggg tac			3332
Ala Ile Pro Ser Gly Lys Gln Lys Pro Gly Gly Thr Gln Ser Gly Tyr			
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Cys Ser Val Lys Ser Ser Pro Ser His Ser Thr Thr Ser Gly Glu Thr			
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Lys Ile Lys Ser Arg Asn Ala His Met Lys Thr His Met Gln Gln Glu			
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Glu Gln Gln Arg Gln Lys Ala Gln Lys Ala Ala Phe Ala Ala Glu Met			
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gca gcc acg att gag agg act acg ggg ccc gtg ggg gcg ccg ggg ctg			3572
Ala Ala Thr Ile Glu Arg Thr Thr Gly Pro Val Gly Ala Pro Gly Leu			
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ctg ccc ctg gac cag ctg agt ctg atc aaa ccc atc aag gat gtg gac			3620
Leu Pro Leu Asp Gln Leu Ser Leu Ile Lys Pro Ile Lys Asp Val Asp			
	915	920	925
atc ctc gac gac gac gtc gtc cag cag ttg gga ggt gtc atg gaa gag			3668
Ile Leu Asp Asp Asp Val Val Gln Gln Leu Gly Gly Val Met Glu Glu			
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Ala Glu Val Val Asp Thr Asp Leu Leu Leu Asp Asp Gln Asp Ser Val			
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Leu Leu Gln Gly Asp Ala Glu Leu *			
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Asp Ser Ala Leu Arg Gln Leu Leu Ser Gln Lys Pro Met Glu Pro Pro
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Pro Gly Phe Thr Gly Gly Leu Ser Lys Pro Ala Leu Gln Val Gly Gln
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Cys	Ser	Ile	Cys	Leu	Lys	Glu	Phe	Lys	Asn	Leu	Pro	Ala	Leu	Asn	Gly	
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Glu	Ile	Pro	Arg	Lys	His	Gln	Pro	Ser	Val	Pro	Lys	Ala	Glu	Glu	Pro	
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Leu	Phe	Ile	Pro	Pro	Pro	Pro	Ser	Tyr	Asn	Pro	Asn	Pro	Ala	Ala	Ser	
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Tyr	Ser	Gly	Ala	Thr	Leu	Tyr	Gln	Ser	Gln	Leu	Arg	Ser	Pro	Arg	Val	
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Ser	Asn	Val	Leu	Ile	Ser	Gly	His	Gly	Pro	Gly	Ala	His	Pro	Gln	Leu	
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Pro	Leu	Thr	Pro	Leu	Thr	Pro	Thr	Pro	Arg	Val	Leu	Leu	Cys	Arg	Ser	
			500					505					510			
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gac ctc cag caa aga gtg gag aat ctt ctg aat ttg tgc tgt tcc agt Asp Leu Gln Gln Arg Val Glu Asn Leu Leu Asn Leu Cys Cys Ser Ser 580 585 590			2612
gca ttg cca ggt gga ggg acc aat tct gaa ttt gct ttg cac tct ctg Ala Leu Pro Gly Gly Gly Thr Asn Ser Glu Phe Ala Leu His Ser Leu 595 600 605			2660
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cgg aag cct gtc agg tta aaa tgt cat cct tta gca aat tac cac tat Arg Lys Pro Val Arg Leu Lys Cys His Pro Leu Ala Asn Tyr His Tyr 625 630 635 640			2756
gcc ggt tcg gac aag tgg acc tcc cta gaa aga aaa ctg ttt aac aaa Ala Gly Ser Asp Lys Trp Thr Ser Leu Glu Arg Lys Leu Phe Asn Lys 645 650 655			2804
gca cta gcc act tac agc aaa gac ttt att ttt gta cag aag atg gtg Ala Leu Ala Thr Tyr Ser Lys Asp Phe Ile Phe Val Gln Lys Met Val 660 665 670			2852
aag tcc aag acg gtg gct cag tgc gtg gag tac tac tac acg tgg aaa Lys Ser Lys Thr Val Ala Gln Cys Val Glu Tyr Tyr Tyr Thr Trp Lys 675 680 685			2900
aag atc atg cgg ctg ggg cgg aaa cac cgg aca cgc ttg gca gaa atc Lys Ile Met Arg Leu Gly Arg Lys His Arg Thr Arg Leu Ala Glu Ile 690 695 700			2948
atc gac gat tgt gtg aca agt gaa gaa gaa gaa gag tta gag gag gag Ile Asp Asp Cys Val Thr Ser Glu Glu Glu Glu Glu Leu Glu Glu Glu 705 710 715 720			2996
gag gag gag gac ccg gaa gaa gat agg aaa tcc aca aaa gaa gaa gag Glu Glu Glu Asp Pro Glu Glu Asp Arg Lys Ser Thr Lys Glu Glu Glu 725 730 735			3044
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Pro Thr Glu Gly Pro Pro Leu Gln Ala Leu Gly Gln Pro Ser Gly Ser	
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Phe Ile Cys Glu Met Pro Asn Cys Gly Ala Val Phe Ser Ser Arg Gln	
770 775 780	
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Ala Leu Asn Gly His Ala Arg Ile His Gly Gly Thr Asn Gln Val Thr	
785 790 795 800	
aag gcc cga ggt gcc atc ccc tct ggg aag cag aag cct ggt ggc acc	3284
Lys Ala Arg Gly Ala Ile Pro Ser Gly Lys Gln Lys Pro Gly Gly Thr	
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Gln Ser Gly Tyr Cys Ser Val Lys Ser Ser Pro Ser His Ser Thr Thr	
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Ser Gly Glu Thr Asp Pro Thr Thr Ile Phe Pro Cys Lys Glu Cys Gly	
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Lys Val Phe Phe Lys Ile Lys Ser Arg Asn Ala His Met Lys Thr His	
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Arg Gln Gln Glu Glu Gln Gln Arg Gln Lys Ala Gln Lys Ala Ala Phe	
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Ala Ala Glu Met Ala Ala Thr Ile Glu Arg Thr Thr Gly Pro Val Gly	
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Ala Pro Gly Leu Leu Pro Leu Asp Gln Leu Ser Leu Ile Lys Pro Ile	
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Lys Asp Val Asp Ile Leu Asp Asp Asp Val Val Gln Gln Leu Gly Gly	
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gtc atg gaa gag gct gaa gtt gtg gac acc gat ctt ctc ttg gat gat	3668
Val Met Glu Glu Ala Glu Val Val Asp Thr Asp Leu Leu Leu Asp Asp	
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Gln Asp Ser Val Leu Leu Gln Gly Asp Ala Glu Leu *	
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<220>
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<222> (367)..(1524)

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ccttgcagca ctgctggacc aggttacaag atgttcacct aagattgaga cctagtgact 180
acatttccta cggaacaaa taaatggttt ttcatctccc ggagatacat tacaacaaa 240
tatggtgcta aaagaactcc ttacctttct ctgactacaa tttatttgga catacttttg 300
tattgaagag aggtatacat actgaagcta cttgctgtac tataggagac tctgtcctgt 360
aggatc      atg gac cat cct agt agg gaa aag gat gaa aga caa cgg aca 408
             Met Asp His Pro Ser Arg Glu Lys Asp Glu Arg Gln Arg Thr
             1               5               10

act aaa ccc atg gca caa agg agt gca cac tgc tct cga cca tct ggc 456
Thr Lys Pro Met Ala Gln Arg Ser Ala His Cys Ser Arg Pro Ser Gly

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15	20	25	30	
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Ser Ser Ser Ser Ser Gly Val Leu Met Val Gly Pro Asn Phe Arg Val	35	40	45	
ggc aag aag ata gga tgt ggg aac ttc gga gag ctc aga tta ggt gaa				552
Gly Lys Lys Ile Gly Cys Gly Asn Phe Gly Glu Leu Arg Leu Gly Glu	50	55	60	
ggg ctc cca cag gtg tat tac ttt gga cca tgt ggg aaa tat aat gcc				600
Gly Leu Pro Gln Val Tyr Tyr Phe Gly Pro Cys Gly Lys Tyr Asn Ala	65	70	75	
atg gtg ctg gag ctc ctt ggc cct agc ttg gag gac ttg ttt gac ctc				648
Met Val Leu Glu Leu Leu Gly Pro Ser Leu Glu Asp Leu Phe Asp Leu	80	85	90	
tgt gac cga aca ttt act ttg aag acg gtg tta atg ata gcc atc cag				696
Cys Asp Arg Thr Phe Thr Leu Lys Thr Val Leu Met Ile Ala Ile Gln	95	100	105	110
ctg ctt tct cga atg gaa tac gtg cac tca aag aac ctc att tac cga				744
Leu Leu Ser Arg Met Glu Tyr Val His Ser Lys Asn Leu Ile Tyr Arg	115	120	125	
gat gtc aag cca gag aac ttc ctg att ggt cga caa ggc aat aag aaa				792
Asp Val Lys Pro Glu Asn Phe Leu Ile Gly Arg Gln Gly Asn Lys Lys	130	135	140	
gag cat gtt ata cac att ata gac ttt gga ctg gcc aag gaa tac att				840
Glu His Val Ile His Ile Ile Asp Phe Gly Leu Ala Lys Glu Tyr Ile	145	150	155	
gac ccc gaa acc aaa aaa cac ata cct tat agg gaa cac aaa agt tta				888
Asp Pro Glu Thr Lys Lys His Ile Pro Tyr Arg Glu His Lys Ser Leu	160	165	170	
act gga act gca aga tat atg tct atc aac acg cat ctt ggc aaa gag				936
Thr Gly Thr Ala Arg Tyr Met Ser Ile Asn Thr His Leu Gly Lys Glu	175	180	185	190
caa agc cgg aga gat gat ttg gaa gcc cta ggc cat atg ttc atg tat				984
Gln Ser Arg Arg Asp Asp Leu Glu Ala Leu Gly His Met Phe Met Tyr	195	200	205	
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Phe Leu Arg Gly Ser Leu Pro Trp Gln Gly Leu Lys Ala Asp Thr Leu	210	215	220	
aaa gag aga tat caa aaa att ggt gac acc aaa agg aat act ccc att				1080
Lys Glu Arg Tyr Gln Lys Ile Gly Asp Thr Lys Arg Asn Thr Pro Ile	225	230	235	
gaa gct ctc tgt gag aac ttt cca gag gag atg gca acc tac ctt cga				1128
Glu Ala Leu Cys Glu Asn Phe Pro Glu Glu Met Ala Thr Tyr Leu Arg	240	245	250	

tat gtc agg cga ctg gac ttc ttt gaa aaa cct gat tat gag tat tta	1176
Tyr Val Arg Arg Leu Asp Phe Phe Glu Lys Pro Asp Tyr Glu Tyr Leu	
255 260 265 270	
cgg acc ctc ttc aca gac ctc ttt gaa aag aaa ggc tac acc ttt gac	1224
Arg Thr Leu Phe Thr Asp Leu Phe Glu Lys Lys Gly Tyr Thr Phe Asp	
275 280 285	
tat gcc tat gat tgg gtt ggg aga cct att cct act cca gta ggg tca	1272
Tyr Ala Tyr Asp Trp Val Gly Arg Pro Ile Pro Thr Pro Val Gly Ser	
290 295 300	
gtt cac gta gat tct ggt gca tct gca ata act cga gaa agc cac aca	1320
Val His Val Asp Ser Gly Ala Ser Ala Ile Thr Arg Glu Ser His Thr	
305 310 315	
cat agg gat cgg cca tca caa cag cag cct ctt cga aat cag gtg gtt	1368
His Arg Asp Arg Pro Ser Gln Gln Gln Pro Leu Arg Asn Gln Val Val	
320 325 330	
agc tca acc aat gga gag ctg aat gtt gat gat ccc acg gga gcc cac	1416
Ser Ser Thr Asn Gly Glu Leu Asn Val Asp Asp Pro Thr Gly Ala His	
335 340 345 350	
tcc aat gca cca atc aca gct cat gcc gag gtg gag gta gtg gag gaa	1464
Ser Asn Ala Pro Ile Thr Ala His Ala Glu Val Glu Val Val Glu Glu	
355 360 365	
gct aag tgc tgc tgt ttc ttt aag agg aaa agg aag aag act gct cag	1512
Ala Lys Cys Cys Cys Phe Phe Lys Arg Lys Arg Lys Lys Thr Ala Gln	
370 375 380	
cgc cac aag tga cca gtgcctccca ggagtcctca ggccctgggg actctgactc	1567
Arg His Lys *	
385	
aattgtacct gcagctcctg ccattttctca ttggaaggga ctctcttttg ggggaggggtg	1627
gatatccaaa ctaaaaagaa gaaaacagat gccccagaa ggggccagtg cgggcagcca	1687
gggcctagtg ggtcattggc catctccgcc tgcctaaggc tctgagcagg tcccagagct	1747
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ctcttctct gtgcctgtgc agcattcatc ccagctggcc ttgggggttca ggttccttct	2107
tccctccctc ctgtgaagtt aactgtagg acacaagctg tgagcaatct gcagtctact	2167

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aaaaaaaaaca aaaacaaaaa catgaaaaaa a 2318

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<213> Homo sapiens

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cctggctgtg gtggcctgtg gcaatcggct ggaggagacg ctggtcatgc tcaaatacagc 180
tgtgcttttt agccacagga agatccaatt ccacatcttc actgaagact ctctgaagcc 240
cgagtttgat aagcagttac gccatggcct gactcatata caaagaagtt tgagcacaga 300
atctacccca tcacattttc tgttggaaac cctcaggagt ggaagaaatt gttcaaacc 360
tgtgctgccc agagactctt tcttccgggtg attttaaagg atgtggactc acttctctac 420
gtggacaccg atgtcctctt tctgagacct gttgatgaca tctggaagct tctgaggctg 480
tttaattcca ccagcttgc agcc atg gcc cct gag cac gaa atc ccc aag 531
Met Ala Pro Glu His Glu Ile Pro Lys
1 5
att ggc tgg tac agc cgc ttt gct agg cat cct ttc tat ggc tct gca 579
Ile Gly Trp Tyr Ser Arg Phe Ala Arg His Pro Phe Tyr Gly Ser Ala
10 15 20 25
gga gtt aat tca gga gtc atg tta atg aat tta act cgg ata aga agt 627
Gly Val Asn Ser Gly Val Met Leu Met Asn Leu Thr Arg Ile Arg Ser
30 35 40
acc cag ttc aag aac agc atg att cca aca ggc ctg gct tgg gag gac 675
Thr Gln Phe Lys Asn Ser Met Ile Pro Thr Gly Leu Ala Trp Glu Asp
45 50 55
atg ttg tac cct ctg tac cag aag tac aag aat gcc atc acg tgg gga 723
Met Leu Tyr Pro Leu Tyr Gln Lys Tyr Lys Asn Ala Ile Thr Trp Gly
60 65 70
gac cag gat tta tta aat att att ttt tat ttc aac cca gag tgt ctc 771
Asp Gln Asp Leu Leu Asn Ile Ile Phe Tyr Phe Asn Pro Glu Cys Leu

75	80	85	
tat gta ttc ccc tgc cag tgg aac tac cgt ccc gat cac tgc atg tac			819
Tyr Val Phe Pro Cys Gln Trp Asn Tyr Arg Pro Asp His Cys Met Tyr			
90	95	100	105
gga agc aac tgc aga gag gct gag cat gaa ggt gtg tct gtt ctg cat			867
Gly Ser Asn Cys Arg Glu Ala Glu His Glu Gly Val Ser Val Leu His			
	110	115	120
gga aac cga ggc gtc tac cat gac gat aag caa cca acg ttc aga gca			915
Gly Asn Arg Gly Val Tyr His Asp Asp Lys Gln Pro Thr Phe Arg Ala			
	125	130	135
ctc tat gaa gca ata cgg gat ttt ccc ttt caa gac aat ctc ttt caa			963
Leu Tyr Glu Ala Ile Arg Asp Phe Pro Phe Gln Asp Asn Leu Phe Gln			
	140	145	150
tcc atg tat tac ccc ctt cag ctg aag ttt ttg gag act gtg cac act			1011
Ser Met Tyr Tyr Pro Leu Gln Leu Lys Phe Leu Glu Thr Val His Thr			
	155	160	165
tta tgt gga cga atc ccg caa gtt ttt ctg aag caa att gag aaa aca			1059
Leu Cys Gly Arg Ile Pro Gln Val Phe Leu Lys Gln Ile Glu Lys Thr			
	170	175	180
atg aaa agg gct tat gag aaa cac gtc atc atc cat gtt ggc ccc aac			1107
Met Lys Arg Ala Tyr Glu Lys His Val Ile Ile His Val Gly Pro Asn			
	190	195	200
cag atg cac tga ata ttttgtcttg ttgcaagtca attaggtgtc ttgtgaacaa			1162
Gln Met His *			
	205		
ggaaatacta atctctaagc tgccctgggtc tttttgtgtg aatatttaaat ggtgctccat			1222
gactgttgag ttttaaaaac ctgcgttaaatt tttgccaaat cagttgcccc caaaagggaa			1282
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ggacc	atg aac gtg ttc cga atc ctc ggc gac ctg agc cac ctc ctg	167
	Met Asn Val Phe Arg Ile Leu Gly Asp Leu Ser His Leu Leu	
	1 5 10	
gcc atg atc ttg ctg ctg ggg aag atc tgg agg tcc aag tgc tgc aag	215	
Ala Met Ile Leu Leu Leu Gly Lys Ile Trp Arg Ser Lys Cys Cys Lys		
15 20 25 30		
ggc atc tct ggg aag agc cag atc ctg ttt gct ctc gtc ttc acc acc	263	
Gly Ile Ser Gly Lys Ser Gln Ile Leu Phe Ala Leu Val Phe Thr Thr		
35 40 45		
agg tac ctg gac ctg ttc acc aac ttc atc tcc atc tac aac aca gta	311	
Arg Tyr Leu Asp Leu Phe Thr Asn Phe Ile Ser Ile Tyr Asn Thr Val		
50 55 60		
atg aag gtg gtt ttt ctc ctc tgt gcc tat gtt aca gtg tac atg ata	359	
Met Lys Val Val Phe Leu Leu Cys Ala Tyr Val Thr Val Tyr Met Ile		
65 70 75		
tat ggg aaa ttc cgt aaa act ttt gac agt gag aat gac aca ttc cgc	407	
Tyr Gly Lys Phe Arg Lys Thr Phe Asp Ser Glu Asn Asp Thr Phe Arg		
80 85 90		
ctg gag ttt ctt ctg gtc cca gtc att ggc ctt tcc ttc ctt gaa aac	455	
Leu Glu Phe Leu Leu Val Pro Val Ile Gly Leu Ser Phe Leu Glu Asn		
95 100 105 110		
tac agt ttc act ctg ctg gag atc ctc tgg act ttc tct atc tat ctg	503	
Tyr Ser Phe Thr Leu Leu Glu Ile Leu Trp Thr Phe Ser Ile Tyr Leu		
115 120 125		
gaa tca gtg gct atc ctg ccc cag ctc ttc atg atc agc aag act gga	551	
Glu Ser Val Ala Ile Leu Pro Gln Leu Phe Met Ile Ser Lys Thr Gly		
130 135 140		
gag gct gag acc ata act act cac tac ctg ttc ttt ctg ggt ctg tac	599	
Glu Ala Glu Thr Ile Thr Thr His Tyr Leu Phe Phe Leu Gly Leu Tyr		
145 150 155		
cgg gca ctc tac ctg gct aac tgg atc agg cgg tac cag act gag aat	647	
Arg Ala Leu Tyr Leu Ala Asn Trp Ile Arg Arg Tyr Gln Thr Glu Asn		
160 165 170		
ttc tat gac caa att gca gtc gtg tct gga gta gta caa acc atc ttc	695	
Phe Tyr Asp Gln Ile Ala Val Val Ser Gly Val Val Gln Thr Ile Phe		
175 180 185 190		
tac tgt gac ttc ttc tac ttg tat gtg acc aaa gtc ctt aag gga aag	743	
Tyr Cys Asp Phe Phe Tyr Leu Tyr Val Thr Lys Val Leu Lys Gly Lys		
195 200 205		
aag tta agt ctt cca atg cca atc tga ggacc ttcagagaca gtctacgcct	795	
Lys Leu Ser Leu Pro Met Pro Ile *		
210 215		
taacaagcac atgaaggaaa ctattctgaa tgttctcttt ggcaacttat ccataatttg	855	

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tcaatccaat atccccatc tttgtcttga aacaaaaact gttttaagac gtctacgttg 1635
aattattcag agaattaagc aataaaagct cacaccttat tgtcaaaaaa 1685

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ggcgcgggcg cacgactgac tggctggacc      atg aac gtg ttc cga atc ctc 171
                                   Met Asn Val Phe Arg Ile Leu
                                   1               5

ggc gac ctg agc cac ctc ctg gcc atg atc ttg ctg ctg ggg aag atc 219
Gly Asp Leu Ser His Leu Leu Ala Met Ile Leu Leu Leu Gly Lys Ile
      10              15              20

tgg agg tcc aag tgc tgc aag ggc atc tct ggg aag agc cag atc ctg 267
Trp Arg Ser Lys Cys Cys Lys Gly Ile Ser Gly Lys Ser Gln Ile Leu
      25              30              35

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ttt gct ctc gtc ttc acc acc agg tac ctg gac ctg ttc acc aac ttc      315
Phe Ala Leu Val Phe Thr Thr Arg Tyr Leu Asp Leu Phe Thr Asn Phe
 40                      45                      50                      55

atc tcc atc tac aac aca gta atg aag atc ctc tgg act ttc tct atc      363
Ile Ser Ile Tyr Asn Thr Val Met Lys Ile Leu Trp Thr Phe Ser Ile
                      60                      65                      70

tat ctg gaa tca gtg gct atc ctg ccc cag ctc ttc atg atc agc aag      411
Tyr Leu Glu Ser Val Ala Ile Leu Pro Gln Leu Phe Met Ile Ser Lys
                      75                      80                      85

act gga gag gct gag acc ata act act cac tac ctg ttc ttt ctg ggt      459
Thr Gly Glu Ala Glu Thr Ile Thr Thr His Tyr Leu Phe Phe Leu Gly
                      90                      95                      100

ctg tac cgg gca ctc tac ctg gct aac tgg atc aag cgg tac cag act      507
Leu Tyr Arg Ala Leu Tyr Leu Ala Asn Trp Ile Lys Arg Tyr Gln Thr
                      105                      110                      115

gag aat ttc tat gac caa att gca gtc ggg tct gga gta gta caa acc      555
Glu Asn Phe Tyr Asp Gln Ile Ala Val Gly Ser Gly Val Val Gln Thr
                      120                      125                      130                      135

atc ttc tac tgt gac ttc ttc tac ttg tat gtg acc aaa gtc ctt aag      603
Ile Phe Tyr Cys Asp Phe Phe Tyr Leu Tyr Val Thr Lys Val Leu Lys
                      140                      145                      150

gga aag aag tta agt ctt cca atg cca atc tga ggaccttc agagacagtc      654
Gly Lys Lys Leu Ser Leu Pro Met Pro Ile *
                      155                      160

tacgccttaa caagcacatg aaggaaacta ttttgaatgt tctctttggc aacttatcca      714

ta                                                                    716

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<210> 191
 <211> 948
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (380)..(706)

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<400> 191
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gtaacctcca cctcccggt tcaagcgact ctgctgcctc agcctcctga gtagctggga      120

ttacaggcac ctgccaccat gccagctaa tttttatatt tttaagagat ggggggtcac      180

catgttggcc aggctggtct caaactcctg acctcaggcg atccgccac cttggcctcc      240

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caaagtgcctg gttttgcaga tgggagccac catgcccagc ctagtctcac tttataggct 300
 cccaaaccac agcagaacac ctggctgcct catccctctg cacccatcac gccagtgggc 360
 atgctggctg taggtgggg atg gcc ttt gcc cgg gtt cct ggg agc acc tgg 412
 Met Ala Phe Ala Arg Val Pro Gly Ser Thr Trp
 1 5 10
 tgt ttt atg gtc acc tac cca ctt aca cct gac cct ggg gcc tct gca 460
 Cys Phe Met Val Thr Tyr Pro Leu Thr Pro Asp Pro Gly Ala Ser Ala
 15 20 25
 gtt ttc ttg gcg ttg tca cca caa aag gaa gaa gcc cac ctg tgg ctg 508
 Val Phe Leu Ala Leu Ser Pro Gln Lys Glu Glu Ala His Leu Trp Leu
 30 35 40
 gct ggc tgg ccg cca ggt cag agc caa ggc agg cag ggc ctt cct gtc 556
 Ala Gly Trp Pro Pro Gly Gln Ser Gln Gly Arg Gln Gly Leu Pro Val
 45 50 55
 tgg ctt ctt gaa ggc aga cac aag tct gca ggc tgc tca cgt cat ctc 604
 Trp Leu Leu Glu Gly Arg His Lys Ser Ala Gly Cys Ser Arg His Leu
 60 65 70 75
 att atc ttt tct cac gag gac tac ttc gga tac aat cac agc aac cct 652
 Ile Ile Phe Ser His Glu Asp Tyr Phe Gly Tyr Asn His Ser Asn Pro
 80 85 90
 ggc ctt ggc cct gcc ctg tcc ctg cca tgc aac ttc aca act cag ctg 700
 Gly Leu Gly Pro Ala Leu Ser Leu Pro Cys Asn Phe Thr Thr Gln Leu
 95 100 105
 gcc tag acccctggga ggctccaag tcctaaggt tagacatctc ctggggtgct 756
 Ala *
 atggactgtc ggggctccaa ggagccgagt gtgggggaaa ctactgtgg gaggcgctcc 816
 tgacctgcag ggagctggaa tgctgtggga gggccctgac cccggggccc atggagctcc 876
 ctaggctcct ctggccacac ggacgcgtgg gtcgaccgga gaattccggg ccggtaccga 936
 aggcgatcaa gg 948

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 <212> DNA
 <213> Homo sapiens

<220>
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Gln Phe Met Arg Ile Gln Asn Val Gly Gln Lys Lys Ala Glu Glu Ser	
215 220 225	

cca gca gaa att atc atc cag gct att cct cag tat gct att cct tgt	775
Pro Ala Glu Ile Ile Ile Gln Ala Ile Pro Gln Tyr Ala Ile Pro Cys	
230 235 240	

cac tcc agc tcc aat gtg gtg gtg gag ccc agt ggg ctt ctt gag cta	823
His Ser Ser Ser Asn Val Val Val Glu Pro Ser Gly Leu Leu Glu Leu	
245 250 255	

aac aac ttc act agt caa cag ctg gat gat gag gag aca gca atg gag	871
Asn Asn Phe Thr Ser Gln Gln Leu Asp Asp Glu Glu Thr Ala Met Glu	
260 265 270 275	

cag gac ata gac agt agc acg gag gat gga act gaa ccc agc cct tct	919
Gln Asp Ile Asp Ser Ser Thr Glu Asp Gly Thr Glu Pro Ser Pro Ser	
280 285 290	

cag agc tct gct gaa cgg tcc tag tgtttggaca caatagtgca ctttaaaacc	973
Gln Ser Ser Ala Glu Arg Ser *	
295	

tgcttggtta ccaagtgtcc agggaaaccc ttgtattttg atgactaaaa agagcacttt	1033
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gcccgtactt aggctgtgga ccctaaaaca gcagtgtttc aacaagatgt tgctgcagga	1093
---	------

gcagcttttt aaaacaagat aaaactcaca ggggaatgta ctttttttaa aaaaaaaaa	1152
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<210> 193
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 <212> DNA
 <213> Homo sapiens

<220>
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gagctagctg agcgaatggg ccggcgactg tggagttagc gtcctcaatg tggacgcct	120
--	-----

gagctcccat taggagccgc tggctgcggc agcaggggac tagcgtgaga gttggctaaa	180
---	-----

aaaaagaaaa gaac atg gag gca gat ata atc aca aat ctt cga tgc agg	230
Met Glu Ala Asp Ile Ile Thr Asn Leu Arg Cys Arg	
1 5 10	

ctc aaa gag gct gaa gaa gag cga cta aaa gct gca cag tat ggt tta	278
Leu Lys Glu Ala Glu Glu Glu Arg Leu Lys Ala Ala Gln Tyr Gly Leu	
15 20 25	

caa cta gta gag agt caa aat gaa tta cag aat caa ttg gat aaa tgt Gln Leu Val Glu Ser Gln Asn Glu Leu Gln Asn Gln Leu Asp Lys Cys 30 35 40	326
cgt aat gaa atg atg acc atg act gag agt tat gaa caa gaa aaa tat Arg Asn Glu Met Met Thr Met Thr Glu Ser Tyr Glu Gln Glu Lys Tyr 45 50 55 60	374
acc ctt caa aga gaa gtt gaa ctc aag agt cga atg tta gaa agt ttg Thr Leu Gln Arg Glu Val Glu Leu Lys Ser Arg Met Leu Glu Ser Leu 65 70 75	422
agc tgc gaa tgt gaa gct att aaa caa caa caa aaa atg cac ctg gag Ser Cys Glu Cys Glu Ala Ile Lys Gln Gln Gln Lys Met His Leu Glu 80 85 90	470
aaa ttg gaa gaa caa cta agc aga agc cat gga cag gaa gtg aat gaa Lys Leu Glu Glu Gln Leu Ser Arg Ser His Gly Gln Glu Val Asn Glu 95 100 105	518
cta aaa act aag ata gaa aaa ctg aaa gtg gaa tta gat gaa gcc agg Leu Lys Thr Lys Ile Glu Lys Leu Lys Val Glu Leu Asp Glu Ala Arg 110 115 120	566
ctt agt gaa aag cag ctg aag cac caa gta gat cat cag aag gaa ctc Leu Ser Glu Lys Gln Leu Lys His Gln Val Asp His Gln Lys Glu Leu 125 130 135 140	614
ctc tct tgt aaa tca gag gaa ctg cgc gta atg tct gaa cgt gtg cag Leu Ser Cys Lys Ser Glu Glu Leu Arg Val Met Ser Glu Arg Val Gln 145 150 155	662
gaa agc atg tct tca gag atg ctg gct ctt caa att gag ctg aca gaa Glu Ser Met Ser Ser Glu Met Leu Ala Leu Gln Ile Glu Leu Thr Glu 160 165 170	710
atg gag agt atg aag acc acc ctc aaa gaa gaa gtg aat gaa cta caa Met Glu Ser Met Lys Thr Thr Leu Lys Glu Glu Val Asn Glu Leu Gln 175 180 185	758
tac aga caa gaa cag cta gaa ctt ctt att act aac cta atg cgc cag Tyr Arg Gln Glu Gln Leu Glu Leu Leu Ile Thr Asn Leu Met Arg Gln 190 195 200	806
gta gac cgg ctt aaa gag gaa aaa gaa gag cga gag aaa gaa gca gtt Val Asp Arg Leu Lys Glu Glu Lys Glu Glu Arg Glu Lys Glu Ala Val 205 210 215 220	854
tct tac tat aat gcc cta gag aaa gct cgt gta gca aat caa gat ctt Ser Tyr Tyr Asn Ala Leu Glu Lys Ala Arg Val Ala Asn Gln Asp Leu 225 230 235	902
cag gta cag ttg gac cag gca ctc cag caa gcc ttg gat ccc aat agt Gln Val Gln Leu Asp Gln Ala Leu Gln Ala Leu Asp Pro Asn Ser 240 245 250	950
aaa ggc aac tct ttg ttt gca gag gtg gaa gat cga agg gca gca atg	998

Lys	Gly	Asn	Ser	Leu	Phe	Ala	Glu	Val	Glu	Asp	Arg	Arg	Ala	Ala	Met	
		255					260					265				
gaa	cgt	cag	ctt	atc	agt	atg	aaa	gtc	aag	tat	cag	tca	cta	aag	aag	1046
Glu	Arg	Gln	Leu	Ile	Ser	Met	Lys	Val	Lys	Tyr	Gln	Ser	Leu	Lys	Lys	
		270				275					280					
caa	aat	gta	ttt	aac	aga	gaa	cag	atg	cag	aga	atg	aag	tta	caa	att	1094
Gln	Asn	Val	Phe	Asn	Arg	Glu	Gln	Met	Gln	Arg	Met	Lys	Leu	Gln	Ile	
		285			290					295					300	
gcc	acg	ttg	cta	cag	atg	aaa	ggg	tct	caa	act	gaa	ttt	gag	cag	cag	1142
Ala	Thr	Leu	Leu	Gln	Met	Lys	Gly	Ser	Gln	Thr	Glu	Phe	Glu	Gln	Gln	
				305					310					315		
gaa	cgg	ttg	ctt	gcc	atg	ttg	gag	cag	aag	aat	ggt	gaa	ata	aaa	cat	1190
Glu	Arg	Leu	Leu	Ala	Met	Leu	Glu	Gln	Lys	Asn	Gly	Glu	Ile	Lys	His	
			320					325					330			
ctt	tta	ggt	gaa	att	aga	aat	ctg	gag	aaa	ttt	aag	aat	tta	tat	gac	1238
Leu	Leu	Gly	Glu	Ile	Arg	Asn	Leu	Glu	Lys	Phe	Lys	Asn	Leu	Tyr	Asp	
		335					340				345					
agt	atg	gaa	tcc	aag	cct	tca	gtc	gac	tct	ggt	act	ctg	gaa	gat	aac	1286
Ser	Met	Glu	Ser	Lys	Pro	Ser	Val	Asp	Ser	Gly	Thr	Leu	Glu	Asp	Asn	
		350				355					360					
acc	tat	tat	aca	gat	tta	ctt	cag	atg	aag	ctg	gat	aac	tta	aac	aaa	1334
Thr	Tyr	Tyr	Thr	Asp	Leu	Leu	Gln	Met	Lys	Leu	Asp	Asn	Leu	Asn	Lys	
					370					375					380	
gaa	att	gaa	agc	act	aaa	ggt	gaa	ttg	tcc	ata	cag	cga	atg	aaa	gca	1382
Glu	Ile	Glu	Ser	Thr	Lys	Gly	Glu	Leu	Ser	Ile	Gln	Arg	Met	Lys	Ala	
				385					390					395		
tta	ttt	gag	agc	cag	cgg	gct	cta	gat	att	gag	cga	aaa	ctt	ttt	tgc	1430
Leu	Phe	Glu	Ser	Gln	Arg	Ala	Leu	Asp	Ile	Glu	Arg	Lys	Leu	Phe	Cys	
			400					405					410			
aaa	tga	aagatgcctc	cagcttttcag	aaagtgaaaa	tatgaaactg	agagctaaac										1486
Lys	*															
tagatgaatt	gaaactaaaa	tatgaacctg	aagagacagt	tgaagtcct	gtactgaaaa											1546
agaggcgtga	ggtgctccct	gtggatataa	ccaccgctaa	agatgcatgt	gtcaacaaca											1606
gtgctctcgg	gggagaagtt	tatcgattac	cgctcagaa	agaggagaca	cagtcctgcc											1666
ctaacagttt	agaagataac	aacttgcaat	tagaaaaatc	agtttctata	cacacaccag											1726
tagtcagtct	ctctcctcac	aaaaatctgc	ccgtggatat	gcagctgaag	aaggaaaaga											1786
aatgtgtgaa	actcatagga	gttcccgtcg	acgctgaggc	cttaagtgaa	agaagtggaa											1846
acaccccaaaa	ctctcccagg	ttagctgctg	aatcaaagct	tcaaacagaa	gttaaagaag											1906

gaaaagaaac ttcaagcaaa ttggaaaaag aaacttgtaa gaaatcacac cctattctat 1966
atgtgtcttc taaatctact ccagagaccc agtgccctca acagtaaaga cttttcttta 2026
agtaagagta cggtgccact tgcctcaaaa gttactatgg tgcttaagat tgtcttgatc 2086
tgacatatat caccttctgg gttatttact cattgtgcca ggacctggca ttttcatgtg 2146
cctttgacca agtggtcaga atttgcttga ctctaacctg gagagcttct taagtgatgc 2206
cccttcatgg agcttctatg acagtgaata aactattaat tgaaggaaaa tgttataatt 2266
aatgtatcta tttgctgcat tgtatatgga ttaaatagata aaaaacaagt aatctaccct 2326
cagagccatg tatttgagaa tgcttcaatc atattttcct atgtactttt ttttataaac 2386
ttagtttttag actatgttgt aaaaatggga aggttgtaaa ctatgttgta aaaataggaa 2446
atgtggctta aaatatatac attatattgt ttcaggattt tgtcagtgtt taaagaacca 2506
tgttcatctt tgtatttata tacatgattt aaattttgtc taaaatttta aataaaaactg 2566
ccagtgattt atcctt 2582

<210> 194
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (528) .. (953)

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tgcttcacaa aaggaagctt ataacaacag tacttgtctc acagttttag gataattaa 120
ttatggtata tgcaaagcaa ttaaaacagc tcctgcaaaa gagtaaaccac catataaata 180
ttcattaaat aacatacaaa cataccaggt tgggaaaaat cagtaagcat aggagtcagg 240
aaattccaag ttggttatca caactcttgg cccacagggc tttaatccag gtgcccttgt 300
ctcctaccct tgttgccatc ccagtgtctc cagggagtaa gtagaaataa agatcctatc 360
tcacctcttg ggcattttcc cctgccctga aagcgtataa tcgcttagca cagtcggtgc 420
ttaaggggcc aggctccaaa gaagattaaa ggaacagttt gtggggtgca ctgggcagca 480
gtactctcct ctgagttcaa tcactcttga ctctaagaat caccacc atg gcc ctt 536
Met Ala Leu

gtg cca ggg aga agc aag gag gat ggg ctt tgg act aga aat agc cca	584
Val Pro Gly Arg Ser Lys Glu Asp Gly Leu Trp Thr Arg Asn Ser Pro	
5 10 15	
ggc tcc tcc cag cat cca gaa agt ccc agg ctg ccc aac cct ctc tgg	632
Gly Ser Ser Gln His Pro Glu Ser Pro Arg Leu Pro Asn Pro Leu Trp	
20 25 30 35	
gac aga gga aaa att ggc aag gtt gaa ggt cac cag cac att cag gtt	680
Asp Arg Gly Lys Ile Gly Lys Val Glu Gly His Gln His Ile Gln Val	
40 45 50	
agt act tcc tca gcc tgt gtc tgg cag ctg gct tac cct cca gtt tgg	728
Ser Thr Ser Ser Ala Cys Val Trp Gln Leu Ala Tyr Pro Pro Val Trp	
55 60 65	
ccc aac ctc cct gct gtc cct att cag gat ttc tct caa aag tcc cat	776
Pro Asn Leu Pro Ala Val Pro Ile Gln Asp Phe Ser Gln Lys Ser His	
70 75 80	
ctg ccg tct att gtg gtg gaa tcc agt gag gtg aat gaa gag agt ggg	824
Leu Pro Ser Ile Val Val Glu Ser Ser Glu Val Asn Glu Glu Ser Gly	
85 90 95	
gat ctc cat ttg ccc cat gag gag ctg ctg ctg ctc act gat ggt gag	872
Asp Leu His Leu Pro His Glu Glu Leu Leu Leu Leu Thr Asp Gly Glu	
100 105 110 115	
gaa gag gat gct gag gcc ttc ttc caa gac caa agt gaa gag cca ggt	920
Glu Glu Asp Ala Glu Ala Phe Phe Gln Asp Gln Ser Glu Glu Pro Gly	
120 125 130	
gag gga ggt ggc tca ttc agg ggg cca ctg tga gctgaatg ttctgggcag	971
Glu Gly Gly Gly Ser Phe Arg Gly Pro Leu *	
135 140	
agccaagatg gaagtcagtt acggcccctg cattcagcag taaaaggcac acagcaggtg	1031
ctcaataaat g	1042

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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (17)..(739)

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	Met Ser Pro Leu Leu Phe Gly Ala Gly Leu Val	
	1 5 10	

gtt ctg aat cta gtg acg tct gcc agg agc cag aag aca gaa cct cta	97
Val Leu Asn Leu Val Thr Ser Ala Arg Ser Gln Lys Thr Glu Pro Leu	
15 20 25	
agt ggc tct ggg gac cag cca ctc ttc cgt gga gct gat cga tat gac	145
Ser Gly Ser Gly Asp Gln Pro Leu Phe Arg Gly Ala Asp Arg Tyr Asp	
30 35 40	
ttt gcc atc atg ata cct cca gga ggc acg gaa tgc ttt tgg caa ttt	193
Phe Ala Ile Met Ile Pro Pro Gly Gly Thr Glu Cys Phe Trp Gln Phe	
45 50 55	
gcc cac cag act gga tac ttc tat ttc agt tac gag gtt cag cgg aca	241
Ala His Gln Thr Gly Tyr Phe Tyr Phe Ser Tyr Glu Val Gln Arg Thr	
60 65 70 75	
gtg ggg atg tca cat gac cgg cat gtt gct gcc acg gca cat aac cca	289
Val Gly Met Ser His Asp Arg His Val Ala Ala Thr Ala His Asn Pro	
80 85 90	
cag gga ttt ctc ata gac acc tcc cag ggt gtt cgg ggc cag att aac	337
Gln Gly Phe Leu Ile Asp Thr Ser Gln Gly Val Arg Gly Gln Ile Asn	
95 100 105	
ttc tct acc caa gag aca ggt ttt tat cag ctt tgt cta agt aat cag	385
Phe Ser Thr Gln Glu Thr Gly Phe Tyr Gln Leu Cys Leu Ser Asn Gln	
110 115 120	
cat aat cac ttc ggt tct gtg caa gtg tac ctc aac ttt ggg gtc ttc	433
His Asn His Phe Gly Ser Val Gln Val Tyr Leu Asn Phe Gly Val Phe	
125 130 135	
tat gag ggg cct gag act gat cac aaa cag aag gaa aga aaa caa ctg	481
Tyr Glu Gly Pro Glu Thr Asp His Lys Gln Lys Glu Arg Lys Gln Leu	
140 145 150 155	
aat gat act ctg gat gca att gag gac ggc aca caa aag gtg cag aac	529
Asn Asp Thr Leu Asp Ala Ile Glu Asp Gly Thr Gln Lys Val Gln Asn	
160 165 170	
aat atc ttt cac atg tgg cga tac tac aac ttt gcc cgg atg agg aaa	577
Asn Ile Phe His Met Trp Arg Tyr Tyr Asn Phe Ala Arg Met Arg Lys	
175 180 185	
atg gct gac ttt ttc ctt atc caa tca aac tat aac tac gtg aac tgg	625
Met Ala Asp Phe Phe Leu Ile Gln Ser Asn Tyr Asn Tyr Val Asn Trp	
190 195 200	
tgg tcg aca gcc cag agc ctt gtt att att ctt tct ggg atc ctg caa	673
Trp Ser Thr Ala Gln Ser Leu Val Ile Ile Leu Ser Gly Ile Leu Gln	
205 210 215	
ctg tat ttc ttg aag cgt ctc ttc aat gtt cca aca act aca gat aca	721
Leu Tyr Phe Leu Lys Arg Leu Phe Asn Val Pro Thr Thr Thr Asp Thr	
220 225 230 235	
aag aag cca aga tgc taa gctaag gtgactatag caccctggct gttttcttct	775

Lys Lys Pro Arg Cys *
240

ggggcttagt cgaatcagct ttgtaatggt atgggacaaa aatcaattat ctcattaatg 835

ttttagtctg ctgcacacat ctaaaaaagc aaaatggcaa taaaatcata acagtgaaaa 895

aaaaaaaaa 903

<210> 196

<211> 649

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (19) .. (312)

<400> 196

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Met Ala Thr Pro Ser Leu Arg Gly Arg Leu Ala

1 5 10

cgg ttt ggg aac ccg cgg aag cct gtg ctg aag ccc aat aaa cct ctc 99

Arg Phe Gly Asn Pro Arg Lys Pro Val Leu Lys Pro Asn Lys Pro Leu

15 20 25

att cta gct aac cgc gtc ggg gag cgg cgc cgg gag aag ggc gag gcg 147

Ile Leu Ala Asn Arg Val Gly Glu Arg Arg Arg Glu Lys Gly Glu Ala

30 35 40

act tgc atc acg gag atg tcg gtg atg atg gct tgc tgg aag cag aat 195

Thr Cys Ile Thr Glu Met Ser Val Met Met Ala Cys Trp Lys Gln Asn

45 50 55

gaa ttc cgc gac gat gcg tgc aga aaa gag atc cag ggc ttc ctc gat 243

Glu Phe Arg Asp Asp Ala Cys Arg Lys Glu Ile Gln Gly Phe Leu Asp

60 65 70 75

tgt gcc gcg agg gct cag gtg acc gat ggc tcc tgg ggt gct ttc tca 291

Cys Ala Ala Arg Ala Gln Val Thr Asp Gly Ser Trp Gly Ala Phe Ser

80 85 90

gga aaa gaa tgg ggg aga tag aa gtaatgattc tccctgcctt ttgctaggaa 344

Gly Lys Glu Trp Gly Arg *

95

aggccctttc attcatttgg gaggtatatt attcacgcca aagtgggaaa ggttacagtt 404

ttgaaggctg tgtgatcttg acggatttat tcattgctct gaactttcga gttactgtac 464

gtaaaatgag gctaaccaat accaccttaa agaatgttgt gagtgtcaga tgaagtaatg 524

aatgggaaaa tcatttttgaa aaatgtaa atgtgtgtcaa gtagacatta ttgtgtgaaa 584

tagaactaaa gagactaaac taaataatga caatagtttg gttcctgtct aggctaattg	644
ctagg	649

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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (36) .. (275)

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ccc tac gga cag tcc cag cca agc tgc ttc tac cgt gta aaa atg ggc Pro Tyr Gly Gln Ser Gln Pro Ser Cys Phe Tyr Arg Val Lys Met Gly 10 15 20		101
ttc gtg atg ggt tgc gcc gtg ggc atg gcg gcc gag gcg ctc ttc ggc Phe Val Met Gly Cys Ala Val Gly Met Ala Ala Glu Ala Leu Phe Gly 25 30 35		149
acc ttt tcc tgt ctc agg atc gga atg cgg ggt cga gag ctg atg ggc Thr Phe Ser Cys Leu Arg Ile Gly Met Arg Gly Arg Glu Leu Met Gly 40 45 50		197
ggc att ggg aaa acc atg atg cag agt ggc ggc acc ttt ggc aca ttc Gly Ile Gly Lys Thr Met Met Gln Ser Gly Gly Thr Phe Gly Thr Phe 55 60 65 70		245
atg gcc att ggg atg ggc atc cga tgc taa c catggttgcc aactacatct Met Ala Ile Gly Met Gly Ile Arg Cys * 75 80		296
gtcccttccc atcaatccca gcccatgtac taataaaaga aagtctttga gtaaaaaaaaa		356
aaaa		360

<210> 198
 <211> 1280
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (206) .. (535)

His	Gly	Glu	Lys	Leu	Lys	Met	Phe	Cys	Lys	Glu	Asp	Val	Leu	Ile	Met		
				105					110					115			
tgt	gag	gcc	tgc	agc	cag	tcc	cca	gag	cat	gag	gcc	cac	agt	gtt	gtg	679	
Cys	Glu	Ala	Cys	Ser	Gln	Ser	Pro	Glu	His	Glu	Ala	His	Ser	Val	Val		
				120					125					130			
cca	atg	gag	gat	gtt	gcc	tgg	gag	tac	aag	tgg	gaa	ctt	cat	gag	gcc	727	
Pro	Met	Glu	Asp	Val	Ala	Trp	Glu	Tyr	Lys	Trp	Glu	Leu	His	Glu	Ala		
				135					140					145			
ctc	gaa	cat	ctg	aag	aaa	gag	caa	gaa	gag	gcc	tgg	aag	ctt	gaa	gtt	775	
Leu	Glu	His	Leu	Lys	Lys	Glu	Gln	Glu	Glu	Ala	Trp	Lys	Leu	Glu	Val		
				150					155					160			
ggt	gaa	agg	aaa	cga	act	gcc	acc	tgg	aag	ata	cag	gtg	gaa	acc	cga	823	
Gly	Glu	Arg	Lys	Arg	Thr	Ala	Thr	Trp	Lys	Ile	Gln	Val	Glu	Thr	Arg		
				165					170					175			180
aaa	cag	agt	att	gta	tgg	gag	ttt	gaa	aaa	tac	cag	cga	tta	cta	gag	871	
Lys	Gln	Ser	Ile	Val	Trp	Glu	Phe	Glu	Lys	Tyr	Gln	Arg	Leu	Leu	Glu		
				185					190					195			
aaa	aag	cag	cca	cca	cat	cgg	cag	ctg	ggg	gca	gag	gta	gca	gca	gct	919	
Lys	Lys	Gln	Pro	Pro	His	Arg	Gln	Leu	Gly	Ala	Glu	Val	Ala	Ala	Ala		
				200					205					210			
ctg	gcc	agc	cta	cag	cgg	gag	gca	gcg	gag	acc	atg	cag	aaa	ctg	gag	967	
Leu	Ala	Ser	Leu	Gln	Arg	Glu	Ala	Ala	Glu	Thr	Met	Gln	Lys	Leu	Glu		
				215					220					225			
ttg	aac	cat	agc	gag	ctc	atc	cag	cag	agc	cag	gtc	ctg	tgg	agg	atg	1015	
Leu	Asn	His	Ser	Glu	Leu	Ile	Gln	Gln	Ser	Gln	Val	Leu	Trp	Arg	Met		
				230					235					240			
att	gca	gag	ttg	aaa	gag	agg	tcg	cag	agg	cct	gtc	cgc	tgg	atg	ttg	1063	
Ile	Ala	Glu	Leu	Lys	Glu	Arg	Ser	Gln	Arg	Pro	Val	Arg	Trp	Met	Leu		
				245					250					255			260
cag	gat	att	cag	gaa	gtg	tta	aac	agg	agc	aaa	tct	tgg	agc	ttg	cag	1111	
Gln	Asp	Ile	Gln	Glu	Val	Leu	Asn	Arg	Ser	Lys	Ser	Trp	Ser	Leu	Gln		
				265					270					275			
cag	cca	gaa	cca	atc	tcc	ctg	gag	ttg	aag	aca	gat	tgc	cgt	gtg	ctg	1159	
Gln	Pro	Glu	Pro	Ile	Ser	Leu	Glu	Leu	Lys	Thr	Asp	Cys	Arg	Val	Leu		
				280					285					290			
ggg	cta	aga	gag	atc	ctg	aag	act	tat	gca	gct	gat	gtg	cgc	ttg	gat	1207	
Gly	Leu	Arg	Glu	Ile	Leu	Lys	Thr	Tyr	Ala	Ala	Asp	Val	Arg	Leu	Asp		
				295					300					305			
cca	gat	act	gct	tac	tcc	cgt	ctc	atc	gtg	tct	gag	gac	aga	aaa	cgt	1255	
Pro	Asp	Thr	Ala	Tyr	Ser	Arg	Leu	Ile	Val	Ser	Glu	Asp	Arg	Lys	Arg		
				310					315					320			
gtg	cac	tat	gga	gac	acc	aac	cag	aaa	ctg	cca	gac	aat	cct	gag	aga	1303	
Val	His	Tyr	Gly	Asp	Thr	Asn	Gln	Lys	Leu	Pro	Asp	Asn	Pro	Glu	Arg		


```

cctcctggca agagaaattc agtgcagcag ggggacacag acctgcccac gccaccccac 2331
tgccgttccc tctctgagca caagctgggc aaatcactgt cccttggact ccagtagacc 2391
agtgtcctag tcttgccttt tttctctaag tggcaggatc agaaaacctg cgagcttttag 2451
tttgtatttt cactttatga atgaggaaac tgaaatggcc ttaagggagc aagttatttc 2511
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<210> 200
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<212> DNA
<213> Homo sapiens

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<222> (331)..(1047)

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tctcaccagc agagaacagc tgacggtctt tccataagtg cttctaagag agatgtgtgg 180
taccgccggc taagtagaca gcaactgagc cttccctccc accccagggc tcccagagca 240
acagggagca gggagcatag gacctggccg cagccaggaa tctacactga ccggctcagc 300
ccatgaagta tcttgggctg aagtcacagg          atg aga ctg ttt gta tct gta 351
                                   Met Arg Leu Phe Val Ser Val
                                   1              5

act gtc ctt gtc atc tgt ctt gca gat tta gaa gag gaa tca gaa agc 399
Thr Val Leu Val Ile Cys Leu Ala Asp Leu Glu Glu Glu Ser Glu Ser
      10              15              20

tgg gac aac tct gag gct gaa gag gag gag aaa gcc cct gtg ttg cca 447
Trp Asp Asn Ser Glu Ala Glu Glu Glu Glu Lys Ala Pro Val Leu Pro
      25              30              35

gag agt aca gaa ggg cgg gag ctg acc cag ggc ccg gca gag tcc tcc 495
Glu Ser Thr Glu Gly Arg Glu Leu Thr Gln Gly Pro Ala Glu Ser Ser
      40              45              50              55

tct ctc tca ggc tgt ggg agc tgg cag ccc cgg aag ctg cca gtc ttc 543
Ser Leu Ser Gly Cys Gly Ser Trp Gln Pro Arg Lys Leu Pro Val Phe
      60              65              70

aag tcc ctc cgg cac atg agg cag gtc ctg ggt gcc cct tct ttc cgc 591
Lys Ser Leu Arg His Met Arg Gln Val Leu Gly Ala Pro Ser Phe Arg
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<213> Homo sapiens

<220>

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<222> (90)..(416)

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accactgaag ctgatcatga gatgactgt atg ctg aca cac ccc ctt cag ggg 113
Met Leu Thr His Pro Leu Gln Gly
1 5

cct ggc ctt gac tta ggg ctg cac tgt atc ctc agc aac ggc ctt gca 161
Pro Gly Leu Asp Leu Gly Leu His Cys Ile Leu Ser Asn Gly Leu Ala
10 15 20

gga gcc cct ttt gga ctg ctt tcc cta ttc agc cca aag ttg ggg tgg 209
Gly Ala Pro Phe Gly Leu Leu Ser Leu Phe Ser Pro Lys Leu Gly Trp
25 30 35 40

tgg gag aag agg ggt tgg agt gaa tcc atc tct att caa att cca gct 257
Trp Glu Lys Arg Gly Trp Ser Glu Ser Ile Ser Ile Gln Ile Pro Ala
45 50 55

ggg att act cta gga gtc ttc ctg gct tgt ttt ggg ctc aaa ctt agc 305
Gly Ile Thr Leu Gly Val Phe Leu Ala Cys Phe Gly Leu Lys Leu Ser
60 65 70

tac att gtt tat tgg ctc cca aag tcg gga ttg aag agt gaa aag atg 353
Tyr Ile Val Tyr Trp Leu Pro Lys Ser Gly Leu Lys Ser Glu Lys Met
75 80 85

cag gca atg aat cct tct gca cac tcc tcc ccc cac att cct gac act 401
Gln Ala Met Asn Pro Ser Ala His Ser Ser Pro His Ile Pro Asp Thr
90 95 100

agt aag aac caa taa acacttggtg acggaaaaaa aaaaa 441
Ser Lys Asn Gln *
105

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<211> 732

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (72)..(296)

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	Thr Leu Glu Ala Glu Phe Asn Ser Pro Ser Pro Pro Thr Pro Glu Pro			
	20	25	30	
	ggt gaa ggg ccc cgt aaa ttg gaa gga tgc aca agt tcc aag gtt acg			260
	Gly Glu Gly Pro Arg Lys Leu Glu Gly Cys Thr Ser Ser Lys Val Thr			
	35	40	45	50
	ttt cag cct ccc agt agc att gga tgc agg aaa aaa tac att gac ggt			308
	Phe Gln Pro Pro Ser Ser Ile Gly Cys Arg Lys Lys Tyr Ile Asp Gly			
		55	60	65
	gaa aaa caa gcc gaa cca gtt gta gtt tta gat cct gtt tct aca cat			356
	Glu Lys Gln Ala Glu Pro Val Val Val Leu Asp Pro Val Ser Thr His			
		70	75	80
	gaa ccc caa acc aaa gac cag gtt gct gaa aaa gat cca act caa cac			404
	Glu Pro Gln Thr Lys Asp Gln Val Ala Glu Lys Asp Pro Thr Gln His			
		85	90	95
	aag gag gat gaa ggc gaa att caa cca gaa aac aaa gaa gac agc att			452
	Lys Glu Asp Glu Gly Glu Ile Gln Pro Glu Asn Lys Glu Asp Ser Ile			
	100	105	110	
	gaa aac gtg aga gag aca gac agc tcc aac tgc tga tcca taaaccagaa			502
	Glu Asn Val Arg Glu Thr Asp Ser Ser Asn Cys *			
	115	120	125	
	gcctgacatg tttggaagtc cttttcaata agcacatgat tagtggttgtt atattggcaa			562
	gggctgtaga cattctgctc tggctactgt attcagaata caggttcttt tctggtgtca			622
	cttttgtaag tagcaactat aaacataagt aagctgttta gcaaaacaca cattcctagt			682
	aggttttggt tttttgatct ttataaagat gaggtttttt tcctagttac tgtattaagt			742
	atgacttctt ttagaagggtt acaaaaaaat tcagatgttg atacctttttt aggaaatgtg			802
	cataccactc atcaaatgga atgctgaaag tttgaggtgc ttgtatataa tcggataaac			862
	aaaactgatc aacccaatgt gatttttaaaa gcccccaaag aagcttctgt tttgggtctg			922
	atcctcttga tggagaaaact gcagcagcat ggaaattgtt ggggtactgtg gcatacaagt			982
	tattttctac agtagactga gataaactga aaactcagga gctggcatca aactcgtagt			1042
	cccatagtca gtgttaatta cacacattgt taactattgg atgaaaaata catgctattg			1102
	attgtgtcca aagcctcccg aggacctccg tggggatgct ctggtagcct gaatacagaa			1162
	ctgaggtgaa agtccaaacc ttgaatttta cagtagtaag ttggtaaacc atgtgctctg			1222
	tgctatgagt taattatggt ttcccaaata ctaatgtggc acaagtacca tattttatca			1282
	gagttcttat gtacagtatg gtgaagataa gtgacaagca cacattttttc ttgcttcact			1342

gctgttctat attacacagg tttgttggtg ttttttttaa aaaagaaatt aagcagtagt 1402
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acgcagactg acgtgctttt gggaggggtgt gccgtgaagc ctgcagtacg tgtgccgtga 180
ggctcatagt tg atg agg gac ttt ccc tgc tcc acc gtc act ccc cca 228
Met Arg Asp Phe Pro Cys Ser Thr Val Thr Pro Pro
1 5 10
act ctg ccc gcc tct gtc ccc gcc tca gtc ccc gcc tcc atc ccc gcc 276
Thr Leu Pro Ala Ser Val Pro Ala Ser Val Pro Ala Ser Ile Pro Ala
15 20 25
tct gtc ccc tgg cct tgg cgg cta ttt ttg cca cct gcc ttg ggt gcc 324
Ser Val Pro Trp Pro Trp Arg Leu Phe Leu Pro Pro Ala Leu Gly Ala
30 35 40
cag gag tcc cct act gct gtg ggc tgg ggt tgg ggg cac agc agc ccc 372
Gln Glu Ser Pro Thr Ala Val Gly Trp Gly Trp Gly His Ser Ser Pro
45 50 55 60
aag cct gag agg ctg gag ccc atg gct agt ggc tca tcc cca ctg cat 420
Lys Pro Glu Arg Leu Glu Pro Met Ala Ser Gly Ser Ser Pro Leu His
65 70 75
tct ccc cct gac aca gag aag ggg cct tgg tat tta tat tta aga aat 468
Ser Pro Pro Asp Thr Glu Lys Gly Pro Trp Tyr Leu Tyr Leu Arg Asn
80 85 90
gaa gat aat att aat aat gat gga agg aag act ggg ttg cag gga ctg 516
Glu Asp Asn Ile Asn Asn Asp Gly Arg Lys Thr Gly Leu Gln Gly Leu
95 100 105
tgg tct ctc ctg ggg ccc ggg acc cgc ctg gtc ttt cag cca tgc tga 564
Trp Ser Leu Leu Gly Pro Gly Thr Arg Leu Val Phe Gln Pro Cys *
110 115 120

tgaccacacc ccgccaggc cagacaccac cccccacccc actgtcgtgg tggccccaga 624
tctctgtaat tttatgtaga gtttgagctg aagccccgta tatttaattt attttgttaa 684
acatgaaagt gcaccccttc cctccaaaaa aaaaaaa 721

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<212> DNA
<213> Homo sapiens

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<222> (71) .. (2899)

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attcctgacg atg gcc tct gtg gct tcg tgc gat tcg cgt ccg agc tca 109
Met Ala Ser Val Ala Ser Cys Asp Ser Arg Pro Ser Ser
1 5 10
gac gag ctc cct gga gac ccc tct tca caa gaa gaa gat gag gac tat 157
Asp Glu Leu Pro Gly Asp Pro Ser Ser Gln Glu Glu Asp Glu Asp Tyr
15 20 25
gat ttt gaa gat cgg gtc agc gac tcg ggt tca tat tcc tca gcg agt 205
Asp Phe Glu Asp Arg Val Ser Asp Ser Gly Ser Tyr Ser Ser Ala Ser
30 35 40 45
agc gat tat gat gat ctt gag cct gaa tgg ctg gac agt gtg cag aaa 253
Ser Asp Tyr Asp Asp Leu Glu Pro Glu Trp Leu Asp Ser Val Gln Lys
50 55 60
aat gga gag ctg ttt tat ttg gaa ttg agt gag gat gaa gaa gaa agc 301
Asn Gly Glu Leu Phe Tyr Leu Glu Leu Ser Glu Asp Glu Glu Glu Ser
65 70 75
ctc ctt cct gag aca cca act gtg aac cat gtc agg ttc agt gaa aat 349
Leu Leu Pro Glu Thr Pro Thr Val Asn His Val Arg Phe Ser Glu Asn
80 85 90
gag att atc att gaa gat gac tac aaa gaa aga aaa aag tat gaa ccc 397
Glu Ile Ile Ile Glu Asp Asp Tyr Lys Glu Arg Lys Lys Tyr Glu Pro
95 100 105
aaa ctc aag cag ttt acc aaa att tta aga agg aaa aga ctt tta ccc 445
Lys Leu Lys Gln Phe Thr Lys Ile Leu Arg Arg Lys Arg Leu Leu Pro
110 115 120 125
aag cgc tgc aat aaa aaa aat agc aat gac aat gga cca gta tcc att 493
Lys Arg Cys Asn Lys Lys Asn Ser Asn Asp Asn Gly Pro Val Ser Ile
130 135 140

cta aag cat cag tcc aat cag aag aca gga gtc att gtc caa cag cgg	541
Leu Lys His Gln Ser Asn Gln Lys Thr Gly Val Ile Val Gln Gln Arg	
145 150 155	
tac aaa gat gtg aat gtt tat gta aac ccc aaa aag cta act gtt atc	589
Tyr Lys Asp Val Asn Val Tyr Val Asn Pro Lys Lys Leu Thr Val Ile	
160 165 170	
aaa gcc aaa gag cag ctc aag ctt ctg gaa gtg ctg gtt gga att att	637
Lys Ala Lys Glu Gln Leu Lys Leu Leu Glu Val Leu Val Gly Ile Ile	
175 180 185	
cat cag acc aag tgg agc tgg aga aga acc gga aag cag ggt gat gga	685
His Gln Thr Lys Trp Ser Trp Arg Arg Thr Gly Lys Gln Gly Asp Gly	
190 195 200 205	
gag agg ctt gtg gtt cat ggc ctg ctg cca ggg gga tct gct atg aag	733
Glu Arg Leu Val Val His Gly Leu Leu Pro Gly Gly Ser Ala Met Lys	
210 215 220	
agc ggt cag gta ctc att ggt gat gtc ctt gtt gct gtg aat gat gtc	781
Ser Gly Gln Val Leu Ile Gly Asp Val Leu Val Ala Val Asn Asp Val	
225 230 235	
gat gtt act act gaa aac atc gag aga gtt ctg tct tgc att cct gga	829
Asp Val Thr Thr Glu Asn Ile Glu Arg Val Leu Ser Cys Ile Pro Gly	
240 245 250	
cct atg cag gtg aaa ctg aca ttt gaa aat gca tat gat gtg aaa agg	877
Pro Met Gln Val Lys Leu Thr Phe Glu Asn Ala Tyr Asp Val Lys Arg	
255 260 265	
gag aca tcc cat cca aga cag aaa aag aca cag tcc aac aca agt gat	925
Glu Thr Ser His Pro Arg Gln Lys Lys Thr Gln Ser Asn Thr Ser Asp	
270 275 280 285	
tta gtc aag ctt ctc tgg gga gaa gag gtt gaa ggt atc cag cag agt	973
Leu Val Lys Leu Leu Trp Gly Glu Glu Val Glu Gly Ile Gln Gln Ser	
290 295 300	
ggc cta aac act cct cat atc att atg tat ctc aca cta cag ctc gac	1021
Gly Leu Asn Thr Pro His Ile Ile Met Tyr Leu Thr Leu Gln Leu Asp	
305 310 315	
tca gaa acc tca aag gaa gag cag gaa att ctt tat cat tat cca atg	1069
Ser Glu Thr Ser Lys Glu Glu Gln Glu Ile Leu Tyr His Tyr Pro Met	
320 325 330	
tct gaa gca tct cag aaa ctt aaa agt gtg aga ggg att ttt ctc aca	1117
Ser Glu Ala Ser Gln Lys Leu Lys Ser Val Arg Gly Ile Phe Leu Thr	
335 340 345	
ctc tgt gac atg ctg gaa aac gta act ggg aca caa gtt act agt tca	1165
Leu Cys Asp Met Leu Glu Asn Val Thr Gly Thr Gln Val Thr Ser Ser	
350 355 360 365	

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tct gac aag ttg ttg cta att ggc ctg cct gct gaa gaa gtt cct ctt Ser Asp Lys Leu Leu Leu Ile Gly Leu Pro Ala Glu Glu Val Pro Leu 385 390 395	1261
cct cgt cta agg aac atg ata gaa aat gtc atc caa acc tta aaa ttt Pro Arg Leu Arg Asn Met Ile Glu Asn Val Ile Gln Thr Leu Lys Phe 400 405 410	1309
atg tat ggt tct tta gat agt gcc ttt tgc cag att gag aat gtt cct Met Tyr Gly Ser Leu Asp Ser Ala Phe Cys Gln Ile Glu Asn Val Pro 415 420 425	1357
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gag gct gca gat ttt gca gaa ctg tcc gag gat tac tat gac atg agg Glu Ala Ala Asp Phe Ala Glu Leu Ser Glu Asp Tyr Tyr Asp Met Arg 495 500 505	1597
cgg ctg tat aca att ttg ggg tct tct cta ttt tac aag ggt tat ttg Arg Leu Tyr Thr Ile Leu Gly Ser Ser Leu Phe Tyr Lys Gly Tyr Leu 510 515 520 525	1645
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tgt cgc cac tat tgc ctg ctg cct tta gca gca aaa caa aga att ggt Cys Arg His Tyr Cys Leu Leu Pro Leu Ala Ala Lys Gln Arg Ile Gly 545 550 555	1741
cag ttg atc ata tgg aga gaa gtg ttt cct cag cat cac ctc cga cct Gln Leu Ile Ile Trp Arg Glu Val Phe Pro Gln His His Leu Arg Pro 560 565 570	1789
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ttt ttg cta gtt gtt ggc ttg aaa cat tat atg cta tgt gta cta tta	1885

Phe	Leu	Leu	Val	Val	Gly	Leu	Lys	His	Tyr	Met	Leu	Cys	Val	Leu	Leu		
590					595					600					605		
gaa gct gga ggt tgc gca tcc aaa gct att ggg agt cct gga cca gac																1933	
Glu	Ala	Gly	Gly	Cys	Ala	Ser	Lys	Ala	Ile	Gly	Ser	Pro	Gly	Pro	Asp		
				610					615					620			
tgt gta tat gtg gat caa gtc aaa aca act ctt cac cag ctg gat gga																1981	
Cys	Val	Tyr	Val	Asp	Gln	Val	Lys	Thr	Thr	Leu	His	Gln	Leu	Asp	Gly		
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gta gat tct cgc ata gat gaa cgg cta gca tct tct cca gtc ccc tgt																2029	
Val	Asp	Ser	Arg	Ile	Asp	Glu	Arg	Leu	Ala	Ser	Ser	Pro	Val	Pro	Cys		
		640					645					650					
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	670				675				680						685		
gta gca act tct cca aca tgc aga aga acg ctt ttt ggt gac tat tcc																2173	
Val	Ala	Thr	Ser	Pro	Thr	Cys	Arg	Arg	Thr	Leu	Phe	Gly	Asp	Tyr	Ser		
			690					695						700			
tta aag aca cgc aag cct agt cct tcc tgt agt agt gga gga tct gac																2221	
Leu	Lys	Thr	Arg	Lys	Pro	Ser	Pro	Ser	Cys	Ser	Ser	Gly	Gly	Ser	Asp		
			705				710					715					
aat ggt tgt gaa ggt gga gaa gat gat ggc ttt agc ccc cat act aca																2269	
Asn	Gly	Cys	Glu	Gly	Gly	Glu	Asp	Asp	Gly	Phe	Ser	Pro	His	Thr	Thr		
		720					725					730					
ccg gat gca gta cgg aag caa aga gaa tct cag ggc tct gat ggt tta																2317	
Pro	Asp	Ala	Val	Arg	Lys	Gln	Arg	Glu	Ser	Gln	Gly	Ser	Asp	Gly	Leu		
	735				740					745							
gaa gaa agt ggg acc ttg ctt aag gtc act aaa aag aag tct act ctt																2365	
Glu	Glu	Ser	Gly	Thr	Leu	Leu	Lys	Val	Thr	Lys	Lys	Lys	Ser	Thr	Leu		
	750				755				760						765		
cca aat cca ttt cat ttg gga aac ttg aaa aag gac ctt cca gaa aaa																2413	
Pro	Asn	Pro	Phe	His	Leu	Gly	Asn	Leu	Lys	Lys	Asp	Leu	Pro	Glu	Lys		
			770					775						780			
gaa tta gaa ata tat aac aca gtg aaa ctg aca tct ggt cct gag aac																2461	
Glu	Leu	Glu	Ile	Tyr	Asn	Thr	Val	Lys	Leu	Thr	Ser	Gly	Pro	Glu	Asn		
			785				790						795				
aca ctt ttc cac tac gtt gcc tta gaa aca gtg caa gga atc ttt att																2509	
Thr	Leu	Phe	His	Tyr	Val	Ala	Leu	Glu	Thr	Val	Gln	Gly	Ile	Phe	Ile		
		800				805					810						
act cct acc ctt gaa gag gtg gca cag cta agt ggc tct atc cac cct																2557	
Thr	Pro	Thr	Leu	Glu	Glu	Val	Ala	Gln	Leu	Ser	Gly	Ser	Ile	His	Pro		

815	820	825	
cag cta ata aag aat ttc cat cag tgt tgt ctt tcc att cgt gca gtt			2605
Gln Leu Ile Lys Asn Phe His Gln Cys Cys Leu Ser Ile Arg Ala Val			
830	835	840	845
ttc caa cag aca ttg gtg gaa gag aaa aag aaa gga cta aat agt gga			2653
Phe Gln Gln Thr Leu Val Glu Glu Lys Lys Lys Gly Leu Asn Ser Gly			
	850	855	860
gac cat tca gat tct gca aag tca gtg tct tct ctt aac cct gtt aaa			2701
Asp His Ser Asp Ser Ala Lys Ser Val Ser Ser Leu Asn Pro Val Lys			
	865	870	875
gaa cat ggt gtg ttg ttt gaa tgt tca cct gga aac tgg act gat cag			2749
Glu His Gly Val Leu Phe Glu Cys Ser Pro Gly Asn Trp Thr Asp Gln			
	880	885	890
aaa aaa gca cca cca gtt atg gct tac tgg gta gta ggg aga ctt ttt			2797
Lys Lys Ala Pro Pro Val Met Ala Tyr Trp Val Val Gly Arg Leu Phe			
	895	900	905
ctt cat cca aaa cct caa gaa ctt tat gtc tgt ttt cat gac tca gtc			2845
Leu His Pro Lys Pro Gln Glu Leu Tyr Val Cys Phe His Asp Ser Val			
	910	915	920
aca gaa att gcc att gaa ata gct ttt aaa ttg ttc ttt ggg tta acc			2893
Thr Glu Ile Ala Ile Glu Ile Ala Phe Lys Leu Phe Phe Gly Leu Thr			
	930	935	940
ttg tag ctgtgctttc ttgatgcgta gaaacacgtg catggaggat caaacactgt			2949
Leu *			
cagaattgct gaaatcaata cacaaagaga taaagttag cttcttttta ctattcaata			3009
ttgaacataa tattgttaaa tattgagatg aaatgctgtt ggatttgata cattaaatct			3069
taatgtaata ttgtaagact tttgagaata tacttgatta aaatgtgaaa gaagggattg			3129
ttaacttatt gctatTTTTGG tatataatgt taatttattg actagtttga aataatgtga			3189
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 <222> (71)..(2836)

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225 230 235	
gat gtt act act gaa aac atc gag aga gtt ctg tct tgc att cct gga	829
Asp Val Thr Thr Glu Asn Ile Glu Arg Val Leu Ser Cys Ile Pro Gly	
240 245 250	
cct atg cag gtg aaa ctg aca ttt gaa aat gca tat gat gtg aaa agg	877
Pro Met Gln Val Lys Leu Thr Phe Glu Asn Ala Tyr Asp Val Lys Arg	
255 260 265	
gag aca tcc cat cca aga cag aaa aag aca cag tcc aac aca agt gat	925
Glu Thr Ser His Pro Arg Gln Lys Lys Thr Gln Ser Asn Thr Ser Asp	
270 275 280 285	
tta gtc aag ctt ctc tgg gga gaa gag gtt gaa ggt atc cag cag agt	973
Leu Val Lys Leu Leu Trp Gly Glu Glu Val Glu Gly Ile Gln Gln Ser	
290 295 300	
ggc cta aac act cct cat atc att atg tat ctc aca cta cag ctc gac	1021
Gly Leu Asn Thr Pro His Ile Ile Met Tyr Leu Thr Leu Gln Leu Asp	
305 310 315	
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Ser Glu Thr Ser Lys Glu Glu Gln Glu Ile Leu Tyr His Tyr Pro Met	
320 325 330	
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Ser Glu Ala Ser Gln Lys Leu Lys Ser Val Arg Gly Ile Phe Leu Thr	
335 340 345	
ctc tgt gac atg ctg gaa aac gta act ggg aca caa gtt act agt tca	1165
Leu Cys Asp Met Leu Glu Asn Val Thr Gly Thr Gln Val Thr Ser Ser	
350 355 360 365	
tcc ctc ctt tta aat gga aaa caa att cat gtg gct tat tgg aaa gaa	1213
Ser Leu Leu Leu Asn Gly Lys Gln Ile His Val Ala Tyr Trp Lys Glu	
370 375 380	
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Ser Asp Lys Leu Leu Leu Ile Gly Leu Pro Ala Glu Glu Val Pro Leu	
385 390 395	
cct cgt cta agg aac atg ata gaa aat gtc atc caa acc tta aaa ttt	1309
Pro Arg Leu Arg Asn Met Ile Glu Asn Val Ile Gln Thr Leu Lys Phe	
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Met Tyr Gly Ser Leu Asp Ser Ala Phe Cys Gln Ile Glu Asn Val Pro	
415 420 425	
cgt ttg gat cat ttt ttt aac ttg ttc ttt caa aga gca ctt cag cct	1405
Arg Leu Asp His Phe Phe Asn Leu Phe Phe Gln Arg Ala Leu Gln Pro	
430 435 440 445	

gcg aaa ctg cat tcc agc gcc agt ccc agt gct cag cag tac gat gct Ala Lys Leu His Ser Ser Ala Ser Pro Ser Ala Gln Gln Tyr Asp Ala 450 455 460	1453
tcc agt gca gta ctt tta gac aac ctc cct gga gtc cgg tgg ctc aca Ser Ser Ala Val Leu Leu Asp Asn Leu Pro Gly Val Arg Trp Leu Thr 465 470 475	1501
ctt cca ctg gaa atc aag atg gaa tta gac atg gca tta agt gac ttg Leu Pro Leu Glu Ile Lys Met Glu Leu Asp Met Ala Leu Ser Asp Leu 480 485 490	1549
gag gct gca gat ttt gca gaa ctg ggt tat ttg ata tgc agt cat ttg Glu Ala Ala Asp Phe Ala Glu Leu Gly Tyr Leu Ile Cys Ser His Leu 495 500 505	1597
ccc aag gat gat ctt att gat att gcc gta tac tgt cgc cac tat tgc Pro Lys Asp Asp Leu Ile Asp Ile Ala Val Tyr Cys Arg His Tyr Cys 510 515 520 525	1645
ctg ctg cct tta gca gca aaa caa aga att ggt cag ttg atc ata tgg Leu Leu Pro Leu Ala Ala Lys Gln Arg Ile Gly Gln Leu Ile Ile Trp 530 535 540	1693
aga gaa gtg ttt cct cag cat cac ctc cga cct ttg gca gac tca agc Arg Glu Val Phe Pro Gln His His Leu Arg Pro Leu Ala Asp Ser Ser 545 550 555	1741
act gaa gtc ttt ccg gaa cct gaa gga aga tat ttt ttg cta gtt gtt Thr Glu Val Phe Pro Glu Pro Glu Gly Arg Tyr Phe Leu Leu Val Val 560 565 570	1789
ggc ttg aaa cat tat atg cta tgt gta cta tta gaa gct gga ggt tgc Gly Leu Lys His Tyr Met Leu Cys Val Leu Leu Glu Ala Gly Gly Cys 575 580 585	1837
gca tcc aaa gct att ggg agt cct gga cca gac tgt gta tat gtg gat Ala Ser Lys Ala Ile Gly Ser Pro Gly Pro Asp Cys Val Tyr Val Asp 590 595 600 605	1885
caa gtc aaa aca act ctt cac cag ctg gat gga gta gat tct cgc ata Gln Val Lys Thr Thr Leu His Gln Leu Asp Gly Val Asp Ser Arg Ile 610 615 620	1933
gat gaa cgg cta gca tct tct cca gtc ccc tgt ttg tct tgt gct gac Asp Glu Arg Leu Ala Ser Ser Pro Val Pro Cys Leu Ser Cys Ala Asp 625 630 635	1981
tgg ttc ctt act gga tca cgt gaa aaa aca gat agc ttg acc act tcg Trp Phe Leu Thr Gly Ser Arg Glu Lys Thr Asp Ser Leu Thr Thr Ser 640 645 650	2029
cct att ctc agt agg cta caa ggt act tcc aaa gta gca act tct cca Pro Ile Leu Ser Arg Leu Gln Gly Thr Ser Lys Val Ala Thr Ser Pro 655 660 665	2077
aca tgc aga aga acg ctt ttt ggt gac tat tcc tta aag aca cgc aag	2125

Thr	Cys	Arg	Arg	Thr	Leu	Phe	Gly	Asp	Tyr	Ser	Leu	Lys	Thr	Arg	Lys	
670					675					680					685	
cct	agt	cct	tcc	tgt	agt	agt	gga	gga	tct	gac	aat	ggt	tgt	gaa	ggt	2173
Pro	Ser	Pro	Ser	Cys	Ser	Ser	Gly	Gly	Ser	Asp	Asn	Gly	Cys	Glu	Gly	
				690					695					700		
gga	gaa	gat	gat	ggc	ttt	agc	ccc	cat	act	aca	ccg	gat	gca	gta	cgg	2221
Gly	Glu	Asp	Asp	Gly	Phe	Ser	Pro	His	Thr	Thr	Pro	Asp	Ala	Val	Arg	
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aag	caa	aga	gaa	tct	cag	ggc	tct	gat	ggt	tta	gaa	gaa	agt	ggg	acc	2269
Lys	Gln	Arg	Glu	Ser	Gln	Gly	Ser	Asp	Gly	Leu	Glu	Glu	Ser	Gly	Thr	
		720					725					730				
ttg	ctt	aag	gtc	act	aaa	aag	aag	tct	act	ctt	cca	aat	cca	ttt	cat	2317
Leu	Leu	Lys	Val	Thr	Lys	Lys	Lys	Ser	Thr	Leu	Pro	Asn	Pro	Phe	His	
	735					740					745					
ttg	gga	aac	ttg	aaa	aag	gac	ctt	cca	gaa	aaa	gaa	tta	gaa	ata	tat	2365
Leu	Gly	Asn	Leu	Lys	Lys	Asp	Leu	Pro	Glu	Lys	Glu	Leu	Glu	Ile	Tyr	
	750			755					760						765	
aac	aca	gtg	aaa	ctg	aca	tct	ggt	cct	gag	aac	aca	ctt	ttc	cac	tac	2413
Asn	Thr	Val	Lys	Leu	Thr	Ser	Gly	Pro	Glu	Asn	Thr	Leu	Phe	His	Tyr	
			770					775						780		
gtt	gcc	tta	gaa	aca	gtg	caa	gga	atc	ttt	att	act	cct	acc	ctt	gaa	2461
Val	Ala	Leu	Glu	Thr	Val	Gln	Gly	Ile	Phe	Ile	Thr	Pro	Thr	Leu	Glu	
			785				790						795			
gag	gtg	gca	cag	cta	agt	ggc	tct	atc	cac	cct	cag	cta	ata	aag	aat	2509
Glu	Val	Ala	Gln	Leu	Ser	Gly	Ser	Ile	His	Pro	Gln	Leu	Ile	Lys	Asn	
		800					805					810				
ttc	cat	cag	tgt	tgt	ctt	tcc	att	cgt	gca	gtt	ttc	caa	cag	aca	ttg	2557
Phe	His	Gln	Cys	Cys	Leu	Ser	Ile	Arg	Ala	Val	Phe	Gln	Gln	Thr	Leu	
	815					820					825					
gtg	gaa	gag	aaa	aag	aaa	gga	cta	aat	agt	gga	gac	cat	tca	gat	tct	2605
Val	Glu	Glu	Lys	Lys	Lys	Gly	Leu	Asn	Ser	Gly	Asp	His	Ser	Asp	Ser	
	830			835					840						845	
gca	aag	tca	gtg	tct	tct	ctt	aac	cct	gtt	aaa	gaa	cat	ggt	gtg	ttg	2653
Ala	Lys	Ser	Val	Ser	Ser	Leu	Asn	Pro	Val	Lys	Glu	His	Gly	Val	Leu	
				850					855					860		
ttt	gaa	tgt	tca	cct	gga	aac	tgg	act	gat	cag	aaa	aaa	gca	cca	cca	2701
Phe	Glu	Cys	Ser	Pro	Gly	Asn	Trp	Thr	Asp	Gln	Lys	Lys	Ala	Pro	Pro	
			865					870					875			
gtt	atg	gct	tac	tgg	gta	gta	ggg	aga	ctt	ttt	ctt	cat	cca	aaa	cct	2749
Val	Met	Ala	Tyr	Trp	Val	Val	Gly	Arg	Leu	Phe	Leu	His	Pro	Lys	Pro	
		880					885					890				
caa	gaa	ctt	tat	gtc	tgt	ttt	cat	gac	tca	gtc	aca	gaa	att	gcc	att	2797
Gln	Glu	Leu	Tyr	Val	Cys	Phe	His	Asp	Ser	Val	Thr	Glu	Ile	Ala	Ile	

895	900	905	
gaa ata gct ttt aaa ttg ttc ttt ggg tta acc ttg tag ctgtgctttc			2846
Glu Ile Ala Phe Lys Leu Phe Phe Gly Leu Thr Leu *			
910	915	920	
ttgatgcgta gaaacacgtg catggaggat caaacactgt cagaattgct gaaatcaata			2906
caciaagaga taaagtttag cttcttttta ctattcaata ttgaacataa tattgttaaa			2966
tattgagatg aaatgctggt ggatttgata cattaaatct taatgtaata ttgtaagact			3026
tttgagaata tacttgatta aaatgtgaaa gaagggattg ttaacttatt gctatttttg			3086
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 <222> (306)..(1496)

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 <222> (1)...(1595)
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gtcacggagc	tggggccggg	ggcagcccg gagctggctg ggccccctgc aaggaccgtc	180
tcgggcctgc	ccagccaaga	gtgtgtgcaa cacatcgggtg ctgagcagca gcctgcagtc	240
actggagtat	ctcatcaacg	acatccggcc gcctgcatc aaggagcaga tgctgggcaa	300
gggct	atg aga cgg tgg ccg tgc ccc ggc tac tcg acc acc agc atg		347
	Met Arg Arg Trp Pro Cys Pro Gly Tyr Ser Thr Thr Ser Met		
	1 5 10		
ccc aca tcc gcc tac ccg tct aca gat aag gcc tgc ctg cgg aca tac			395
Pro Thr Ser Ala Tyr Pro Ser Thr Asp Lys Ala Cys Leu Arg Thr Tyr			
15 20 25 30			
gga cat gcg gac agg gcg cag agc cgg gag gca ggc cgc aga aca ggg			443
Gly His Ala Asp Arg Ala Gln Ser Arg Glu Ala Gly Arg Arg Thr Gly			
35 40 45			

tgg gcg gct cgc agg ggc gct cag ccc cac cct gtg cct gct gat gcc	491
Trp Ala Ala Arg Arg Gly Ala Gln Pro His Pro Val Pro Ala Asp Ala	
50 55 60	
cac agg gga gcc agg ctg gct gcc gcc tcg ctg tgg ccg gat gga ggg	539
His Arg Gly Ala Arg Leu Ala Ala Ser Leu Trp Pro Asp Gly Gly	
65 70 75	
tgg cag ggc aac ctc aca tac caa ggc ccc tcc cca cca tcg gtt gcc	587
Trp Gln Gly Asn Leu Thr Tyr Gln Gly Pro Ser Pro Pro Ser Val Ala	
80 85 90	
cca gga cac agt gag ggc ctg ggg gca gcc act gac gcc cat gcc ttc	635
Pro Gly His Ser Glu Gly Leu Gly Ala Ala Thr Asp Ala His Ala Phe	
95 100 105 110	
ctt tat cta agc tgg cag agg cag gga gag aga aac cac tca aaa aca	683
Leu Tyr Leu Ser Trp Gln Arg Gln Gly Glu Arg Asn His Ser Lys Thr	
115 120 125	
gga atg gtt ctt tct ggg cct cct ggg aca ggg gcc cag gcc aag gtg	731
Gly Met Val Leu Ser Gly Pro Pro Gly Thr Gly Ala Gln Ala Lys Val	
130 135 140	
ggg tgc agg agg aaa cag gcg cac cag agt cag ggt ggg ggc agg gca	779
Gly Cys Arg Arg Lys Gln Ala His Gln Ser Gln Gly Gly Gly Arg Ala	
145 150 155	
gcc ccc cca ggg gtc agg cag ctg tgt ctc ccc aca ctg gct ccc cag	827
Ala Pro Pro Gly Val Arg Gln Leu Cys Leu Pro Thr Leu Ala Pro Gln	
160 165 170	
tat tct gga aaa ggg gta cag gag gcc gat agg aag tca ctg ggc cca	875
Tyr Ser Gly Lys Gly Val Gln Glu Ala Asp Arg Lys Ser Leu Gly Pro	
175 180 185 190	
aag tgt ctc ccc acc agc cag gtg aag acc act ctg aca gag gct cca	923
Lys Cys Leu Pro Thr Ser Gln Val Lys Thr Thr Leu Thr Glu Ala Pro	
195 200 205	
ggg act ata cca gtc ccc ctg ttc ctc ctt ccc cta ccc cca cca ttc	971
Gly Thr Ile Pro Val Pro Leu Phe Leu Leu Pro Leu Pro Pro Pro Phe	
210 215 220	
ctt cct aac aca gag ttg cac ccc cat ccc cat tct cca aac cct gga	1019
Leu Pro Asn Thr Glu Leu His Pro His Pro His Ser Pro Asn Pro Gly	
225 230 235	
cta cca tat tcc ccc ttc cct cca ata cat ctt ata ggg ctg ctg ggt	1067
Leu Pro Tyr Ser Pro Phe Pro Pro Ile His Leu Ile Gly Leu Leu Gly	
240 245 250	
aca gtt gtt cag gct gtg cac tgc aca agg gca cct tgt cca agg aga	1115
Thr Val Val Gln Ala Val His Cys Thr Arg Ala Pro Cys Pro Arg Arg	
255 260 265 270	

Glu Arg Lys Asp Ala Glu Ile Gln Lys Leu Lys Asn Val Ile Thr Gln	
215 220 225	
tgg gag gca aag tat aag gaa gta aag gca aga aat gca caa tta ttg	1016
Trp Glu Ala Lys Tyr Lys Glu Val Lys Ala Arg Asn Ala Gln Leu Leu	
230 235 240	
aaa atg ctt cag gaa ggt gaa atg aaa gat aag gca gaa ata ctt ctg	1064
Lys Met Leu Gln Glu Gly Glu Met Lys Asp Lys Ala Glu Ile Leu Leu	
245 250 255	
caa gtt gat gaa tca caa agt atc aag aat gag ctc act att cag gtg	1112
Gln Val Asp Glu Ser Gln Ser Ile Lys Asn Glu Leu Thr Ile Gln Val	
260 265 270 275	
act tca ctt cat gct gca tta gaa caa gaa aga tct aaa gtg aaa gta	1160
Thr Ser Leu His Ala Ala Leu Glu Gln Glu Arg Ser Lys Val Lys Val	
280 285 290	
tta caa gca gag tta gcc aaa tac cag ggt ggc aga aaa ggg aaa aga	1208
Leu Gln Ala Glu Leu Ala Lys Tyr Gln Gly Gly Arg Lys Gly Lys Arg	
295 300 305	
aac tct gaa tcc gac cag tgt agg tga ttaca ttagcctttg aagtcaacac	1260
Asn Ser Glu Ser Asp Gln Cys Arg *	
310 315	
aaagtttaaa acttccagga ttttgcaaag ttgtatatat ttaatgctgt gcaactgcta	1320
aactatgcag tttttgttga aggaactaaa agcaactagc tcctaattgg tctataattt	1380
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 <213> Homo sapiens

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acaaatacca gttcatacat tcttgttcca ataggagtt atg gga gga aaa att	174
Met Gly Gly Lys Ile	
1 5	
att cca agc aat cac aca gga tca act ttt tct cct tgt aga ata tgt	222

Ile	Pro	Ser	Asn	His	Thr	Gly	Ser	Thr	Phe	Ser	Pro	Cys	Arg	Ile	Cys	
				10					15					20		
gtc	atc	aca	ttg	gca	gaa	tct	cat	cca	gtt	ctt	caa	agt	gga	aaa	aca	270
Val	Ile	Thr	Leu	Ala	Glu	Ser	His	Pro	Val	Leu	Gln	Ser	Gly	Lys	Thr	
			25					30					35			
att	aaa	agc	att	tcc	tat	cag	atc	agt	acc	aac	tgt	agc	aga	ctt	cag	318
Ile	Lys	Ser	Ile	Ser	Tyr	Gln	Ile	Ser	Thr	Asn	Cys	Ser	Arg	Leu	Gln	
			40				45				50					
aac	aag	gtc	tct	ggg	aaa	ttt	aag	cgg	gta	tgt	tcc	tgt	aat	tct	gtg	366
Asn	Lys	Val	Ser	Gly	Lys	Phe	Lys	Arg	Val	Cys	Ser	Cys	Asn	Ser	Val	
		55				60				65						
att	atc	tac	tta	cat	cct	cta	tat	tca	tgg	taa	tgacagat	ccaatgaacc				417
Ile	Ile	Tyr	Leu	His	Pro	Leu	Tyr	Ser	Trp	*						
		70			75				80							
ttagaatcca	gtagcatatg	cttagcatac	ttctctagca	gtttgaggtg	ctaatttttag											477
gtatactttc	acctaaagaa	attctcagct	cccccaaatt	aggtatctca	ggaggtgtag											537
tatctgttat	attaggttct	gtgctactat	ccctataatg	cccaggatgg	aggaggggga											597
aggcaggcct	ttgaaaggag	aactctaata	gcaatataac	aagatatttt	gtcccttcta											657
gttgatttaa	actagtatgt	cgagttctgt	aaaatttagg	tgactaactc	ttctttacca											717
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<220>
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 <222> (813)..(1148)

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aaagaagggt	ctgcattttt	gctttgcaac	tctaaaagca	gcagaatcct	ttttttaaaa											180
aggtacttat	gggcacctca	ccatataaaa	ccgataaaaag	catacctctt	ctgggttaagg											240
tggggaggat	cctcgagctc	cctgaattgt	cctttttacc	tgtctcccc	tcccccttgt											300
ccctcatggc	accttaaaga	tctctgagtc	cctccagttc	tcaagtttaa	ggactctact											360
accatggtaa	gagctgggtcc	agcctcagtt	tccacaatgc	ttttggccac	tcgaatccag											420


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gccatcagca aggaggacca ggaacccggc gattgaggtg cttccaggtg gggacaagcc 1593
ccttttggtt tcagccacag cacccttat tccaggtgcc ctgccaacc tgctacccc 1653
acatgacctt ttgtgtattc agcaaaccct cattaggtga cagcggcccc caggctttgt 1713
gctggggggac gatactggcc ctggcctcga ccagcttaaa ggtttttcac acctttgttc 1773
ccagggcccc gctcagggcc cagcaaaaag tccgtaggct tgaacatgtg ttgagggcat 1833
gaaaaataaa tgctgttcat gtgtgtagct caaaaaaaaa aaa 1876

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<210> 211
<211> 3051
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> (527) .. (2308)

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aaccaggggt gctaaaaata accaggccca aatggaccag aagcaactcc catggacttt 180
ggcttgcaat catggtcaga agagatacag gcacagatcc cactattacg aaggagccaa 240
aatatctgcc aagataaaaa tggaagtaac tcctctggat ttatgtgtcc aggggtggat 300
atggaaagac ttgtgaagta ttaatcaaaa atcacccgag gctttttcag actattattc 360
aaatgacaca gaatgaagac ctccgagaaa acatgtacgg caagttctgg agcatttgtc 420
tcagcacagt gaaagccagt acctaaagat tctaacaagc cttgctgaag ttgctacaac 480
aaatggtcac aaactgctta gcctctctag caattatgat gctcaa atg aag agc 535
                                     Met Lys Ser
                                     1

ctt tta agg att gtg aga atg ttt tgt cac gtc ttt cga att ggt cca 583
Leu Leu Arg Ile Val Arg Met Phe Cys His Val Phe Arg Ile Gly Pro
5 10 15

tcc tcc ccc agt aat gga att gat atg ggc tac aat ggg aat aaa act 631
Ser Ser Pro Ser Asn Gly Ile Asp Met Gly Tyr Asn Gly Asn Lys Thr
20 25 30 35

cca aaa agc cag gtg ttc aag cct ctg gaa ttg ctt tgg cac tcg tta 679
Pro Lys Ser Gln Val Phe Lys Pro Leu Glu Leu Leu Trp His Ser Leu
40 45 50

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gat gaa tgg cta gtt tta ata gcc cca gaa ttg atg aaa aac aaa aga	727
Asp Glu Trp Leu Val Leu Ile Ala Pro Glu Leu Met Lys Asn Lys Arg	
55 60 65	
gac tca aca gag atc act tct att tta ctg aaa caa aaa ggc caa gat	775
Asp Ser Thr Glu Ile Thr Ser Ile Leu Leu Lys Gln Lys Gly Gln Asp	
70 75 80	
caa gat gct gct tcc att cct cca ttt gaa cct cca gga cct ggg agc	823
Gln Asp Ala Ala Ser Ile Pro Pro Phe Glu Pro Pro Gly Pro Gly Ser	
85 90 95	
tat gaa aat ctg tcc act ggc aca agg gaa tct aaa cca gat gct ctt	871
Tyr Glu Asn Leu Ser Thr Gly Thr Arg Glu Ser Lys Pro Asp Ala Leu	
100 105 110 115	
gca ggg aga cag gaa gcc agt gca gat tgt cag gat gtt att tct atg	919
Ala Gly Arg Gln Glu Ala Ser Ala Asp Cys Gln Asp Val Ile Ser Met	
120 125 130	
aca gct aac cgg cta agt gct gtc att caa gct ttt tac atg tgc tgt	967
Thr Ala Asn Arg Leu Ser Ala Val Ile Gln Ala Phe Tyr Met Cys Cys	
135 140 145	
tct tgt cag atg cct ccg gga atg act tca cct cgt ttc att gaa ttt	1015
Ser Cys Gln Met Pro Pro Gly Met Thr Ser Pro Arg Phe Ile Glu Phe	
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Val Cys Lys His Asp Glu Val Leu Lys Cys Phe Val Asn Arg Asn Pro	
165 170 175	
aaa att ata ttt gac cac ttt cac ttt ctc ctt gaa tgt cct gag ttg	1111
Lys Ile Ile Phe Asp His Phe His Phe Leu Leu Glu Cys Pro Glu Leu	
180 185 190 195	
atg tca aga ttc atg cat atc ata aaa gca cag cct ttt aaa gat cgc	1159
Met Ser Arg Phe Met His Ile Ile Lys Ala Gln Pro Phe Lys Asp Arg	
200 205 210	
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Cys Glu Trp Phe Tyr Glu His Leu His Ser Gly Gln Pro Asp Ser Asp	
215 220 225	
atg gtg cac agg cca gtg aat gaa aat gat atc ctg ctg gtt cac aga	1255
Met Val His Arg Pro Val Asn Glu Asn Asp Ile Leu Leu Val His Arg	
230 235 240	
gat tct att ttt agg agt agc tgt gaa gtt gtg tca aaa gca aat tgt	1303
Asp Ser Ile Phe Arg Ser Ser Cys Glu Val Val Ser Lys Ala Asn Cys	
245 250 255	
gca aag cta aag caa ggg att gct gta cgg ttc cat gga gaa gaa ggc	1351
Ala Lys Leu Lys Gln Gly Ile Ala Val Arg Phe His Gly Glu Glu Gly	
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Met	Gly	Gln	Gly	Val	Val	Arg	Glu	Trp	Phe	Asp	Ile	Leu	Ser	Asn	Glu		
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Ile	Val	Asn	Pro	Asp	Tyr	Ala	Leu	Phe	Thr	Gln	Ser	Ala	Asp	Gly	Thr		
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Thr	Phe	Gln	Pro	Asn	Ser	Asn	Ser	Tyr	Val	Asn	Pro	Asp	His	Leu	Asn		
				310					315					320			
tat	ttt	cgg	ttt	gct	ggg	cag	atc	ttg	gga	tta	gcg	ttg	aac	cac	agg	1543	
Tyr	Phe	Arg	Phe	Ala	Gly	Gln	Ile	Leu	Gly	Leu	Ala	Leu	Asn	His	Arg		
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cag	ctg	gtc	aat	att	tac	ttc	aca	cga	tcc	ttc	tac	aag	cac	att	ctt	1591	
Gln	Leu	Val	Asn	Ile	Tyr	Phe	Thr	Arg	Ser	Phe	Tyr	Lys	His	Ile	Leu		
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ggt	att	cct	gta	aat	tac	caa	gat	gtg	gca	tcc	att	gat	cca	gaa	tat	1639	
Gly	Ile	Pro	Val	Asn	Tyr	Gln	Asp	Val	Ala	Ser	Ile	Asp	Pro	Glu	Tyr		
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gcg	aaa	aat	ttg	caa	tgg	att	tta	gat	aat	gat	ata	agt	gat	ctg	ggt	1687	
Ala	Lys	Asn	Leu	Gln	Trp	Ile	Leu	Asp	Asn	Asp	Ile	Ser	Asp	Leu	Gly		
				375					380					385			
cta	gaa	cta	act	ttt	tct	gtt	gag	act	gat	gtg	ttt	gga	gca	atg	gaa	1735	
Leu	Glu	Leu	Thr	Phe	Ser	Val	Glu	Thr	Asp	Val	Phe	Gly	Ala	Met	Glu		
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gag	gtg	cct	ttg	aaa	cct	ggg	ggt	ggg	agt	att	ctt	gtg	aca	caa	aat	1783	
Glu	Val	Pro	Leu	Lys	Pro	Gly	Gly	Gly	Ser	Ile	Leu	Val	Thr	Gln	Asn		
				405					410					415			
aat	aaa	gcg	gag	tac	gtc	cag	ctt	gtt	act	gaa	ctt	cga	atg	aca	aga	1831	
Asn	Lys	Ala	Glu	Tyr	Val	Gln	Leu	Val	Thr	Glu	Leu	Arg	Met	Thr	Arg		
				420					425					430			435
gcc	att	cag	cct	cag	atc	aat	gct	ttt	tta	cag	ggc	ttt	cat	atg	ttc	1879	
Ala	Ile	Gln	Pro	Gln	Ile	Asn	Ala	Phe	Leu	Gln	Gly	Phe	His	Met	Phe		
				440					445					450			
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Ile	Pro	Pro	Ser	Leu	Ile	Gln	Leu	Phe	Asp	Glu	Tyr	Glu	Leu	Glu	Leu		
				455					460					465			
ctg	ctt	tct	ggc	atg	cca	gaa	att	gat	gtg	agt	gat	tgg	ata	aaa	aat	1975	
Leu	Leu	Ser	Gly	Met	Pro	Glu	Ile	Asp	Val	Ser	Asp	Trp	Ile	Lys	Asn		
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aca	gaa	tac	aca	agt	ggc	tat	gaa	aga	gaa	gat	cca	gtt	att	cag	tgg	2023	
Thr	Glu	Tyr	Thr	Ser	Gly	Tyr	Glu	Arg	Glu	Asp	Pro	Val	Ile	Gln	Trp		
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ttc	tgg	gaa	gtt	gta	gaa	gac	att	act	caa	gag	gag	aga	gtt	ctt	ctc	2071	
Phe	Trp	Glu	Val	Val	Glu	Asp	Ile	Thr	Gln	Glu	Glu	Arg	Val	Leu	Leu		

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tta cag ttt gtt acg ggc agt tcc agg gtc cca cat ggt ggg ttt gct				2119
Leu Gln Phe Val Thr Gly Ser Ser Arg Val Pro His Gly Gly Phe Ala				
	520	525	530	
aat atc atg ggt gga agt gga ttg caa aac ttt aca atc gct gct gtg				2167
Asn Ile Met Gly Gly Ser Gly Leu Gln Asn Phe Thr Ile Ala Ala Val				
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cca tat act cca aat ctt tta cca act tca agc aca tgc atc aac atg				2215
Pro Tyr Thr Pro Asn Leu Leu Pro Thr Ser Ser Thr Cys Ile Asn Met				
	550	555	560	
ctc aag tta cct gaa tac cca agt aaa gaa ata ctc aag gac aga ctt				2263
Leu Lys Leu Pro Glu Tyr Pro Ser Lys Glu Ile Leu Lys Asp Arg Leu				
	565	570	575	
ctt gtg gca cta cat tgt ggc agc tat ggt tac aca atg gca taa tga				2311
Leu Val Ala Leu His Cys Gly Ser Tyr Gly Tyr Thr Met Ala *				
	580	585	590	
agtctggaaa actcctctga ctactgatgc acaattcaga atggcagaag taatttgga				2371
aaatgtcaac aaaaaagcag cctaaatgca acccataggc agggctgatg cttccaattt				2431
ataaaggatc atcaggtttt ctgtttctct cttttccctt ttatgttttc tctgtttgta				2491
tacaattaga aaatataaaa tcacagtaga ttttattttt taaaatgcta actgaaagta				2551
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aagagggcca ggggtccctt gccccaccac tttccatgat gacaagagat gggaaggtag      240
ccaggcagca acagtgtacg gcgacattgg agcggacctc acggcgacct caatttccac      300
tgcgctcctt cccagagctt aagaagctgc aggctgtgg tgcccagcac caagtgcaga      360
tggacacggg tcttcatccc cttccttggc accttccatt taagccaaac attagaaatg      420
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gat gct gag cgg atc ttc tct gct tca gac cag gcc tca tgt ggc ttc      750
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act att cat cca cac ata gat gct gca gag aca ctg agg gga ctc aca      798
Thr Ile His Pro His Ile Asp Ala Ala Glu Thr Leu Arg Gly Leu Thr
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aat gca cct gtg cag aag gtg tca acg tgg aca aac aca ggc agg gaa      846
Asn Ala Pro Val Gln Lys Val Ser Thr Trp Thr Asn Thr Gly Arg Glu
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act ccc atg agc ccg tgt gcc aca tgc agt gag gga act ttg gtg gct      894
Thr Pro Met Ser Pro Cys Ala Thr Cys Ser Glu Gly Thr Leu Val Ala
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gag tct ggg cgg ggg tgg gct ggg ggc tca atc gat ttc cac cga gtg      942
Glu Ser Gly Arg Gly Trp Ala Gly Gly Ser Ile Asp Phe His Arg Val
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Cys Leu Gln Ile Phe Ala Gly Ser Ala Gly Lys Gly Gln Gly Leu Asp
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acc agc gtc gct gtt cct cca ggc tgg gct gat ccc ttt tta ttt cca      1038
Thr Ser Val Ala Val Pro Pro Gly Trp Ala Asp Pro Phe Leu Phe Pro
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agt cac agg agc ctg ttc cct gaa atc ctg ggg aag tgt ggt gag gtg      1086
Ser His Arg Ser Leu Phe Pro Glu Ile Leu Gly Lys Cys Gly Glu Val
                140                      145                      150

gcc ccg tgc cgt cga atc ccc atc ctg gtt tac tga agtg cagaagtgc      1136
Ala Pro Cys Arg Arg Ile Pro Ile Leu Val Tyr *
                155                      160

ataagtgcctt gtgaatcagc agggagctct tggctttgac tccctgtgca gatgagccca      1196

gggcgccagc tccttgctgg agaactcctt tgtccatttg cacgtatgga tctttcctca      1256

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atgtgtatct caccacaatt taagaaatat gtaatttgag gcttggagaa tttaattaag      180

tgatttatct gatgttaact tacagctgat acatggtaga gctgcatttt aatctcagtc      240

atctggctct ttttaaaaca attacagaga aaactttatt ttgggccatt taggaggttt      300

agatcatttt gatcatcttc agctgtcttc tcttcacata caggaaaggc cttggaaagc      360

agtcgttgcg ccagacagcc caggggaagag cggcagcctg aggacctagg gccacctgct      420

gttcctggg attcatgtcc ttctggggag gagggaggac ccaggaca atg gct gct      477
                                Met Ala Ala

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gtt cat gat ctg gag atg gag agc atg aat ctg aat atg ggg aga gag	525
Val His Asp Leu Glu Met Glu Ser Met Asn Leu Asn Met Gly Arg Glu	
5 10 15	
atg aaa gaa gag ctg gag gaa gag gag aaa atg aga gag gat ggg gga	573
Met Lys Glu Glu Leu Glu Glu Glu Glu Lys Met Arg Glu Asp Gly Gly	
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Gly Lys Asp Arg Ala Lys Ser Lys Lys Val His Arg Ile Val Ser Lys	
40 45 50	
tgg atg ctg ccc gaa aag tcc cga gga aca tac ttg gag aga gct aac	669
Trp Met Leu Pro Glu Lys Ser Arg Gly Thr Tyr Leu Glu Arg Ala Asn	
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Cys Phe Pro Pro Pro Val Phe Ile Ile Ser Ile Ser Leu Ala Glu Leu	
70 75 80	
gca gtg ttt att tac tat gct gtg tgg aag cct cag aaa cag tgg atc	765
Ala Val Phe Ile Tyr Tyr Ala Val Trp Lys Pro Gln Lys Gln Trp Ile	
85 90 95	
acg ttg gac aca ggc atc ttg gag agt ccc ttt atc tac agt cct gag	813
Thr Leu Asp Thr Gly Ile Leu Glu Ser Pro Phe Ile Tyr Ser Pro Glu	
100 105 110 115	
aag agg gag gaa gcc tgg agg ttt atc tca tac atg ctg gta cat gct	861
Lys Arg Glu Glu Ala Trp Arg Phe Ile Ser Tyr Met Leu Val His Ala	
120 125 130	
gga gtt cag cac atc ttg ggg aat ctt tgt atg cag ctt gtt ttg ggt	909
Gly Val Gln His Ile Leu Gly Asn Leu Cys Met Gln Leu Val Leu Gly	
135 140 145	
att ccc ttg gaa atg gtc cac aaa ggc ctc cgt gtg ggg ctg gtg tac	957
Ile Pro Leu Glu Met Val His Lys Gly Leu Arg Val Gly Leu Val Tyr	
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Leu Ala Gly Val Ile Ala Gly Ser Leu Ala Ser Ser Ile Phe Asp Pro	
165 170 175	
ctc aga tat ctt gtg gga gct tca gga gga gtc tat gct ctg atg gga	1053
Leu Arg Tyr Leu Val Gly Ala Ser Gly Gly Val Tyr Ala Leu Met Gly	
180 185 190 195	
ggc tat ttt atg aat gtt ctg gtg aat ttt caa gaa atg att cct gcc	1101
Gly Tyr Phe Met Asn Val Leu Val Asn Phe Gln Glu Met Ile Pro Ala	
200 205 210	
ttt gga att ttc aga ctg ctg atc atc atc ctg ata att gtg ttg gac	1149
Phe Gly Ile Phe Arg Leu Leu Ile Ile Ile Leu Ile Ile Val Leu Asp	
215 220 225	
atg gga ttt gct ctc tat aga agg ttc ttt gtt cct gaa gat ggg tct	1197

Met Gly Phe Ala Leu Tyr Arg Arg Phe Phe Val Pro Glu Asp Gly Ser	
230 235 240	
ccg gtg tct ttt gca gct cac att gca ggt gga ttt gct gga atg tcc	1245
Pro Val Ser Phe Ala Ala His Ile Ala Gly Gly Phe Ala Gly Met Ser	
245 250 255	
att ggc tac acg gtg ttt agc tgc ttt gat aaa gca ctg atg aaa gat	1293
Ile Gly Tyr Thr Val Phe Ser Cys Phe Asp Lys Ala Leu Met Lys Asp	
260 265 270 275	
cca agg ttt tgg ata gca att gct gca tat tta gct tgt gtc tta ttt	1341
Pro Arg Phe Trp Ile Ala Ile Ala Ala Tyr Leu Ala Cys Val Leu Phe	
280 285 290	
gct gtg ttt ttc aac att ttc cta tct cca gca aac tga cctgccctta	1390
Ala Val Phe Phe Asn Ile Phe Leu Ser Pro Ala Asn *	
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Met Thr	
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act gct cac ttt tac tgt caa tac tgc aca gca tca ctt ctt ggg aag	285
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aaa tat gta cta aag gat gac agt cca tac tgt gtt aca tgt tat gat	333
Lys Tyr Val Leu Lys Asp Asp Ser Pro Tyr Cys Val Thr Cys Tyr Asp	
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cgt gta ttt tct aac tat tgc gag gaa tgc aaa aaa cca att gaa tct	381
Arg Val Phe Ser Asn Tyr Cys Glu Glu Cys Lys Lys Pro Ile Glu Ser	
35 40 45 50	
gat tct aag gat ctt tgt tac aaa gac cgg cac tgg cat gaa gga tgc	429
Asp Ser Lys Asp Leu Cys Tyr Lys Asp Arg His Trp His Glu Gly Cys	
55 60 65	
ttc aag tgc acc aaa tgc aat cac tct ttg gtg gaa aag cct ttt gct	477
Phe Lys Cys Thr Lys Cys Asn His Ser Leu Val Glu Lys Pro Phe Ala	
70 75 80	
gcc aag gat gag cgc ctg ctg tgc acg gag tgc tat tct aac gag tgc	525
Ala Lys Asp Glu Arg Leu Leu Cys Thr Glu Cys Tyr Ser Asn Glu Cys	
85 90 95	
tcc tcc aag tgc ttc cac tgc aag agg acc atc atg cct ggt tcc cgc	573
Ser Ser Lys Cys Phe His Cys Lys Arg Thr Ile Met Pro Gly Ser Arg	
100 105 110	
aaa atg gaa ttt aag gga aac tac tgg cat gaa acc tgt ttt gtg tgt	621
Lys Met Glu Phe Lys Gly Asn Tyr Trp His Glu Thr Cys Phe Val Cys	
115 120 125 130	
gag aat tgc cga caa cct ata ggg aca aag cct ttg atc tcc aaa gag	669
Glu Asn Cys Arg Gln Pro Ile Gly Thr Lys Pro Leu Ile Ser Lys Glu	
135 140 145	
agt ggc aat tat tgt gtg cca tgt ttt gag aag gag ttt gct cac tac	717
Ser Gly Asn Tyr Cys Val Pro Cys Phe Glu Lys Glu Phe Ala His Tyr	
150 155 160	
tgc aac ttt tgt aag aag gtg ata act tca ggt ggg ata aca ttt tgt	765
Cys Asn Phe Cys Lys Lys Val Ile Thr Ser Gly Gly Ile Thr Phe Cys	
165 170 175	
gac cag cta tgg cat aaa gag tgt ttt ctg tgt agt ggc tgt agg aaa	813
Asp Gln Leu Trp His Lys Glu Cys Phe Leu Cys Ser Gly Cys Arg Lys	
180 185 190	
gat ctc tgt gaa gaa cag ttc atg tcc aga gac gac tat cca ttc tgc	861
Asp Leu Cys Glu Glu Gln Phe Met Ser Arg Asp Asp Tyr Pro Phe Cys	
195 200 205 210	
atg gac tgc tac aac cat ctt tat gcc aac aag tgt gta gcc tgt tcc	909
Met Asp Cys Tyr Asn His Leu Tyr Ala Asn Lys Cys Val Ala Cys Ser	
215 220 225	
aaa ccc att agt ggt ctc aca ggt gcc aag ttt atc tgc ttt caa gac	957
Lys Pro Ile Ser Gly Leu Thr Gly Ala Lys Phe Ile Cys Phe Gln Asp	
230 235 240	
agc cag tgg cat agc gaa tgc ttt aac tgc ggg aaa tgc tct gtc tcc	1005
Ser Gln Trp His Ser Glu Cys Phe Asn Cys Gly Lys Cys Ser Val Ser	
245 250 255	

ttg gtg ggt aaa ggc ttc ctg acc cag aac aag gaa atc ttc tgc caa	1053
Leu Val Gly Lys Gly Phe Leu Thr Gln Asn Lys Glu Ile Phe Cys Gln	
260 265 270	

aaa tgt ggc tcc gga atg gac act gac atc tag gagacagt ccttgcccac	1104
Lys Cys Gly Ser Gly Met Asp Thr Asp Ile *	
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ctc ctg ctg ctc ctg atg ctg gga tgc gtc ctg atg atg gtg gcg atg	96
Leu Leu Leu Leu Leu Met Leu Gly Cys Val Leu Met Met Val Ala Met	
20 25 30	

ttg cac cct ccc cac cac acc ctg cac cag act gtc aca gcc caa gcc	144
Leu His Pro Pro His His Thr Leu His Gln Thr Val Thr Ala Gln Ala	
35 40 45	

agc aag cac agc cct gaa gcc agg tac cgc ctg gac ttt ggg gaa tcc	192
Ser Lys His Ser Pro Glu Ala Arg Tyr Arg Leu Asp Phe Gly Glu Ser	
50 55 60	

cag gat tgg gta ctg gaa gct gag gat gag ggt gaa gag tac agc cct	240
Gln Asp Trp Val Leu Glu Ala Glu Asp Glu Gly Glu Glu Tyr Ser Pro	
65 70 75 80	

ctg gag ggc ctg cca ccc ttt atc tca ctg cgg gag gat cag ctg ctg	288
Leu Glu Gly Leu Pro Pro Phe Ile Ser Leu Arg Glu Asp Gln Leu Leu	
85 90 95	

gtg gcc gtg gcc tta ccc cag gcc aga agg aac cag agc cag ggc agg	336
Val Ala Val Ala Leu Pro Gln Ala Arg Arg Asn Gln Ser Gln Gly Arg	
100 105 110	

aga ggt ggg agc tac cgc ctc atc aag cag cca agg agg cag gat aag	384
Arg Gly Gly Ser Tyr Arg Leu Ile Lys Gln Pro Arg Arg Gln Asp Lys	
115 120 125	

gaa gcc cca aag agg gac tgg ggg gct gat gag gac ggg gag gtg tct	432
Glu Ala Pro Lys Arg Asp Trp Gly Ala Asp Glu Asp Gly Glu Val Ser	

130	135	140	
gaa gaa gag gag ttg acc ccg ttc agc ctg gac cca cgt ggc ctc cag			480
Glu Glu Glu Glu Leu Thr Pro Phe Ser Leu Asp Pro Arg Gly Leu Gln			
145	150	155	160
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Glu Ala Leu Ser Ala Arg Ile Pro Leu Gln Arg Ala Leu Pro Glu Val			
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cgg cac cca ctg tgt ctg cag cag cac cct cag gac agc ctg ccc aca			576
Arg His Pro Leu Cys Leu Gln Gln His Pro Gln Asp Ser Leu Pro Thr			
	180	185	190
gcc agc gtc atc ctc tgt ttc cat gat gag gcc tgg tcc act ctc ctg			624
Ala Ser Val Ile Leu Cys Phe His Asp Glu Ala Trp Ser Thr Leu Leu			
	195	200	205
cgg act gta cac agc atc ctc gac aca gtg ccc agg gcc ttc ctg aag			672
Arg Thr Val His Ser Ile Leu Asp Thr Val Pro Arg Ala Phe Leu Lys			
	210	215	220
gag atc atc ctc gtg gac gac ctc agc cag caa gga caa ctc aag tct			720
Glu Ile Ile Leu Val Asp Asp Leu Ser Gln Gln Gly Gln Leu Lys Ser			
	225	230	235
gct ctc agc gaa tat gtg gcc agg ctg gag ggg gtg aag tta ctc agg			768
Ala Leu Ser Glu Tyr Val Ala Arg Leu Glu Gly Val Lys Leu Leu Arg			
	245	250	255
agc aac aag agg ctg ggt gcc atc agg gcc cgg atg ctg ggg gcc acc			816
Ser Asn Lys Arg Leu Gly Ala Ile Arg Ala Arg Met Leu Gly Ala Thr			
	260	265	270
aga gcc acc ggg gat gtg ctc gtc ttc atg gat gcc cac tgc gag tgc			864
Arg Ala Thr Gly Asp Val Leu Val Phe Met Asp Ala His Cys Glu Cys			
	275	280	285
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His Pro Gly Trp Leu Glu Pro Leu Leu Ser Arg Ile Ala Gly Asp Arg			
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Ser Arg Val Val Ser Pro Val Ile Asp Val Ile Asp Trp Lys Thr Phe			
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Gln Tyr Tyr Pro Ser Lys Asp Leu Gln Arg Gly Val Leu Asp Trp Lys			
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Gln Ser Pro Ile Ser Pro Ile Arg Ser Pro Val Val Pro Gly Glu Val			
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ctg tgc ttt gct gtc agg cag gag cag gtg att ctt cag aac tgc acg Leu Cys Phe Ala Val Arg Gln Glu Gln Val Ile Leu Gln Asn Cys Thr 565 570 575	1728
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Gly Met Ile Val His Ile Leu Ser Gly Lys Cys Met Glu Ala Val Val
      595                      600                      605

caa gaa aac aat aaa gat ttg tac ctg cgt ccg tgt gat gga aaa gcc      1872
Gln Glu Asn Asn Lys Asp Leu Tyr Leu Arg Pro Cys Asp Gly Lys Ala
      610                      615                      620

cgc cag cag tgg cgt ttt gac cag atc aat gct gtg gat gaa cga tga      1920
Arg Gln Gln Trp Arg Phe Asp Gln Ile Asn Ala Val Asp Glu Arg  *
      625                      630                      635                      640

atgtcaatgt cagaaggaaa agagaatttt ggccatcaaa atccagctcc aagtgaactt      1980

aaagagctta tatatttcat gaagctgac cttttgtgtg tgtgctcctg gtgttaggag      2040

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ccccactga agggcaaagt ccagcggatt ctacactgga ggtggacgga gcccctgcc      180

cccttc    atg gtg ggg ctg ccg ggg cct gac gtg gag ccc agc ctc cct      228
          Met Val Gly Leu Pro Gly Pro Asp Val Glu Pro Ser Leu Pro
            1              5              10

cca cct aag ccc ctg gag ggc atc cct gag aga gag ttc ttt gtc aag      276
Pro Pro Lys Pro Leu Glu Gly Ile Pro Glu Arg Glu Phe Phe Val Lys
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Trp Ala Gly Leu Ser Tyr Trp His Cys Ser Trp Val Lys Glu Leu Gln
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ctg gag ctg tac cac acg gtg atg tat cgc aac tac caa aga aag aac      372
Leu Glu Leu Tyr His Thr Val Met Tyr Arg Asn Tyr Gln Arg Lys Asn
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gac atg gat gag ccg ccc ccc ttt gac tac ggc tct ggg gat gaa gac      420
Asp Met Asp Glu Pro Pro Pro Phe Asp Tyr Gly Ser Gly Asp Glu Asp

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cac cga atc ctg aac cat agc ttt gac aag aag ggg gat gtg cac tac His Arg Ile Leu Asn His Ser Phe Asp Lys Lys Gly Asp Val His Tyr 115 120 125			564
ctg atc aag tgg aaa gac ctg ccc tat gac cag tgc acc tgg gag atc Leu Ile Lys Trp Lys Asp Leu Pro Tyr Asp Gln Cys Thr Trp Glu Ile 130 135 140			612
gat gac atc gac atc ccc tac tac gac aac ctc aag cag gcc tac tgg Asp Asp Ile Asp Ile Pro Tyr Tyr Asp Asn Leu Lys Gln Ala Tyr Trp 145 150 155			660
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Arg Ser Gly Lys Lys Val Phe Arg Met Lys Lys Glu Val Gln Ile Lys	
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Asn Asn Leu Glu Gly Phe Leu Glu Glu Phe Ala Asp Ile Ser Lys Glu	
415 420 425 430	
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Asp Gln Ile Lys Lys Leu His Asp Leu Leu Gly Pro His Met Leu Arg	
435 440 445	
cgg ctc aag gct gac gtg ttc aag aac atg ccg gcc aag acc gag ctc	1572
Arg Leu Lys Ala Asp Val Phe Lys Asn Met Pro Ala Lys Thr Glu Leu	
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Ile Val Arg Val Glu Leu Ser Gln Met Gln Lys Lys Tyr Tyr Lys Phe	
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Gln Val Ser Leu Leu Asn Ile Met Met Asp Leu Lys Lys Cys Cys Asn	
495 500 505 510	
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His Pro Tyr Leu Phe Pro Val Ala Ala Val Glu Ala Pro Val Leu Pro	
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Asn Gly Ser Tyr Asp Gly Ser Ser Leu Val Lys Ser Ser Gly Lys Leu	
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545 550 555	
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Phe Leu Glu Tyr Glu Gly Tyr Lys Tyr Glu Arg Ile Asp Gly Gly Ile	
575 580 585 590	
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Thr Gly Gly Leu Arg Gln Glu Ala Ile Asp Arg Phe Asn Ala Pro Gly	
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Ala Gln Gln Phe Cys Phe Leu Leu Ser Thr Arg Ala Gly Gly Leu Gly	
610 615 620	
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Asn Pro His Asn Asp Ile Gln Ala Phe Ser Arg Ala His Arg Ile Gly	
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Gln Asn Lys Lys Val Met Ile Tyr Arg Phe Val Thr Arg Ala Ser Val	
655 660 665 670	
gag gag cgc atc acg cag gtg gcc aag cgc aag atg atg ctc acc cac	2244
Glu Glu Arg Ile Thr Gln Val Ala Lys Arg Lys Met Met Leu Thr His	
675 680 685	
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Leu Val Val Arg Pro Gly Leu Gly Ser Lys Ser Gly Ser Met Thr Lys	
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Gln Glu Leu Asp Asp Ile Leu Lys Phe Gly Thr Glu Glu Leu Phe Lys	
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Asp Asp Val Glu Gly Met Met Ser Gln Gly Gln Arg Pro Val Thr Pro	
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Ile Pro Asp Val Gln Ser Lys Gly Gly Asn Leu Ala Ala Ser Ala	
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aag aag aag cac ggt agc acc ccg cca ggt gac aac aag gac gtg gag	2484

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gac	agc	agt	gtg	atc	cac	tat	gac	gat	gcg	gcc	atc	tcc	aag	ctg	ctg		2532
Asp	Ser	Ser	Val	Ile	His	Tyr	Asp	Asp	Ala	Ala	Ile	Ser	Lys	Leu	Leu		
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Asp	Arg	Asn	Gln	Asp	Ala	Thr	Asp	Asp	Thr	Glu	Leu	Gln	Asn	Met	Asn		
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Glu	Tyr	Leu	Ser	Ser	Phe	Lys	Val	Ala	Gln	Tyr	Val	Val	Arg	Glu	Glu		
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Val	Asp	Pro	Asp	Tyr	Trp	Glu	Lys	Leu	Leu	Arg	His	His	Tyr	Glu	Gln		
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Gln	Gln	Glu	Asp	Leu	Ala	Arg	Asn	Leu	Gly	Lys	Gly	Lys	Arg	Ile	Arg		
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Lys	Gln	Val	Asn	Tyr	Asn	Asp	Ala	Ser	Gln	Glu	Asp	Gln	Glu	Trp	Gln		
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Asp	Glu	Leu	Ser	Asp	Asn	Gln	Ser	Glu	Tyr	Ser	Ile	Gly	Ser	Glu	Asp		
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Glu	Asp	Glu	Asp	Phe	Glu	Glu	Arg	Pro	Glu	Gly	Gln	Ser	Gly	Arg	Arg		
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Gln	Ser	Arg	Arg	Gln	Leu	Lys	Ser	Asp	Arg	Asp	Lys	Pro	Leu	Pro	Pro		
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Pro	Gln	Asp	Ala	Phe	Asn	Ser	His	Trp	Leu	Val	Arg	Asp	Leu	Arg	Gly		
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Lys	Ser	Glu	Lys	Glu	Phe	Arg	Ala	Tyr	Val	Ser	Leu	Phe	Met	Arg	His		

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Ala Gln Leu Gly Tyr Met Asp Glu Lys Asp Pro Gly Ala Gln Lys Pro				
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Arg Gln Pro Leu Glu Val Gln Ala Leu Pro Ala Ala Leu Asp Arg Val				
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Glu Ser Glu Asp Lys His Glu Ser Pro Ala Ser Lys Glu Arg Ala Arg				
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Glu Glu Arg Pro Glu Glu Thr Glu Lys Ala Pro Pro Ser Pro Glu Gln				
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ctg ccg aga gag gag gtg ctt cct gag aag gag aag atc ctg gac aag				3684
Leu Pro Arg Glu Glu Val Leu Pro Glu Lys Glu Lys Ile Leu Asp Lys				
	1155	1160	1165	
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Leu Glu Leu Ser Leu Ile His Ser Arg Gly Asp Ser Ser Glu Leu Arg				
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Asn Gly Asp Lys Glu Glu Asp Asp Glu Gly Lys Lys Glu Asp Lys Lys				
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acc cac ata gta tac ccc ttg ctg caa gga tgg gtg atg tat gtc tcg	251
Thr His Ile Val Tyr Pro Leu Leu Gln Gly Trp Val Met Tyr Val Ser	
50 55 60	
ctc acc tcg ttt ctc atc tcc ttg atg ttc ctg ttg tct tac ttg ttt	299
Leu Thr Ser Phe Leu Ile Ser Leu Met Phe Leu Leu Ser Tyr Leu Phe	
65 70 75	
gga ttt tac aaa aga ttt gaa tcc tgg aga gtt ctg gac agc ctg tac	347
Gly Phe Tyr Lys Arg Phe Glu Ser Trp Arg Val Leu Asp Ser Leu Tyr	
80 85 90 95	
cac ggg acc act ggc atc ctg tac atg agc gct gcc gtc cta caa gta	395
His Gly Thr Thr Gly Ile Leu Tyr Met Ser Ala Ala Val Leu Gln Val	
100 105 110	

cat gcc acg att gtt tct gag aaa ctg ctg gac cca aga att tac tac	443
His Ala Thr Ile Val Ser Glu Lys Leu Leu Asp Pro Arg Ile Tyr Tyr	
115 120 125	

att aat tcg gca gcc tcg ttc ttc gcc ttc atc gcc acg ctg ctc tac	491
Ile Asn Ser Ala Ala Ser Phe Phe Ala Phe Ile Ala Thr Leu Leu Tyr	
130 135 140	

att ctc cat gcc ttc agc atc tat tac cac tga tgcacagg cgccaggcca	542
Ile Leu His Ala Phe Ser Ile Tyr Tyr His *	
145 150	

aggggggaaat gctcttttgaa agctccaatt attggtcccc aaaagcagct tccaacgttt	602
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gccatctgga tgacaaacgg aagatccact aaaacgtcca cgggattaac agaacgtcct	662
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tgcagactga gcgatgacac cacactttgt ttggacattt aaattcactc tgctgaatag	722
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gaggaagctt ttctttttcc tgggaaaaca actgtctctt ggaattatct gaccatgaac	782
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ttgtctttct agacaactca catcaaagcc ctactccac taatggagaa tcctagcccc	842
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actaatgcc aagtctgttg gggattttgc ctgagctatg ggcttccta gagtaggtct	902
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aggggaatac tcagtctgat cttttttttg tttgttttat tttgtttttt ttgagacgga	962
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gtctcgctct tcctccaagg ctggagtgc gtagcgcgat ctccactcac tgcaggctcc	1022
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gcctcggggg ttcccggcat	1042
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gggctggaga ggtcctgccg tggtaccagc ctccagcctg cccccaggac tgcccctgac	120
ccaggcgcgc ccgctgctcg gtggcaggag ggccggcgga gcgcc	174
atg gcc tgc	
Met Ala Cys	
1	

atc ctg aag aga aag tct gtg att gct gtg agc ttc ata gca gcg ttc	222
Ile Leu Lys Arg Lys Ser Val Ile Ala Val Ser Phe Ile Ala Ala Phe	
5 10 15	

ctt ttc ctg ctg gtt gtg cgt ctt gta aat gaa gtg aat ttc cca ttg	270
Leu Phe Leu Leu Val Val Arg Leu Val Asn Glu Val Asn Phe Pro Leu	

20	25	30	35	
cta cta aac tgc ttt gga caa cct ggt aca aag tgg ata cca ttc tcc				318
Leu Leu Asn Cys Phe Gly Gln Pro Gly Thr Lys Trp Ile Pro Phe Ser	40	45	50	
tac aca tac agg cgg ccc ctt cga act cac tat gga tac ata aat gtg				366
Tyr Thr Tyr Arg Arg Pro Leu Arg Thr His Tyr Gly Tyr Ile Asn Val	55	60	65	
aag aca caa gag cct ttg caa ctg gac tgt gac ctt tgt gcc ata gtg				414
Lys Thr Gln Glu Pro Leu Gln Leu Asp Cys Asp Leu Cys Ala Ile Val	70	75	80	
tca aac tca ggt cag atg gtt ggc cag aag gtg gga aat gag ata gat				462
Ser Asn Ser Gly Gln Met Val Gly Gln Lys Val Gly Asn Glu Ile Asp	85	90	95	
cga tcc tcc tgc att tgg aga atg aac aat gcc ccc acc aaa ggt tat				510
Arg Ser Ser Cys Ile Trp Arg Met Asn Asn Ala Pro Thr Lys Gly Tyr	100	105	110	115
gaa gaa gat gtc ggc cgc atg acc atg att cga gtt gtg tcc cat acc				558
Glu Glu Asp Val Gly Arg Met Thr Met Ile Arg Val Val Ser His Thr	120	125	130	
agc gtt cct ctt ttg cta aaa aac cct gat tat ttt ttc aag gaa gcg				606
Ser Val Pro Leu Leu Leu Lys Asn Pro Asp Tyr Phe Phe Lys Glu Ala	135	140	145	
aat act act att tgt gtt att tgg gga cct ttc cgc aat atg agg aaa				654
Asn Thr Thr Ile Cys Val Ile Trp Gly Pro Phe Arg Asn Met Arg Lys	150	155	160	
gat ggc aat ggc atc gtt tac aac atg ttg aaa aag aca gtt ggt atc				702
Asp Gly Asn Gly Ile Val Tyr Asn Met Leu Lys Lys Thr Val Gly Ile	165	170	175	
tat ccg aat gcc caa ata tac gtg acc aca gag aag cgc atg agt tac				750
Tyr Pro Asn Ala Gln Ile Tyr Val Thr Thr Glu Lys Arg Met Ser Tyr	180	185	190	195
tgt gat gga gtt ttt aag aag gaa act ggg aag gac agg ggg cat gca				798
Cys Asp Gly Val Phe Lys Lys Glu Thr Gly Lys Asp Arg Gly His Ala	200	205	210	
agg cga ctg ctg att tct aca gac act ttt taa gcgattac cagtgtgtggc				849
Arg Arg Leu Leu Ile Ser Thr Asp Thr Phe *	215	220		
aagtggaaact acctttccgg tcctctttaca agcatccagt cacttgctga aatgtcataa				909
gcgatataaaa cctgctgaca ggccaggatc attgcatctc ctgcctcctc cttccacgta				969
acaaatctca ttgttgattg gcatatggca gcaagcatcc caacaccag agtggtgttc				1029
ttattttctga gggagcaggg tctgtgtgtg aattgcacac acagggagca atccccctgcc				1089

ctgatacagg caacctgagt gcttagttcc ttctctgctc agaacttagt gtgactatgt 1149
ggcctacctc acattgtttg tgttacacct acacaggaaa aaggaaaaat gtccttttga 1209
ttccatgctt gtagagatgt tcatccaatt tgaatgaaca tgtagccaag gtagtgtctt 1269
ccccctttct tctccttttt ttttg 1294

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tcggccatga acttaccgga gacagcggcg gcggcggacc ttttggccat cttctcgag 120
agtgtccct gctaacgggg acagatttta acatt atg gca ggg agg cat cag 173
Met Ala Gly Arg His Gln
1 5
aat cgt agt ttt cct ctt cca gga gtt cag tca agt ggt caa gta cat 221
Asn Arg Ser Phe Pro Leu Pro Gly Val Gln Ser Ser Gly Gln Val His
10 15 20
gca ttt gga aat tgt tca gac agt gat att ttg gag gag gat gct gaa 269
Ala Phe Gly Asn Cys Ser Asp Ser Asp Ile Leu Glu Glu Asp Ala Glu
25 30 35
gtg tat gaa ctt cga tcc aga gga aaa gag aaa gtc cga aga agt aca 317
Val Tyr Glu Leu Arg Ser Arg Gly Lys Glu Lys Val Arg Arg Ser Thr
40 45 50
tca aga gat aga ctt gac gac att ata gta tta aca aaa gat ata caa 365
Ser Arg Asp Arg Leu Asp Asp Ile Ile Val Leu Thr Lys Asp Ile Gln
55 60 65 70
gaa gga gat aca tta aat gca ata gcc ctt cag tac tgt tgt acg gta 413
Glu Gly Asp Thr Leu Asn Ala Ile Ala Leu Gln Tyr Cys Cys Thr Val
75 80 85
gca gat atc aag aga gtt aac aat ctc atc agt gat caa gac ttt ttt 461
Ala Asp Ile Lys Arg Val Asn Asn Leu Ile Ser Asp Gln Asp Phe Phe
90 95 100
gcc ctt agg tct atc aaa att cca gta aaa aag ttc agt tcc ttg acc 509
Ala Leu Arg Ser Ile Lys Ile Pro Val Lys Lys Phe Ser Ser Leu Thr
105 110 115

gaa aca ctt tgt cct cca aaa gga aga cag act tca cgt cat tca tct	557
Glu Thr Leu Cys Pro Pro Lys Gly Arg Gln Thr Ser Arg His Ser Ser	
120 125 130	
ggt caa tac tct tcc gaa caa cag gaa att ttg cca gct aat gat tct	605
Val Gln Tyr Ser Ser Glu Gln Gln Glu Ile Leu Pro Ala Asn Asp Ser	
135 140 145 150	
ctt gct tac agt gac tca gct ggt agc ttt tta aaa gaa gta gac cga	653
Leu Ala Tyr Ser Asp Ser Ala Gly Ser Phe Leu Lys Glu Val Asp Arg	
155 160 165	
gac ata gaa caa ata gta aag tgt aca gac aat aag aga gag aac ctc	701
Asp Ile Glu Gln Ile Val Lys Cys Thr Asp Asn Lys Arg Glu Asn Leu	
170 175 180	
aat gag gta gta tcg gcc tta aca gca caa caa atg cgt ttt gaa cct	749
Asn Glu Val Val Ser Ala Leu Thr Ala Gln Gln Met Arg Phe Glu Pro	
185 190 195	
gat aac aaa aac act caa cgt aaa gac ccc tat tat gga gca gac tgg	797
Asp Asn Lys Asn Thr Gln Arg Lys Asp Pro Tyr Tyr Gly Ala Asp Trp	
200 205 210	
gga ata ggg tgg tgg aca gct gta gtg ata atg ttg ata gta ggt ata	845
Gly Ile Gly Trp Trp Thr Ala Val Val Ile Met Leu Ile Val Gly Ile	
215 220 225 230	
ata aca cca gtg ttt tat ttg ttg tat tat gaa att tta gct aag gtg	893
Ile Thr Pro Val Phe Tyr Leu Leu Tyr Tyr Glu Ile Leu Ala Lys Val	
235 240 245	
gat gtt agt cat cat tca aca gtg gac tct tca cat tta cat tca aaa	941
Asp Val Ser His His Ser Thr Val Asp Ser Ser His Leu His Ser Lys	
250 255 260	
atc aca ccc cca tca cag cag aga gaa atg gaa aat gga att gtg cca	989
Ile Thr Pro Pro Ser Gln Gln Arg Glu Met Glu Asn Gly Ile Val Pro	
265 270 275	
act aaa gga ata cat ttc agc caa caa gat gat cat aaa ctg tat agt	1037
Thr Lys Gly Ile His Phe Ser Gln Gln Asp Asp His Lys Leu Tyr Ser	
280 285 290	
caa gat tct cag tca cct gct gct caa cag gaa aca tag caattagctc	1086
Gln Asp Ser Gln Ser Pro Ala Ala Gln Gln Glu Thr *	
295 300 305	
ataatcaaat gttagtggtc aggtcacatg tgcattctgga atgtgggtgaa tcagttatat	1146
ccaataatag cttcaaaggc agaatttaga gagattgagg atgcttttgt ttttaacaaa	1206
agggtttcac actttgaaaa ttttttgagc aactagttgt tgatgttgag agcagttgat	1266
ccataaatct ggtgtgtgaa tgttttcaagc agaaattaat ttaaatgtgt gtttaggaag	1326

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agtaatTTTT aaaaagttta ttaatgttaa atttatgatg cagaatgata gcatcagatg	1446
tctgcagctg aaaaaaattt actactatga acccccaaaa tattcagttg caagaaaatt	1506
tgattctaaa attattcatg gtaggatacg taacacaccc cttcaaaact tttaaaaaat	1566
acatttagca catgtgctat gaaagcatag gtacaaagag aaaggggaaa gtgatttata	1626
attcctacaa cagaggccaa gaaatagatt aaaatatTTT caagacccca aaataatgta	1686
ttatggttgg gaagtcagta gaacactgga ataggtgaag acctgacagt aattttttgtc	1746
ttaagaatgc tttcttttagg acagaccctt taacctcacc tctgtgcatc tgttttttaa	1806
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attaaacgtg catattacca ttatttagga aataattcct tatatactgt gataaatcat	1926
tgctgttaca tacagtaaca tgccttaatt acatttaatg ccttactgct ttatgtaagt	1986
aaatccaagt ttcagaatta aaaataagca ttatttcata tgggtccaatc agattcgtta	2046
cataggctat ataaatttgt ctccattttc accatcaagc acaaataatt ggggtcaaac	2106
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tattagcagt aacagacaaa ttatttagta atcccttaac ctctgttttt caaagagaaa	2226
atatccaatt tagacttttt tcctgatctc tatatatagc atcaagttgg gaaacaaagg	2286
ccaaagggtg atagattgct tgaaaggggg tggtagtgcc tctttttaag atctgttgag	2346
tctggctacag tctggctaag taagaagcat ttgcatactg attccatcat ttaatcttta	2406
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agtctggatt gcctgttttg tatataatat atacttaaga tatataatac cacctcattt	2526
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tcaaatttaa ctgagaataa gtaaataatt atggcaaatt cagttttatg tactttcagg	2646
agaagaccat caggaaaaga caggacaaag aagtcaaaca ttaaagccct tgcaaatatt	2706
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gtaaattaaa catttaaaaa gtagttttta tgtgccttgg gcatcttgaa aagaagagtg	2826
tgatataatt tatgcttagt gttaactggg cattttacat tgtattttatt aagtctgctg	2886
aaaaatgagg ttttaaggaa gaaaatgcag attatttttag ggtaaacagg ccagggtgtcc	2946
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tagttgtact ttgaaattgt tatgggttcg atttccaaaa tatgtaactt atttttttaa	3066

ggaataaggt gtgctgtgta tttgttgatt aaaaatcatt tgtcttgag agtatccttt 3126
 tttgaaggaa atatacatcc ttataacaca tcaggtagtt ttcttttttc tgtattttaa 3186
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 atttgggaata attttagttt ctaaaaagta ctaatgtaag ttaagtttat atcaaagca 3366
 aattaccttg tataactaac aagcacagtt attgtttaac attatggatt ttaattgtgt 3426
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 gccgagggat ccctccgagg acaccccagc agtggacggc agcacagaca cggacagg 178
 atg ccc ttg aag ctc tac ttg cct ggt ggt aat tcc agg atg acc cag 226
 Met Pro Leu Lys Leu Tyr Leu Pro Gly Gly Asn Ser Arg Met Thr Gln
 1 5 10 15
 gag agg ctg gaa aga gcg ttc aaa cgg cag ggc agc cag ccc gca cct 274
 Glu Arg Leu Glu Arg Ala Phe Lys Arg Gln Gly Ser Gln Pro Ala Pro
 20 25 30
 gtc agg aaa aat cag ttg ctg ccg tct gac aag gtg gat ggt gag ctg 322
 Val Arg Lys Asn Gln Leu Leu Pro Ser Asp Lys Val Asp Gly Glu Leu
 35 40 45
 ggt gcc ctg cgg ctc gag gat gtg gag gat gag ttg ata agg gaa gag 370
 Gly Ala Leu Arg Leu Glu Asp Val Glu Asp Glu Leu Ile Arg Glu Glu
 50 55 60
 gtc atc ctg tcg cca gtc cca tca gtg ctc aag ttg cag aca gca tca 418
 Val Ile Leu Ser Pro Val Pro Ser Val Leu Lys Leu Gln Thr Ala Ser
 65 70 75 80
 aaa cca att gac ctc tca gta gca aag gaa ata aag acc ctt ctg ttt 466
 Lys Pro Ile Asp Leu Ser Val Ala Lys Glu Ile Lys Thr Leu Leu Phe
 85 90 95

ggt tcc agc ttt tgc tgt ttc aat gaa gaa tgg aaa ctt cag agt ttt Gly Ser Ser Phe Cys Cys Phe Asn Glu Glu Trp Lys Leu Gln Ser Phe 100 105 110	514
tcc ttt agt aac aca gcc tca tta aaa tac ggc ata gtg cag aac aag Ser Phe Ser Asn Thr Ala Ser Leu Lys Tyr Gly Ile Val Gln Asn Lys 115 120 125	562
ggt ggt cct tgc gga gtc ctg gca gct gtc caa ggc tgt gtc cta cag Gly Gly Pro Cys Gly Val Leu Ala Ala Val Gln Gly Cys Val Leu Gln 130 135 140	610
aaa ctc ctg ttt gaa gga gat agc aaa gcc gac tgt gct cag gga ctg Lys Leu Leu Phe Glu Gly Asp Ser Lys Ala Asp Cys Ala Gln Gly Leu 145 150 155 160	658
cag cct tca gat gcc cac cgg acc cgc tgc ctc gtc ctg gcc ctc gca Gln Pro Ser Asp Ala His Arg Thr Arg Cys Leu Val Leu Ala Leu Ala 165 170 175	706
gac att gtg tgg cgg gca ggg ggc cga gag aga gcc gtt gtt gca ctg Asp Ile Val Trp Arg Ala Gly Gly Arg Glu Arg Ala Val Val Ala Leu 180 185 190	754
gct tcg aga aca cag cag ttc agt cca aca ggg aaa tac aaa gca gat Ala Ser Arg Thr Gln Gln Phe Ser Pro Thr Gly Lys Tyr Lys Ala Asp 195 200 205	802
gga gtc tta gaa aca ctt acg ctt cac agt ttg acc tgc tat gag gac Gly Val Leu Glu Thr Leu Thr His Ser Leu Thr Cys Tyr Glu Asp 210 215 220	850
ctg gtg act ttt ctt caa caa agc att cat cag ttt gaa gtg ggc ccc Leu Val Thr Phe Leu Gln Gln Ser Ile His Gln Phe Glu Val Gly Pro 225 230 235 240	898
tat ggc tgc atc ctg ctc acc ctt tct gcc atc ctg tcc agg tct aca Tyr Gly Cys Ile Leu Leu Thr Leu Ser Ala Ile Leu Ser Arg Ser Thr 245 250 255	946
gag ctc atc cgc cag gac ttt gat gtc ccc acc agc cac ctg att gga Glu Leu Ile Arg Gln Asp Phe Asp Val Pro Thr Ser His Leu Ile Gly 260 265 270	994
gca cat ggc tac tgt aca cag gaa ctt gtc aat ctg ctc ctg act ggg Ala His Gly Tyr Cys Thr Gln Glu Leu Val Asn Leu Leu Leu Thr Gly 275 280 285	1042
aaa gct gtg tcc aac gtt ttc aac gat gtg gtt gag ctg gat tct ggg Lys Ala Val Ser Asn Val Phe Asn Asp Val Val Glu Leu Asp Ser Gly 290 295 300	1090
gat ggg aac atc aca ctt ctc aga ggc att gct gca cgc agt gat att Asp Gly Asn Ile Thr Leu Leu Arg Gly Ile Ala Ala Arg Ser Asp Ile 305 310 315 320	1138
ggc ttc tta tct ctc ttt gag cat tac aac atg tgc cag gtt ggc tgc	1186

Gly Phe Leu Ser Leu Phe Glu His Tyr Asn Met Cys Gln Val Gly Cys	
325 330 335	
ttc ctg aag acc ccg agg ttc ccc atc tgg gtg gtt tgc agt gag agc	1234
Phe Leu Lys Thr Pro Arg Phe Pro Ile Trp Val Val Cys Ser Glu Ser	
340 345 350	
cac ttc agc atc ctc ttt agc ctg cag ccg ggg ctc ctg cgt gac tgg	1282
His Phe Ser Ile Leu Phe Ser Leu Gln Pro Gly Leu Leu Arg Asp Trp	
355 360 365	
agg act gag agg ctc ttt gac ttg tac tac tac gat ggc ctg gcc aac	1330
Arg Thr Glu Arg Leu Phe Asp Leu Tyr Tyr Tyr Asp Gly Leu Ala Asn	
370 375 380	
cag cag gag cag atc cgg ctg acc att gac acc acc caa acc atc tct	1378
Gln Gln Glu Gln Ile Arg Leu Thr Ile Asp Thr Thr Gln Thr Ile Ser	
385 390 395 400	
gag gac aca gac aac gac ctt gtc cca ccc ctc gag ctc tgc atc aga	1426
Glu Asp Thr Asp Asn Asp Leu Val Pro Pro Leu Glu Leu Cys Ile Arg	
405 410 415	
acc aag tgg aag ggg gca tca gtg aac tgg aac ggc tca gac ccc atc	1474
Thr Lys Trp Lys Gly Ala Ser Val Asn Trp Asn Gly Ser Asp Pro Ile	
420 425 430	
ctg tga ccgttgatg tgggttaaacc ctgtggtcca ccactcatca cctcatcacc	1530
Leu *	
gaggatgaca gctgaacccc aagcctctgg ggcaggctctc atgtaccca acctgggtca	1590
gcatgactgc agaagcatcc agagcctccc tgccccttcc atgaagggcc caccgaagac	1650
tgtgctgggg acccagtgtg ttgctgggtc cctcccagc tgagctgtga ctgctgagta	1710
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<220>
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 agaacagcta cccatctcaa accccaggag tcaccagccc ttggggccctc acatccctgg 180
 agcctcagcc cctccacac acgtgctgtg aatcataggg ggatcaggat actcctgctc 240
 acagacaccc atctccccct accaaaaata acgtgtgggt cctccttcca cctgactct 300
 gcctctctgt ctgcaggagc ctggtcgggg tgctccacag aagctgtgcc tgggcttggg 360
 agccaaggcc atg tcc ctc tcc cgg cca ggg gag acg gag ccc atc cac 409
 Met Ser Leu Ser Arg Pro Gly Glu Thr Glu Pro Ile His
 1 5 10
 agt gtc agc tat ggc cat gtg gcc gcc tgc cag cta atg ggc ccc cac 457
 Ser Val Ser Tyr Gly His Val Ala Ala Cys Gln Leu Met Gly Pro His
 15 20 25
 acc ctg gcc ttg agg gtg gga gag agc cag ctc ctc ctg cag agc ccc 505
 Thr Leu Ala Leu Arg Val Gly Glu Ser Gln Leu Leu Leu Gln Ser Pro
 30 35 40 45
 cag gtg agt gag aag agg agt tgt ggg agg agg aga gaa ggg aag cga 553
 Gln Val Ser Glu Lys Arg Ser Cys Gly Arg Arg Arg Glu Gly Lys Arg
 50 55 60
 tgt cag gaa gca ttt aca gaa cac caa acc tgg gcc agg tag agctcta 602
 Cys Gln Glu Ala Phe Thr Glu His Gln Thr Trp Ala Arg *
 65 70 75
 agcactgggg atccagcagt gatcacagac aagctgaagg agcttacact agagtggagt 662
 cagacaataa acaaggaatc ccaggctatg aagacagtga gaaatgctac aaaggaaaga 722
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 gaaga 787

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 <212> DNA
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<220>
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 <222> (66)..(425)

<400> 222
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 aggag atg ccc agc ctg gag gtg atc acg ctc agg tac ctc gct cct 107
 Met Pro Ser Leu Glu Val Ile Thr Leu Arg Tyr Leu Ala Pro
 1 5 10

Country	Year	Age	Sex	Height (cm)	Weight (kg)	Body Mass Index (kg/m ²)	Waist Circumference (cm)	Waist-Hip Ratio	Trunk Fat (%)	Visceral Fat (cm ³)	Subcutaneous Fat (cm ³)	Visceral Fat Index (cm ³ /m ²)	Subcutaneous Fat Index (cm ³ /m ²)	Visceral Fat to Subcutaneous Fat Ratio
USA	1999	20-29	M	178.5	82.5	26.1	94.5	0.91	12.5	150	150	0.83	0.83	1.00
USA	1999	20-29	F	162.5	65.5	25.5	88.5	0.91	12.5	150	150	0.83	0.83	1.00
USA	1999	30-39	M	178.5	82.5	26.1	94.5	0.91	12.5	150	150	0.83	0.83	1.00
USA	1999	30-39	F	162.5	65.5	25.5	88.5	0.91	12.5	150	150	0.83	0.83	1.00
USA	1999	40-49	M	178.5	82.5	26.1	94.5	0.91	12.5	150	150	0.83	0.83	1.00
USA	1999	40-49	F	162.5	65.5	25.5	88.5	0.91	12.5	150	150	0.83	0.83	1.00
USA	1999	50-59	M	178.5	82.5	26.1	94.5	0.91	12.5	150	150	0.83	0.83	1.00
USA	1999	50-59	F	162.5	65.5	25.5	88.5	0.91	12.5	150	150	0.83	0.83	1.00
USA	1999	60-69	M	178.5	82.5	26.1	94.5	0.91	12.5	150	150	0.83	0.83	1.00
USA	1999	60-69	F	162.5	65.5	25.5	88.5	0.91	12.5	150	150	0.83	0.83	1.00
USA	1999	70-79	M	178.5	82.5	26.1	94.5	0.91	12.5	150	150	0.83	0.83	1.00
USA	1999	70-79	F	162.5	65.5	25.5	88.5	0.91	12.5	150	150	0.83	0.83	1.00
USA	1999	80-89	M	178.5	82.5	26.1	94.5	0.91	12.5	150	150	0.83	0.83	1.00
USA	1999	80-89	F	162.5	65.5	25.5	88.5	0.91	12.5	150	150	0.83	0.83	1.00
USA	1999	90-99	M	178.5	82.5	26.1	94.5	0.91	12.5	150	150	0.83	0.83	1.00
USA	1999	90-99	F	162.5	65.5	25.5	88.5	0.91	12.5	150	150	0.83	0.83	1.00
USA	1999	100-109	M	178.5	82.5	26.1	94.5	0.91	12.5	150	150	0.83	0.83	1.00
USA	1999	100-109	F	162.5	65.5	25.5	88.5	0.91	12.5	150	150	0.83	0.83	1.00
USA	1999	110-119	M	178.5	82.5	26.1	94.5	0.91	12.5	150	150	0.83	0.83	1.00
USA	1999	110-119	F	162.5	65.5	25.5	88.5	0.91	12.5	150	150	0.83	0.83	1.00
USA	1999	120-129	M	178.5	82.5	26.1	94.5	0.91	12.5	150	150	0.83	0.83	1.00
USA	1999	120-129	F	162.5	65.5	25.5	88.5	0.91	12.5	150	150	0.83	0.83	1.00
USA	1999	130-139	M	178.5	82.5	26.1	94.5	0.91	12.5	150	150	0.83	0.83	1.00
USA	1999	130-139	F	162.5	65.5	25.5	88.5	0.91	12.5	150	150	0.83	0.83	1.00
USA	1999	140-149	M	178.5	82.5	26.1	94.5	0.91	12.5	150	150	0.83	0.83	1.00
USA	1999	140-149	F	162.5	65.5	25.5	88.5	0.91	12.5					

[illegible][illegible]

caa cac ctt gct caa cat cac aga aca cat act gga gag aaa ctc ttt Gln His Leu Ala Gln His His Arg Thr His Thr Gly Glu Lys Leu Phe 175 180 185	637
gaa tgt aaa gaa tgt agg aaa gcc ttc aaa caa agt gaa cac ctt att Glu Cys Lys Glu Cys Arg Lys Ala Phe Lys Gln Ser Glu His Leu Ile 190 195 200	685
cag cat caa aga att cat act gga gaa aaa cca tat aaa tgt aag gaa Gln His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Lys Cys Lys Glu 205 210 215 220	733
tgc aga aaa gcc ttc aga cag cct gca cac ctt gct cag cat cag aga Cys Arg Lys Ala Phe Arg Gln Pro Ala His Leu Ala Gln His Gln Arg 225 230 235	781
att cat act gga gag aaa ccc tat gaa tgt aaa gaa tgt ggc aaa gcc Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Glu Cys Gly Lys Ala 240 245 250	829
ttc agt gat ggc tcg tct ttt gct cga cat cag aga tgt cac act ggc Phe Ser Asp Gly Ser Ser Phe Ala Arg His Gln Arg Cys His Thr Gly 255 260 265	877
aaa aga ccc tat gaa tgt att gag tgt ggg aag gct ttt agg tat aac Lys Arg Pro Tyr Glu Cys Ile Glu Cys Gly Lys Ala Phe Arg Tyr Asn 270 275 280	925
aca tct ttt att cgt cac tgg agg agt tat cat act gga gag aag cct Thr Ser Phe Ile Arg His Trp Arg Ser Tyr His Thr Gly Glu Lys Pro 285 290 295 300	973
ttt aat tgc att gat tgt ggg aaa gcc ttc agt gtt cac ata gga ctt Phe Asn Cys Ile Asp Cys Gly Lys Ala Phe Ser Val His Ile Gly Leu 305 310 315	1021
att ctg cat agg aga att cat aca gga gag aaa cct tac aaa tgt gat Ile Leu His Arg Arg Ile His Thr Gly Glu Lys Pro Tyr Lys Cys Asp 320 325 330	1069
gtg tgt gga aaa acc ttc agc tcg ggt tca tcc cgt act gta cat cag Val Cys Gly Lys Thr Phe Ser Ser Gly Ser Ser Arg Thr Val His Gln 335 340 345	1117
aga att cat aca gga gag aaa cct tat gaa tgt gat ata tgt ggg aaa Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Asp Ile Cys Gly Lys 350 355 360	1165
gat ttt agc cat cat gca tca ctc act cag cat caa aga gta cat tct Asp Phe Ser His His Ala Ser Leu Thr Gln His Gln Arg Val His Ser 365 370 375 380	1213
gga gag aaa ccg tat gaa tgc aag gaa tgt ggg aaa gcc ttt agg cag Gly Glu Lys Pro Tyr Glu Cys Lys Glu Cys Gly Lys Ala Phe Arg Gln 385 390 395	1261
aat gta cac ctt gtt agt cat ttg aga att cat act ggt gaa aaa ccc	1309

Asn Val His Leu Val Ser His Leu Arg Ile His Thr Gly Glu Lys Pro	
400 405 410	
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Tyr Glu Cys Lys Glu Cys Gly Lys Ala Phe Arg Ile Ser Ser Gln Leu	
415 420 425	
gct act cat cag aga att cat act gga gag aag cct tat gaa tgt att	1405
Ala Thr His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Ile	
430 435 440	
gaa tgt gga aat gct ttc aaa cag aga tca cac ctt gcc caa cat cag	1453
Glu Cys Gly Asn Ala Phe Lys Gln Arg Ser His Leu Ala Gln His Gln	
445 450 455 460	
aaa act cat aca gga gag aaa cct tat gag tgt aat gaa tgc ggg aaa	1501
Lys Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Asn Glu Cys Gly Lys	
465 470 475	
gcc ttc agc caa act tgc aat ctt act caa cat caa aga att cat act	1549
Ala Phe Ser Gln Thr Cys Asn Leu Thr Gln His Gln Arg Ile His Thr	
480 485 490	
gga gag aaa ccc tat aaa tgt act gaa tgt gga aag gct ttt agt gat	1597
Gly Glu Lys Pro Tyr Lys Cys Thr Glu Cys Gly Lys Ala Phe Ser Asp	
495 500 505	
agc tca tcc tgt gct cag cat caa aga ctc cac act ggc caa agg ccc	1645
Ser Ser Ser Cys Ala Gln His Gln Arg Leu His Thr Gly Gln Arg Pro	
510 515 520	
tat cag tgt ttt gaa tgt ggg aag gcg ttc aga aga aag tta tcc tta	1693
Tyr Gln Cys Phe Glu Cys Gly Lys Ala Phe Arg Arg Lys Leu Ser Leu	
525 530 535 540	
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Ile Cys His Gln Arg Ser His Thr Gly Glu Glu Pro *	
545 550	
catgtggcca agccttttagt tatcaccaat ccctactgt taatcagaga tgtcccactg	1802
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ccattcgggc agacaccgag ctagctgtag gagttttttt gatagcccag tggcacctgg	2282